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SICNA
Sorghum Improvement Conference of North America
(www.sorghumgrowers.com)

ICRISAT
International Crops Research Institute for the Semi-Arid Tropics
(www.icrisat.org)

About SICNA

In 1947, sorghum breeders formed an informal working group to meet and review items of interest in sorghum breeding and genetics. This organization was named 'Sorghum Research Committee'. In the 1960s, with the advent of a number of severe disease and insect problems, special half-day sessions, particularly on diseases, became a part of the Sorghum Research Committee. In 1973, a concept was put forward that all sorghum workers, irrespective of discipline and employer, should meet twice a year to discuss mutual concerns with sorghum research and development. The Sorghum Improvement Conference of North America (SICNA) was that new organization. It is composed of eight disciplinary committees, dealing with genetics and breeding, pathology, entomology, chemistry and nutrition, physiology and agronomy, biotechnology, utilization and marketing, and agribusiness and commerce. SICNA meets formally once a year in conjuction with the National Grain Sorghum Producers Board. A general program of research, education, and developmental activities is prepared by the disciplinary committees. Funding is through membership participation and contributions from commercial donors. Essentially. SICNA represents the United States sorghum activities but accepts reports and encourages memberships from sorghum and millet researchers worldwide.

About ICRISAT

The semi-arid tropics (SAT) encompasses parts of 48 developing countries including most of India, parts of southeast Asia, a swathe across sub-Saharan Africa, much of southern and eastern Africa, and parts of Latin America. Many of these countries are among the poorest in the world. Approximately one-sixth of the world's population lives in the SAT, which is typified by unpredictable weather, limited and erratic rainfall, and nutrient-poor soils.

ICRISAT*s mandate crops are sorghum, pearl millet, chickpea, pigeonpea, and groundnut-five crops vital to life for the ever-increasing populations of the SAT. ICRISAT's mission is to conduct research that can lead to enhanced sustainable production of these crops and to improved management of the limited natural resources of the SAT. ICRISAT communicates information on technologies as they are developed through workshops, networks, training, library services, and publishing.

ICRISAT was established in 1972. It is supported by the Consultative Group on International Agricultural Research (CGIAR). an informal association of approximately 50 public and private sector donors. It is co-sponsored by the Food and Agriculture Organization of the United Nations (FAO), the United Nations Development Programme (UNDP), the United Nations Environment Programme (UNEP) and the World Bank. ICRISAT is one of 16 nonprofit CGIAR-supported Future Harvest Centers.

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ISMN Scientific Editors 2003

JA Dahlberg **RP Thakur**

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Editorial

The International Sorghum and Millets Newsletter continues to be an important avenue through which research and news about these two important crops is disseminated to scientific and non-scientific communities around the world. Because sorghum and millets are primarily viewed as crops of poor, marginal agricultural lands, justifying research on these crops can be difficult and we have seen an erosion of support for research in these crops over the years. The publication of this newsletter and the fact that it is distributed to over 1500 people throughout the world indicates the importance of these cereal grains. As water shortage becomes a bigger issue world-wide, these two drought-tolerant crops will play a greater role in agricultural systems, which provide food and sustenance for over 1 billion people.

Volume 44 contains valuable information from preliminary findings of long-term research programs and news from various conferences and meetings that have taken place over the past year.

This issue contains research articles on Genetic Enhancement and Breeding (19 on sorghum, 5 on pearl millet); Biotechnology (2 on sorghum, 2 on pearl millet); Agronomy (7 on sorghum, 3 on pearl millet); Pathology (16 on sorghum, 2 on pearl millet); Entomology (2 on sorghum) and 1 article on workshop highlights and news items and current literature.

We would like to thank the reviewers of these articles for their time and effort in getting back reviews in a timely manner to support publication of this volume. They include: AG Bhasker Raj, FR Bidinger, CT Hash, S Pande, V Panduranga Rao, KN Rai, A Ramakrishna, BVS Reddy, OP Rupela, KL Sahrawat, HC Sharma and HD Upadhyaya (all ICRISAT, Patancheru, India); N Kameswara Rao (IPGRI-SSA, Nairobi); RDVJ Prasada Rao [National Bureau of Plant Genetic Resources (NBPGR), Hyderabad, India]; S Indira, TG Nageshwara Rao, and S Ravi Kumar [National Research Centre for Sorghum (NRCS), Hyderabad, India] and B Bean, S Goldman, S Bean, T Isakict, B Rooney, J Burd and R Kochenower [Sorghum Improvement Conference of North America (SICNA), Texas, USA].

We would also like to thank Sheila Vijayakumar, Technical Editor, for her interest and commitment to high quality and accurate publication and to VS Reddy, Senior Newsletter Officer of Communication Office, ICRISAT for efficiently coordinating the manuscript processing and typesetting for printing. We wish to acknowledge the ICRISAT Library for compiling SATCRIS listing.

We have made some changes in deadlines and have tried to streamline the review process to publish the newsletter so that it gets to you sometime within the first quarter of the New Year. We encourage all authors to please follow ICRISAT guidelines for publication, as this helps our editorial staff publish the newsletter in a more efficient manner.

We have also initiated a new service to all our readers and ISMN 43 has been placed on the World Wide Web at www.icrisat.org under Research Themes "Crop Improvement" under "What's New" as a pdf file. We believe that this will allow the newsletter to reach more people globally and look forward to your comments and suggestions for its improvement.

We encourage our readers to provide us with **feedback** on the articles and news items that appear in this Volume to: **newsletter@cgiar.org** and also to provide us with news, additional research notes, articles, and reviews for publication in the next issue (Vol. 45, 2004) of the ISMN. We look forward to your suggestions and comments so that we can make this newsletter the best that it can be.

JA Dahlberg
SICNA, USA

RP Thakur
ICRISAT, India

News

Enhancing Opportunities for ICRISAT-Private Sector Partnership

ICRISAT's Director General William D Dar was the Chief Guest at the 8th Annual General Meeting of the Seedsmen Association, Hyderabad held on 27 September 2003 at the Bhaskara Auditorium, BM Birla Science Center, Hyderabad, Andhra Pradesh, India.

He was invited to give a keynote address to around 200 members on "Genetically modified crops for rainfed agriculture". The meeting was presided by Sri V Shobhanadreeswar Rao, the Honorable Minister for Agriculture, Government of Andhra Pradesh.

In his 40-minute address, William Dar outlined the role of genetic transformation as a tool in crop improvement, for traits which cannot otherwise be tackled by conventional breeding. He briefly mentioned the progress of work at ICRISAT in developing transformation protocols for ICRISAT mandate crops including the world's first transgenics in groundnut for resistance to peanut clump virus and in pigeonpea and chickpea for pod borer resistance. He outlined the steps taken in maintaining bio-safety measures and asked the private sector seed companies to join hands with ICRISAT to serve the poor farmers in dryland areas. Further, attention was drawn to the existing arrangements and the guidelines developed for further enhancing the ICRISAT-private sector partnership on hybrid parents research in sorghum and pearl millet. Sri V Shobhanadreeswar Rao and respected farmer/seed producer Sri Murahari repeatedly referred to Dar's lecture on the need for private sector partnership with ICRISAT not only on hybrid parents' research but also on genetically modified crops.

The Seedsmen Association also felicitated five agricultural scientists for their outstanding service to dryland farmers. Of the five, three scientists represented ICRISAT: N Seetharama, who is on secondment to the Indian Council of Agricultural Research (ICAR), KN Rai and BVS Reddy. They were presented with a citation of their achievements and a plaque.

William Dar and CLL Gowda were also felicitated for their vision and support to the cause of ICRISAT-private sector partnership in hybrid parents research, which has evolved as a model for private sector partnership in the CGIAR system.

ICRISAT Scientists Honored

Acharya NG Ranga Agricultural University (ANGRAU) awarded the Jannareddy Venkat Reddy Prize to **KN Rai** for his outstanding contributions towards the development of pearl millet varieties. He received the award on 11 March 2003 from His Excellency SS Barnala, Governor of Andhra Pradesh.

HC Sharma, Principal Scientist - Entomology, was honored with the Prof T N Ananthakrishanan Trust Award for 2003. The award carries a cash prize of Rs 5000. a silver plaque and a citation.

The Seed Association of India (SAI), at its Annual General Meeting held on 29 November in Hyderabad, India honored **KN Rai,** Principal Scientist, ICRISAT, Patancheru, for his outstanding achievements in pearl millet hybrid parents' research, which has made significant contributions to the growth of pearl millet hybrid seed industry in India. On this occasion, Rai presented an invited paper on "Partnership-based pearl millet improvement research with a human face". He emphasized the significance of synergy generated from research partnership in addressing the impact-oriented research and development issues. He spoke about ICRISAT's productive partnerships with NARS and the private sector that have led to a diversified hybrid cultivar base and commendable on-farm impact in India.

Vibha Agrotech, a member of ICRISAT's private sector seed consortium for pearl millet and sorghum, honored **KN Rai, BVS Reddy and HC Sharma** for their excellent contribution to the research on these crops. ICRISAT scientists were honored at the inaugural function for the company's modern seed processing facility. The company also recognized and commended RP **Thakur's** contribution towards pearl millet downy mildew research. **CLL Gowda** inaugurated the Office Complex of the seed processing facility on behalf of **William Dar,** Director General, ICRISAT.

Obituary

Dr Hugh Doggett, who worked with ICRISAT as Plant Breeder between August 1973 and December 1976, expired on 20 July 2003, following a stroke. The Doggett family had recently communicated the news to Deepak Pawar, ex-staff member.

Dr Doggett, a British national, was an international authority on sorghum breeding. Many remember him as a dedicated and extremely enthusiastic and energetic scientist. We are saddened by this loss.

His widow, Jane Doggett, can be contacted at: 38 A Cottenham Road, Histon, Cambridge CB4 9ES, UK.

Genetic Enhancement and Breeding

Genetic Diversity Studies in Forage Sorghum

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Introduction

In any crop improvement program, assessment of genetic-diversity is an essential prerequisite for identifying potential parents for hybridization. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. The D^2 statistic is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam 1966). An attempt has been made in this study to assess the nature and magnitude of genetic divergence for green fodder yield and its component traits and brix in available sorghum *(Sorghum bicolor)* germplasm. In India, sorghum is considered for forage based on the tillering ability, leaf-stem ratio, green fodder yield and dry matter yield. Also, palatability, digestibility and crude protein content of fodder are considered important for evaluation of sorghum.

Materials and Methods

Eighty-eight germplasm lines of sorghum were grown at the Indian Grassland and Fodder Research Institute, Dharwad, Karnataka, India during the rainy season in 1999 in a randomized block design with two replications. Each entry was grown in a 4-m row with a spacing of 30 cm between the rows and 15 cm within a row. Five randomly selected plants from each genotype were used to record observations on days to first flowering, plant height, number of tillers, number of leaves, leaf length, leaf width, left-stem ratio, biomass and brix values. The mean of the five plants was subjected to statistical analysis. Wilk's criterion was used to test the significance of pooled differences in mean values of 88 genotypes for all the nine characters. Genetic diversity was estimated as Mahalanobis D^2 statistic and clustering of genotypes was done according to Tocher's method (Rao 1952).

Results and Discussion

The analysis of variance showed highly significant differences among genotypes for all the characters

Table 1. Grouping of 88 forage sorghum genotypes into different clusters.

Cluster	Number	Genotypes
I	15	FM-344, FM-418. FM-443, FM-479, FM-1059, FM-1067, FM-1302, FM-1356, FM-1371. FM-1373, FM-1381, FM-1420, FM-1445, FM-1678, FM-1748
II	19	FM-1, FM-157, FM-162, FM-179, FM-237, FM-238, FM-260, FM-299, FM-561, FM-593, FM-665, FM-863, FM-891, FM-894, FM-897, FM-1041, FM-1051, FM-I616, ICSR-93012
III	11	FM-50, FM-148, FM-154, FM-165, FM-190, FM-194, FM-198, FM-303, FM-339, FM-340, FM-840
IV	7	FM-161, FM-581, FM-629, FM-1223, FM-1350, FM-1351, ICSR-93014
V	4	FM-34, FM-163, FM-427, FM-1533
VI	5	FM-595, FM-685, FM-841, FM-859, FM-893
VII	6	FM-419, FM-439, FM-1183, FM-1279, FM-1280, FM-1407
VIII	1	FM-1310
IX	6	FM-49, FM-234. FM-353, FM-1073, FM-1139, FM-1447
X	1	FM-1028
XI	1	FM-477
XII	1	FM-475
XIII	1	FM-48
XIV	1	FM-1485
XV	1	FM-886
XVI	1	FM-1343
XVII	1	FM-44
XVIII	1	FM-15
XIX	1	FM-580
XX	1	ICSR-93016
XXI	1	FM-45
XXII	1	FM-671
XXIII	1	FM-5

Table 2. Average intra- (along diagonal) and inter-cluster D^2 estimates in forage sorghum.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XXII	XXIII
I	12.10	62.67	95.85	46.95	79.43	25.24	22.78	34.79	31.55	48.33	38.79	45.02	18.28	46.90	54.46	22.57	110.93	110.68	44.08	60.59	89.95	17.68	67.75
II		14.00	36.30	23.96	20.98	47.87	82.02	95.58	33.64	18.07	99.66	106.00	55.76	22.03	19.23	47.22	50.67	50.87	23.93	20.11	31.39	61.44	28.95
III			13.91	52.86	19.57	80.36	115.39	129.00	66.13	49.37	133.13	139.54	87.88	52.72	47.02	79.67	20.83	20.96	54.87	42.97	17.41	94.28	42.56
IV				11.32	36.37	38.19	66.06	78.87	19.59	18.12	83.13	89.71	37.09	21.42	26.84	33.37	68.22	66.59	17.06	27.86	49.39	47.35	26.41
V					8.34	64.79	99.01	112.55	49.58	33.30	116.73	123.17	71.23	37.17	32.76	63.35	34.00	33.29	38.98	29.53	17.86	78.31	29.21
VI						11.95	40.58	53.88	23.01	32.99	57.31	63.07	30.60	30.32	35.65	22.00	94.10	95.44	29.38	43.33	73.76	21.29	60.73
VII							11.94	16.46	50.59	67.58	20.07	25.81	33.15	65.68	73.08	39.48	130.42	130.27	62.97	79.19	109.32	27.75	86.57
VIII								0.00	63.78	81.35	6.79	11.63	43.96	79.61	87.05	51.89	144.27	143.90	76.47	93.00	122.98	39.89	98.59
IX									8.87	19.94	67.97	74.35	25.06	20.93	28.19	18.29	81.43	81.04	18.06	34.32	60.46	32.72	40.55
X										0.00	85.19	91.49	43.20	8.22	11.43	33.97	63.71	64.19	12.55	18 87	43.51	46.67	34.67
XI											0.00	7.10	48.60	83.15	90.66	56.84	148.12	147.79	80.12	96.36	127.38	42.33	103.35
XII												0.00	55.08	89.50	96.79	62.59	154.58	154.39	86.65	102.83	133.48	48.68	109.76
XIII													0.00	43.62	51.79	18.61	103.88	102.39	39.28	56.77	82.82	26.96	54.91
XIV														0.00	10.55	35.00	65.80	66.71	10.66	15.92	47.64	43.40	40.84
XV															0.00	40.94	59.53	61.69	16.92	14.28	40.71	50.95	42.03
XVI																0.00	95.80	95.80	33.49	49.68	72.04	30.49	51.36
XVII																	0.00	10.54	68.26	53.39	29.55	107.76	59.19
XVIII																		0.00	68.44	54.70	32.22	108.01	55.19
XIX																			0.00	18.09	51.28	39.99	38.56
XX																				0.00	41.03	55.11	41.91
XXI																					0.00	89.62	40.25
XXII																						0.00	70.78
XXIII																							0.00

Table 3. Cluster mean values for different characters in forage sorghum.

Cluster	Days to first flowering	Plant height (m)	Number of leaves	Number of tillers	Leaf length (cm)	Leaf width (cm)	Leaf-stem ratio	Brix (%)	Green fodder yield (g plant^{-1})
I	64	1.2	9.8	1.4	78.1	7.9	0.95	6.4	233
II	62	1.9	96	2.1	78.6	6.2	0.67	6.1	246
III	61	2.2	9.7	2.7	81.5	5.2	0.50	6.1	291
IV	69	1.7	9.5	1.6	87.2	6.8	0.85	7.6	205
V	63	2.0	9.5	2.3	82.7	6.9	0.68	6.8	376
VI	61	1.4	7.7	3.9	65.4	3.8	0.75	5.9	114
VII	63	1.1	9.4	1.3	76.1	7.9	1.12	7.3	142
VIII	65	0.9	8.2	1.2	79.4	6.9	1.91	7.3	145
IX	62	1.5	9.8	1.5	80.9	7.3	0.70	5.8	213
X	61	1.7	10.3	1.2	74.2	8.9	0.39	3.4	180
XI	68	0.9	10.9	1.4	75.9	7.5	1.20	5.3	215
XII	65	0.8	9.7	1.5	75.2	7.4	1.21	4.9	275
XIII	68	2.1	10.8	2.0	91.4	9.1	1.51	6.5	245
XIV	68	1.7	11.2	1.0	68.2	9.2	0.65	7.4	610
XV	58	1.8	10.2	2.2	65.4	4.7	1.04	5.6	170
XVI	53	1.4	9.2	1.3	84.7	6.8	0.82	8.2	165
XVII	66	2.4	8.7	3.9	72.5	4.8	0.56	6.8	230
XVIII	72	2.4	10.0	1.5	80.2	7.5	0.51	5.7	345
XIX	70	1.7	8.5	3.7	72.7	3.4	0.52	6.4	310
XX	71	1.8	9.0	2.2	64.2	5.2	0.50	8.5	150
XXI	49	2.1	8.0	2.4	80.9	6.1	0.64	7.0	170
XXII	61	1.3	7.0	3.0	66.0	5.8	0.41	4.3	200
XXIII	66	1.9	8.7	2.0	70.3	8.9	0.81	5.0	515

indicating considerable variability in the experimental material. The contribution of plant height was highest (87.04%) to the total variation followed by leaf length (9.38%) and days to first flowering (3.34%). The clustering based on D^2 statistic grouped the genotypes into 23 clusters (Table 1). Cluster II was the largest and consisted of 19 genotypes followed by clusters I (15 genotypes), III (11 genotypes), IV (7 genotypes), VII and IX (6 genotypes each), VI (5 genotypes), V (4 genotypes) and remaining clusters were solitary.

The intra- and inter-cluster D^2 values among 88 genotypes (Table 2) revealed that cluster V recorded lowest intra-cluster value (8.34) indicating that the genotypes within this cluster were less divergent compared to cluster II which showed highest intra-cluster value (14.00) followed by cluster III (13.91).

Inter-cluster distance of the clusters XII, XI, VIII and VII with cluster XVII was highest followed by cluster XVIII indicating that the genotypes from these clusters can be considered for selection of parents in hybridization program in sorghum improvement. Similar results were reported by Narkhede et al. (2000), Kadam et al. (2001) and Umakanth et al. (2002). In addition, clusters XI and XII have shown higher inter-cluster differences with clusters III, V, XXI and XXIII indicating that the genotypes from these clusters can be selected for hybridization to produce heterotic hybrids from which wide spectrum of variability is expected in segregating generations.

The cluster means estimated over the genotypes for the nine characters (Table 3) reveal considerable inter-cluster variation. The cluster means for days to first flowering ranged between 49 in cluster XXI and 72 days in cluster XVIII. The cluster means for plant height was highest (2.4 m) in clusters XVII and XVIII and lowest in cluster XII (0.8 m). The cluster means for green fodder yield plant^{-1} ranged from 114 g (cluster VI) to 610 g (cluster XIV). The cluster means for number of leaves, leaf length, and leaf width ranged from 7 (cluster XXII) to 11.2 (cluster XIV), 64.2 (cluster XX) to 91.4 cm (cluster XIII) and 3.4 (cluster XIX) to 9.2 cm (cluster XIV) respectively. The cluster mean for leaf-stem ratio ranged from 0.39 (cluster X) to 1.91 (cluster VIII) whereas for brix, it ranged from 3.4 (cluster X) to 8.5 (cluster XX).

The study showed that genetic divergence of cluster XVIII with clusters VII, VIII, XI and XIII and of clusters XI and XII with clusters III, V, XXI and XXIII is comparatively intermediate. Hence, the genotypes from these clusters are expected to produce high frequency of

heterotic hybrids from which substantial variability can be uncovered in segregating generations.

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Genetic Studies for Improvement of Quality Characters in *Rabi* Sorghum Using Landraces

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Introduction

Sorghum *(Sorghum bicolor)* is one of the important cereal crops cultivated in India during *kharif* (rainy) and *rabi* (postrainy) seasons. *Rabi* sorghum is highly valued for its excellent grain quality and also for its food use. The better grain quality fetches high market price often at par or higher than wheat *{Triticum aestivum)* (Nerkar 1998). However, there are certain major constraints in *rabi* sorghum improvement such as narrow genetic base, low variability for yield and grain quality parameters with *rabi* season adaptation. Indian *rabi* sorghum landraces are rich repository of genetic variability and are preserved by the farmers due to local adaptability, good grain quality and for specific food products. Thus, it becomes more relevant to utilize such typical landraces in breeding programs.

Materials and Methods

Five promising *rabi* sorghum varieties (lines), SPV 1155, SPV 1380, SPV 1411, SPV 1413 and SPV 1457 (Table 1), were selected from the All India Coordinated Trial conducted at the Sorghum Research Station, Parbhani, Maharashtra, India. Six landraces (testers), *Giddi Maldandi, Dagdi Solapur, Barshi Joot, Yennigar Jola, Dood Mogara* and *Ramkhe* (Table 1) were selected from breeding material available at the Sorghum Research Station, Parbhani. Thirty hybrids with line x tester mating design were developed during 1999/2000. Hybrids were developed by following manual method of hand emasculation and pollination. The landraces were selected on the basis of their diverse ecogeographic distribution and differences in plant height, flowering and maturity duration, seed color and grain yield.

The material was evaluated in *rabi* 2000/01 in a randomized block design with three replications. Each replication consisting of 44 entries (30 hybrids and 11 parents along with 3 checks) was divided in two tires and randomized within replication. Each genotype was sown in a single row of 5 m length with 45 cm and 15 cm inter- and intra-row spacing, respectively. Recommended dose of fertilizers and carbofuran granules at 4 kg ha^{-1} was applied to the plots.

Table 1. Description of sorghum breeding material used for genetic studies.

Parents	Pedigree/source
Lines	
SPV 1155	(SPV 86 x E 36-1) x Local selection
SPV 1380	SPV 86 x E 36-1
SPV 1411	Selection from GD 31-4-2-3, a restorer from ICRISAT
SPV 1413	RSLG 112-1-54
SPV 1457	RSLG 1613
Testers	
Giddi Maldandi	Dharwad, Karnataka
Dagdi Solapur	Dharwad, Karnataka
Barshi Joot	Barshi local, Maharashtra
Yennigar Jola	Dharwad, Karnataka
Dood Mogara	Dhule, Maharashtra
Ramkhe	Dhule, Maharashtra
Checks	
M 35-1	Selection from Maldandi Bulk
CSH 15R	MS 104A x RS 585
Phule Yashoda	RSLG 112-1-8

Table 2. Sorghum parents with significant general combining ability (GCA) effect for protein content and other important chemical constituents and grain yield.

Parents	Protein (%)	Starch (%)	Soluble/free sugars (%)	Grain yield (%)
Barshi Joot	1.166**[1]	-0.099**	0.045	2.090**
Dagdi Solapur	1.132**	-1.591**	0.095**	-6.870**
Yennigar Jala	0.482**	-0.493**	-0.079**	5.810**
Ramkhe	0.446**	-0.059	0.278**	3.753**
SPV 1457	0.279**	0.377**	0.113**	-0.880**

1. ** = Significant at 1% level.

The quality characters including physical and chemical parameters were evaluated using bulked grain of five selected plants. The proximate composition analysis was carried out as per AOAC (1990) using whole meal flour samples. The genetic analysis was done by adopting line x tester method as suggested by Kempthorne(1957).

Results and Discussion

Grain quality studies in *rabi* sorghum are limited. The results revealed that the majority of the landraces used in this study exhibited higher protein content than improved and popular varieties under cultivation. Protein content was highest (12.42%) in *Dood Mogara* followed by *Yennigar Jola* (11.55%) and SPV 1155 (11.37%). ICRISAT (1980) also reported higher protein range in landraces. The starch in parents ranged from 74.41% *{Barshi Joot)* to 75.95% (SPV 1457) and soluble/free sugars, which impart sweetness to sorghum, ranged from 1% *{Barshi Joot)* to 2.5% *{Giddi Maldandi).* These results were comparable with Ismail (1998).

Genetic studies revealed that the landraces were good general combiners for higher protein content, low starch and high soluble/free sugars content (Table 2). Rao et al. (1982) also observed that positive general combining ability (GCA) effect for protein content was accompanied by negative GCA effect for starch content. The main features of crosses with standard heterosis (%) over M 35-1 for protein content and grain yield are presented in Table 3.

The hybrids had acceptable grain quality as well as grain yield compared to the check M 35-1. The majority of the crosses had semi-compact elliptical panicles with medium to bold and yellow to chalky white grains. The highest heterosis for grain yield was observed for SPV 1155 x *Barshi Joot* while highest heterosis for protein content was observed for SPV 1413 x *Barshi Joot.* Nayeem and Bapat (1984) reported that when wide genetic diversity is present in the parental material

Table 3. Main features of sorghum hybrids with higher standard heterosis for grain/fodder yield and protein.

Cross	Grain yield (g plant^{-1})	Standard heterosis (%) Grain yield (g plant^{-1})	Protein (%)	Fodder yield (g plant^{-1})	Panicle shape[1]	Glume coverage (% grain covered)	Grain size	Grain shape	Grain color (visual score)
SPV 1155 × *Barshi Joot*	80.0	98.8	23.5	56.6	Sce	50	Bold	Sublenticular	Creamy
SPV 1155 × *Yennigar Jola*	79.6	82.1	28.1	75.0	Sce	25	Medium	Oval	Creamy
SPV 1380 × *Ramkhe*	73.2	67.3	14.6	34.1	Sce	25	Medium	Round	Yellow
SPV 1413 × *Ramkhe*	63.8	45.8	23.3	14.9	Ce	50	Medium	Flat	Creamy
SPV 1413 × *Dood Mogara*	62.5	42.8	15.0	23.3	Sce	25	Medium	Sublenticular	Chalky white
SPV 1413 × *Barshi Joot*	57.8	32.1	31.1	13.3	Co	25	Medium	Sublenticular	Creamy
SPV 1411 × *Barshi Joot*	57.3	31.0	21.6	16.6	Sce	25	Bold	Spherical	Yellow
SPV 1411 × *Ramkhe*	55.6	26.0	16.0	27.0	Sce	50	Medium	Globular	Creamy
SPV 1457 × *Giddi Maldandi*	53.2	21.7	7.7	1.1	Sce	50	Small	Sublenticular	Yellow
M 35-1 (check) (Mean values)	43.7		11.3	42.7	Sce	50	Medium	Globular	Creamy

1. Ce = compact elliptical; Co = compact; Sce = semi-compact elliptical.

(improved lines and landraces), it is possible to evolve hybrids/varieties with high grain yield along with acceptable agronomic and grain parameters.

Correlation studies indicated that for protein content improvement in terms of quantity, the starch content must decrease or compensate at biochemical level in the grain, during grain development stage. Shinde et al. (1986) reported superiority of improved line x landrace crosses for heterosis over improved line x improved line crosses due to genetic diversity in the parents. Considering the narrow genetic base and other adaptability features of *rabi* sorghum, such improved line x landrace cresses that are involved in this study are useful for *rabi* sorghum improvement.

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Importance of Economically Significant Constraints for *Kharif* Sorghum in Different Regions of India

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The All India Coordinated Sorghum Improvement Project centers and randomly selected private sector seed companies were asked to score for economic importance of constraints on quality/marketability for *kharif*(rainy) season sorghum *(Sorghum hicolor)* (grain and dual purpose) production in different regions of India on a 1 to 9 scale (1 = most important; 9 = least important). The objective of this study was to identify constraints within each zone, I, II and III, which were classified on the basis of end user needs. Responses obtained are summarized in Tables 1-3. Table 1 summarizes the importance given by 18 public sector sorghum groups while Table 2 summarizes views of 3 private companies. Finally, Table 3 summarizes the relative importance of different traits based on scoring by both sectors.

Scoring for Importance of Stress Factors in Sorghum Production

Insect pests. In almost all the states (Table 1), shoot fly was identified by the public sector as the most important constraint (score 1.0 to 3.0). The other important pest was stem borer (average score 2.9; range 1.0 to 5.0). Stem borer is an important constraint in the states of Uttaranchal, Uttar Pradesh, Rajasthan and Haryana. Head bug is a major constraint of Kovilpatti (Tamil Nadu), followed by Palem (Andhra Pradesh) and Parbhani (Maharashtra). Private companies also identified shoot fly (score = 2) and stem borer (score = 4.1) to be major pests in their areas of operation (Table 2).

Diseases. Grain mold was rated by the public sector as a top priority disease in the states of Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra and Gujarat. It was least important in Rajasthan, Haryana and Gujarat. Ergot was identified as a problem in Dhule and Jalgaon in Maharashtra, Palem in Andhra Pradesh and Surat in Gujarat. Private companies also identified the above two diseases as the most important constraints (score 2 for grain mold and score 3.6 for ergot). All other diseases were given lesser importance both by the public sector

Table 1. Scoring by the public sector for economic importance of constraints for *kharif* sorghum production in different regions of India for grain and dual purpose[1].

Trait	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	Mean
Insect pests																			
Shoot fly	1	3	1	1	1	1	1	1	3	1	1	2	1	1	1	1	1	2	1.4
Stem borer	1	5	5	5	1	3	2	5	3	3	3	3	3	2	2	2	1	1	2.9
Midge	–	5	9	5	–	5	4	1	9	4	5	–	–	5	7	9	2	3	5.1
Head bug	1	5	9	3	2	2	9	5	9	7	9	–	4	7	–	–	3	4	5.1
Diseases																			
Grain mold	1	3	1	1	1	1	1	1	5	1	8	–	5	6	5		9	8	3.5
Ergot	–	6	9	3	2	9	5	1	9	2	9	–	–	5	9	9	4	9	5.9
Rust	–	6	9	1	6	9	2	5	9	9	8	–	–	9	–	–	5	8	6.4
Blight	–	5	9	3	7	2	9	9	9	9	8	–	–	2	–	–	2	3	5.7
Anthracnose	–	8	9	1	7	9	9	9	9	6	–	–	8	1	4	4	1	7	5.9
Abiotic factors																			
Nutrient use	–	6	1	3	–	2	1	5	3	1	1	1	3	8	–	3	3	1	2.7
Drought	1	1	1	1	1	1	1	1	1	7	7	5	7	9	1	1	1	1	2.7
Grain traits																			
Plumpness	–	2	3	1	1	1	5	1	–	1	1	–	3	1	–	–	1	7	2.2
Round grain	–	3	1	1	1	3	2	–	–	1	1	–	3	1	1	1	3	5	2.0
Pearly white grain	1	6	5	1	1	2	1	1	–	1	2	–	–	1	2	2	2	1	1.9
Nutrition	1	–	1	1	1	5	1	–	–	2	3	–	7	5	3	3	1	1	2.5
Protein, starch	1	3	5	1	1	6	2	–	–	3	2	–	–	5	4	4	1	5	3.1
Grain hardness	–	3	9	1	1	4	4	5	–	3	3	–	3	1	–	–	1	4	3.5
Food/Feed/Fodder																			
Hydrocyanic acid	1	5	9	1	1	3	1	1	–	1	1	–	2	2	–	–	1	1	2.2
Protein	1	6	5	1	1	2	1	5	–	1	1	–	7	1	–	–	1	2	2.5
Digestibility/NDF[2]	1	7	1	1	1	1	1	5	–	2	2	–	7	1	1	1	1	2	2.2
Other																			
Market price	1	5	1	1	1	1	1	1	–	2	3	–	1	1	1	3	1	1	1.9

1. A = Kovilpatti, B = Coimbatore in Tamil Nadu; C = Bailhongal, D = Dharwad in Karnataka; E = Palem in Andhra Pradesh; F = Parbhani, G = Akola, H = Dhule in Maharashtra; I = Tancha, J = Surat, K = Deesa in Gujarat; L = Gwalior, M = Indore in Madhya Pradesh; N = Pantnagar in Uttaranchal; O = Kanpur, P = Mauranipur in Uttar Pradesh; Q = Udaipur in Rajasthan; R = Hisar in Haryana. Scoring on 1 to 9 scale where 1 = most important; and 9 = least important.
2. Neutral detergent fiber.

Table 2. Scoring by private sector for economic importance of constraints for *kharif* sorghum production in India for grain and dual purpose[1].

Trait	R&D areas				Seed production area				Marketing areas				Average
	A	B	C	Mean	A	B	C	Mean	A	B	C	Mean	
Insect pests													
Shoot fly	1	3	2	2.0	1	2	2	1.7	1	2	4	2.3	2.0
Stem borer	3	5	5	4.3	3	5	3	3.7	3	6	4	4.3	4.1
Midge	5	4	7	5.3	8	5	8	7.0	7	6	8	7.0	6.4
Head bug	5	5	5	5.0	7	6	9	7.3	6	6	8	6.7	6.3
Diseases													
Grain mold	1	2	1	1.3	5	3	2	3.3	1	2	1	1.3	2.0
Ergot	8	3	6	5.7	1	2	1	1.3	5	5	1	3.7	3.6
Rust	6	6	5	5.7	8	5	5	6.0	6	6	8	6.7	6.1
Blight	7	4	3	4.7	8	3	8	6.3	6	6	7	6.3	5.8
Anthracnose	5	4	5	4.7	6	3	9	6.0	5	5	5	5.0	5.2
Abiotic factors													
Nutrient use	5	3	3	3.7	6	2	3	3.7	6	2	4	4.0	3.8
Drought	4	2	1	2.3	7	2	1	3.3	5	2	1	2.7	2.8
Grain traits													
Plumpness	2	7	3	4.0	3	8	1	4.0	1	7	2	3.3	3.8
Round grain	2	6	1	3.0	3	6	2	3.7	1	6	2	3.0	3.2
Pearly while grain	2	6	1	3.0	3	5	6	4.7	1	6	1	2.7	3.4
Nutrition	5	4	1	3.3	5	3	7	5.0	6	3	4	4.3	4.2
Protein, starch	5	4	1	3.3	5	3	8	5.3	6	3	6	5.0	4.6
Grain hardness	4	5	4	4.3	4	5	3	4.0	5	6	3	4.7	4.3
Food/Feed/Fodder													
Hydrocyanic acid	8	3	1	4.0	8	6	-	7.0	7	4	-	5.5	5.5
Protein	7	3	2	4.0	7	6	-	6.5	8	3	-	5.5	5.3
Digestibility/NDF[2]	8	4	1	4.3	8	6	-	7.0	8	3	1	4.0	5.1
Other													
Market price	2	5	1	2.7	2	3	-	2.5	1	4	1	2.0	2.4

1. A, B and C are the code names for the three private companies that responded to a specific form. Scoring on 1 to 9 scale where 1 = most important; and 9 = least important.
2. Neutral detergent fiber.

and private companies. Across the states, downy mildew and rust were of little importance, except at Dharwad, Karnataka where it was identified as a major constraint. Anthracnose was of particular importance in Uttaranchal, Rajasthan and Karnataka (Dharwad). where fodder sorghum is grown.

Abiotic factors. Drought and nutrient use were identified as major constraints (score 2.7 each) across the states. During the *kharif* season, drought was common in Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Uttar Pradesh and Rajasthan. Hence, breeding efforts should be focused on drought tolerant material for these states. Drought was of lesser significance in Uttaranchal followed by Gujarat and Madhya Pradesh. Nutrient use and cold tolerance scored an average rating of 3.8 and 3.7, respectively.

Grain traits. Pearly white grain received top priority from public sector (1.9), while pearly white coupled with round grain received top priority from private companies. Round shape and plumpness were the next important characters considered by the public sector. Grain hardness scored an average rating of 3.5, and chemical composition of the grain scored 3.1.

Low hydrocyanic acid and high digestibility were important constraints in the fodder belt of Gujarat, Rajasthan, Haryana, Uttaranchal and Madhya Pradesh. These traits were less important to respondents from the private companies.

Market price. All the centers from public sector and private companies identified market price as an important factor which influences *kharif* sorghum production in the country.

Table 3. Analysis of rating of economically important constraints for *kharif* sorghum production in India by the public and private sectors'.

Trait	Mean	Range		SD	CV(%)	Mean	Range		SD	CV(%)
		Minimum	Maximum				Minimum	Maximum		
Insect pests										
Shoot fly	1.4		3	0.77	54	2.0	1	4	1.00	50
Stem borer	2.9		5	1.49	51	4.1	3	6	1.17	28
Midge	5.1		9	2.49	49	6.4	4	8	1.51	23
Head bug	5.1		9	2.83	55	6.3	5	9	1.41	22
Diseases										
Grain mold	3.5		9	2.90	82	2.0	1	5	1.32	66
Ergot	5.9		9	3.10	53	3.6	1	8	2.55	72
Rust	6.4		9	2.82	44	6.1	5	8	1.17	19
Blight	5.7	2	9	3.10	54	5.8	3	8	1.99	34
Anthracnose	5.9		9	3.13	53	5.2	3	9	1.64	31
Abiotic factors										
Nutrient use	2.7		8	2.09	78	3.8	2	6	1.56	41
Drought	2.7		9	2.77	103	2.8	1	7	2.11	76
Grain traits										
Plumpness	2.2		7	1.85	83	3.8	1	8	2.77	73
Round grain	2.0		5	1.25	63	3.2	1	6	2.17	67
Pearly white grain	1.9		6	1.50	80	3.4	1	6	2.30	67
Nutrition	2.5		7	1.88	74	4.2	1	7	1.79	42
Protein, starch	3.1		6	1.71	56	4.6	1	8	2.07	45
Grain hardness	3.5		9	2.35	67	4.3	3	6	1.00	23
Food/Feed/Fodder										
Hydrocyanic acid	2.2		9	2.21	100	5.5	1	8	2.69	51
Protein	2.5		7	2.13	84	5.3	2	8	2.41	47
Digestibility/NDF[2]	2.2		7	2.08	93	5.1	1	8	3.04	62
Other										
Market price	1.9		7	1.73	92	2.4	1	5	1.51	63

1. Scoring on 1 to 9 scale where 1 = most important; and 9 = least important.
2. Neutral detergent fiber.

Conclusions

Among the traits, market price (public: score 1.9; private: score 2.4), shoot fly (public: score 1.4; private: score 2.0), stem borer (public: score 2.9; private: score 4.1), grain mold (public: score 3.5; private: score 2.0), abiotic factors and grain quality (visual) were considered important. Research efforts, therefore, should focus on these traits.

Male Fertility Restoration Studies on A_1 and A_2 Cytoplasms of Sorghum

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Introduction

In sorghum (*Sorghum bicolor),* milo (A_1) cytoplasm is the only source of male sterility for the development of commercial hybrids. Lack of cytoplasmic diversity caused severe problems in the past, mainly due to the vulnerability of crops to cytoplasm-associated diseases.

Table 1. Pollen viability (PV) (%) and seed set (SS) (%) of sorghum parents and hybrids, postrainy season 2002/03, NRCS, Hyderabad, India[1].

Tester	Parameters	IMS9A	RS797A	RS301A$_2$	RS1100A$_2$	RS1103A$_2$	RS1126A$_2$	RS1215A$_2$	Male parent (R)
RS2100	PV	56	57	NP	3*	NP	4*	6*	99
	SS	75	91	0	0**	0**	0**	0**	91
RS2102	PV	66	78	70	88	69	89	93	97
	SS	78	68	70	77	80	88	77	88
RS2103	PV	62	84	73	93	67	96	93	98
	SS	84	64	69	88	66	87	90	91
RS2105	PV	56	69	2	6*	0	0*	6*	85
	SS	92	66	0	0**	0	0**	0**	87
RS2106	PV	69	90	0	5*	0	0	0*	98
	SS	93	78	0	0	0	0	0	91
RS2109	PV	55	60	NP	NP	NP	NP	NP	95
	SS	63	63	0**	0	0	0	0	81
RS2111	PV	87	73	NP	NP	NP	NP	NP	31*
	SS	90	65	0**	0	0	0	0	13
RS2112	PV	82	60	83	89	93	87	86	97
	SS	90	66	70	90	72	91	77	87
RS2113	PV	90	52	NP	NP	NP	NP	1*	97
	SS	92	65	0**	0	0**	0	0**	83
RS2114	PV	53	94	78	50	59	40	42	88
	SS	71	70	72	52	48	14	39	86
RS2115	PV	52	76	NP	NP	0*	NP	0*	97
	SS	92	73	0	0	0	0	0	92
RS2116	PV	64	68	91	61	63	69	85	97
	SS	89	68	79	74	60	78	78	83
RS2117	PV	79	60	71	81	60	88	83	95
	SS	88	72	80	83	68	90	78	92
RS2118	PV	90	62	89	93	93	91	90	98
	SS	79	66	77	91	78	87	63	91
Indore12	PV	81	68	96	90	72	74	84	95
	SS	86	85	84	83	88	78	77	91
C43	PV	89	65	2*	NP	0*	4*	3*	89
	SS	86	62	0	0	0**	0	0	92
AKR150	PV	63	61	NP	NP	NP	NP	NP	95
	SS	87	63	0	0	0	0	0	86
Parent (B)	PV	91	95	92	94	87	97	90	
	SS	84	87	92	87	88	78	76	

1. NP = No pollen, empty anther sac; * = Poor pollen development; ** = Few seeds (<10) in some plants.
Checks: CSH 17 - 51% PV and 76% SS; CSH 16 - 72% PV and 81% SS; CSH 9 - 61% PV and 60% SS.

During 1970, heavy losses in maize (*Zea mays*) production due to occurrence of leaf blight, caused by *Exserohilum turcicum,* over large areas in USA was attributed to using single cytoplasm (T) in maize hybrids. Several alternate cytoplasms have been reported in sorghum from USA and India and their classification was done by Worstell et al. (1984) and Rao et al. (1984). Among the various diverse cytoplasms, A$_2$ derived from Ethiopian line IS 12662C is suitable for use in breeding programs (Schertz and Ritchey 1978). Borikar et al. (1987) also suggested extensive use of A$_2$ cytoplasm for breeding. Hence, this study was undertaken to test A$_1$ and A$_2$ cytoplasmic utility by determining male fertility restoration on the seed parents based on A$_1$ and A$_2$ male-sterile cytoplasms.

Materials and Methods

A total of 119 hybrids were obtained by crossing seven male sterile lines, IMS9A and RS797A of A$_1$ (milo) cytoplasm; RS301A$_2$, RS1100A$_2$, RS1103A$_2$, RS1126A$_2$ and RS1215A$_2$ of A$_2$ (IS 12662C) cytoplasm, with seventeen testers (Table 1) in a line x tester mating design during rainy season 2(K)2. The testcrosses along with

parents (7 B-lines and 17 male parents) and three checks (CSH 9, CSH 16 and CSH 17) were grown in a randomized block design with three replications at the National Research Centre for Sorghum (NRCS), Hyderabad, India during the postrainy season 2002/03. The minimum and maximum atmospheric temperature during reproductive growth of the crop ranged from 8-30°C. Each plot consisted of two 4-m long rows with 60 cm interrow and 15 cm intra-row spacing. Observations were recorded on five plants of each genotype for pollen viability and seed set in each replication and percentage of pollen viability and seed set was calculated (Sridharswamy and Jagadeshwar 1995).

Results and Discussion

The fertility restoration in hybrids, parents and checks was assessed based on the pollen viability and seed set percentage. Pollen development in the female (B) and male (except RS2 111) parents, checks and hybrids with A, cytoplasm was normal but variable in hybrids with A_2 cytoplasm (Table 1). The male parent RS2111 exhibited 31 % pollen viability and 13% seed set, due to sensitivity to low temperature. Checks exhibited 51 to 72% pollen viability and 60 to 81 % seed set. Male fertility restoration with <50% pollen viability and <60% seed set is considered as partial in winter.

All the male parents restored male fertility on both cytoplasmic-male sterile (CMS) lines (IMS9A and RS797A) of A_1 (milo) cytoplasm. The pollen viability and seed set varied from 52 to 94% and 62 to 93%, respectively in A_1 (milo) cytoplasm (Table 1). Highest pollen viability was observed in the cross RS797A x RS2114 (94%) and highest seed set in the cross IMS9A x RS2106 (93%).

Seven male parents (RS2102, RS2103, RS2112, RS2116, RS2117, RS2118 and Indore 12) exhibited good male fertility restoration and RS2114 exhibited partial restoration on A_2 cytoplasm. The remaining nine male parents (RS2100, RS2105, RS2106, RS2109, RS2111, RS2113, RS2115, C43 and AKR150) failed to restore male fertility as their hybrids exhibited sterility and low pollen viability (1 to 6%). Pollen development in anthers in the testcrosses of these male parents was poor or absent, and consequently there was poor or no seed set (<10 seeds). Highest pollen viability (96%) was observed in the crosses RS1126A_2 x RS2103 and RS301A_2 x Indore 12 and highest seed set (91%) in the crosses RS1100A_2 x RS2118 and RS1126A_2 x RS2112.

All the A_1 (milo) cytoplasm-based hybrids depicted good male fertility. Among the 85 A_2 cytoplasm-based hybrids, good male fertility restoration was observed in 37 hybrids, partial male fertility in three hybrids and male sterility in 45 hybrids. The variation in male fertility within the groups of hybrids of the females with specific males revealed differences among females, which would indicate that a male restorer in one particular A_1 female might not necessarily restore in another A_2 female (Worstell et al. 1984). Pollen viability and seed set patterns of A_1 and A_2 cytoplasmic hybrids showed that A_1 cytoplasmic hybrids were more fertile compared to A_2 cytoplasmic hybrids. The higher level of sterility in A_2 cytoplasm hybrids, compared to A_1 was reported earlier by Gangakishan and Borikar (1989) and Senthil et al. (1994).

In this study, eight restorers (among 17) of A_1 cytoplasm restored fertility in A_2 cytoplasm. Therefore, it is possible to exploit A_2 cytoplasm to develop hybrids as an alternate to traditional A_1 (milo) cytoplasm-based hybrids.

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Correlation Analysis Among Growth and Yield Components of Winter Sorghum

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Introduction

Correlation analysis among crop growth and yield and yield components is one of the prerequisite techniques to determine the influence of environment on productivity and potential of a crop. The objective of this experiment was to study the correlation between growth and yield components to understand their individual effects on grain yield of winter sorghum *(Sorghum bicolor).*

Materials and Methods

The experiment was conducted at the Regional Research Station, Bijapur, situated in the Northern Dry Zone of Karnataka state of India. The rainfall received during the cropping season was 424.5 mm in 1994/95 and 384.2 mm in 1995/96, which was 72% and 61% of total rainfall received during winter, respectively. The experiment was laid out on a plot having 1% slope in split-split plot design with three replications and was conducted during postrainy *(rabi)* season of 1994 and 1995 in the deep black soils (Typic-chromosterts, sand 24.8%, silt 14.9% and clay 60.3%) with 0.36% organic carbon, 8.5 pH and 128 kg ha^{-1} of available nitrogen. Different tillage treatments, deep, medium and shallow tillage, were imposed in the main plots. Organic materials [*Leucaena leucocephala* (*subabul*) loppings, farmyard manure (FYM) and vermicompostl were used in sub-plots while within the sub-plots varying levels of nitrogen fertilizers (0, 25 and 50 kg ha^{-1}) were applied. Tillage treatments were imposed during 3rd week of June in 1994 and 3rd week of May during 1995. Deep tillage (22.5 to 30 cm) was carried out through tractor-drawn mold board plow followed by two harrowings. Medium tillage to a depth of 15 to 18 cm was done with bullock-drawn plow, followed by two harrowings. Shallow tillage to a depth of 5 to 7.5 cm was imposed by bullock-drawn harrow three times prior to sowing. *Leucaena* loppings (2.5 t ha^{-1}) and FYM (2.5 t ha^{-1}) were applied during 3rd week of August and 1st week of September and covered manually. Vermicompost (25 kg ha^{-1}), nitrogen fertilizer (50 kg ha^{-1}) and recommended dose of phosphorus (25 kg ha^{-1}) were applied at the time of sowing. Maldandi M 35-1, a postrainy season sorghum cultivar, was sown on 5 October 1994 and 15 September 1995 at a depth of 5 cm with interrow spacing of 60 cm and harvested on 17 February 1995 and 27 January 1996, respectively. Five randomly selected plants from each plot were used to record the observations on growth and yield components at 30-day intervals from 30 days after sowing (DAS) up to harvest. The plant samples were oven-dried at 60 to 65°C and then weighed. Grain and straw from net plot were harvested, sun-dried, weighed to obtained net plot yield.

Observations on leaf area index (LAI), leaf area duration (LAD), absolute growth rate (AGR), crop growth rate (CGR), relative growth rate (RGR), net assimilation rate (NAR) at 91 DAS to harvest and dry matter production and its distribution in various plant parts at harvest were statistically analyzed to evaluate data on individual treatment effects (Snedecor and Cochran 1969). The correlation analysis was carried out according to Johnson and Robinson (1955). The above growth indices are defined below:

1. Leaf area index (LAI) is the proportion of leaf area per plant to the ground area occupied by a plant (Sestak et al. 1971).

$$LAI = \frac{A}{P}$$

where A = Leaf area; and P = Unit land area.

2. Leaf area duration (LAD) is the integral of leaf area index over the growth period and is expressed in days (Power et al. 1967).

$$LAD = \frac{Li + L(i+1) x (t_2 - t_1)}{2}$$

where Li = Leaf area index of ith stage; L (i + 1) = Leaf area index at (i + 0th stage; and t_2-t_1 = Time interval between i and $(i + 1)^{th}$ stage in days.

3. Absolute growth rate (AGR) is the rate of increase in dry matter per plant per unit time and is expressed in g $plant^{-1}$ day^{-1} (Radford 1967).

$$AGR = \frac{(W_2 - W_1)}{(t_2 - t_1)}$$

where W_1 = Dry weight (mass) of plant in g at time t_1; and W_2 = Dry weight (mass) of plant in g at time t_2

4. Crop growth rate (CGR) is rate of dry matter production per plant per unit ground area per unit time and is expressed in g dm^{-2} day^{-1} (Watson 1952).

$$CGR = \frac{(W_2 - W_1)}{(t_2 - t_1)} \times \frac{1}{p}$$

5. Relative growth rate (RGR) is the dry weight (mass) per unit dry weight (mass) per unit time and is expressed in g g^{-1} day^{-1} (Radford 1967).

$$RGR = \frac{Loge W_2 - Loge W_1}{t_2 - t_1}$$

where Loge = Logarithm to the base (Neperian constant).

6. Net assimilation rate (NAR) is the rate increase in dry weight (mass) per unit leaf area per unit time and is expressed as g dm^{-2} day^{-1} (Gregory 1926).

$$NAR = \frac{(W_2 - W_1)\ (Loge L_2 - Loge L_1)}{(t_2 - t_1)(L_2 - L_1)}$$

where L_1 = Leaf area in dm^2 at t_1; and L_2 = Leaf area in dm^2 at L_2.

Results and Discussion

Growth components. The results indicated a significant positive correlation between grain yield and plant height, leaves $plant^{-1}$, leaf area $plant^{-1}$ and dry matter production and its distribution in different plant parts at harvest. Grain yield was highly correlated with ear mass $plant^{-1}$ (0.772), followed by total dry matter production $plant^{-1}$ (0.767), and leaf mass $plant^{-1}$ (0.657) (Table 1). Correlation among growth components was also highly significant. Among the growth components, ear mass $plant^{-1}$ was highly correlated with total dry matter production $plant^{-1}$ (0.977), followed by leaf mass with total dry matter production $plant^{-1}$ (0.892), number of leaves with leaf area $plant^{-1}$ (0.886) and stem mass with total dry matter production $plant^{-1}$ (0.875) (Table 1). Khajan Singh and Lata Chaudhary (2000) reported that stover yield $plant^{-1}$ showed positive and significant correlation with plant height, number of leaves $plant^{-1}$, leaf area $plant^{-1}$ and flag leaf area $plant^{-1}$ in sorghum. These results indicate that the ear mass and total dry matter production $plant^{-1}$ ultimately determines the postrainy sorghum yield per unit area.

Table 1. Correlation coefficient analysis of growth components at harvest and grain yield in postrainy season sorghum[1].

Growth components	Plant height (cm)	Number of leaves $plant^{-1}$	Leaf area (cm^2 $plant^{-1}$)	Leaf mass (g $plant^{-1}$)	Stem mass (g $plant^{-1}$)	Ear mass (g $plant^{-1}$)	TDM (g $plant^{-1}$)	Grain yield (kg ha^{-1})
Plant height (cm)	1.000	0.612**	0.622**	0.600**	0.657**	0.683**	0.710**	0.628**
Number of leaves $plant^{-1}$		1.000	0.886**	0.774**	0.691**	0.772**	0.797**	0.622**
Leaf area (cm^2 $plant^{-1}$)			1.000	0.743**	0.692**	0.750**	0.779**	0.594**
Leaf mass (g $plant^{-1}$)				1.000	0.776**	0.846**	0.892**	0.657**
Stem mass (g $plant^{-1}$)					1.000	0.754**	0.875**	0.625**
Ear mass (g $plant^{-1}$)						1.000	0.977**	0.772**
TDM (g $plant^{-1}$)							1.000	0.767**
Grain yield (kg ha^{-1})								1.000

1, ** = Significant at 1% level; TDM = Total dry matter.

Table 2. Correlation coefficient analysis of growth indices and grain yield in postrainy season sorghum'.

Growth indices[2]	LAI	LAD	AGR	CGR	RGR	NAR	Grain yield (kg ha^{-1})
LAI	1.000	0.846**	0.555**	0.555**	0.353	0.252	0.594**
LAD		1.000	0.593**	0.593**	0.376*	0.249	0.677**
AOR			1.000	0.950**	0.923**	0.912**	0.522**
CGR				1.000	0.923**	0.912**	0.512**
RGR					1.000	0.947**	0.277
NAR						1.000	0.295
Grain yield (kg ha^{-1})							1.000

1. * = Significant at 5% level; ** = Significant at 1% level.
2. LAI = Leaf area index; LAD = Leaf area duration; AGR = Absolute growth rate; CGR = Crop growth rate; RGR - Relative growth rate; NAR = Net assimilation rate.
LAI measured at harvest; others at 91 days after sowing to harvest.

Table 3. Correlation coefficient analysis of yield components and grain yield in postrainy season sorghum[1].

Yield components	Straw yield (t ha^{-1})	Harvest index	Water-use efficiency (kg ha^{-1} cm^{-1})	Ear mass (g plant^{-1})	Grain mass (g plant^{-1})	1000-grain mass (g)	Ear length (cm)	Ear diameter (cm)	Number of grains ear^{-1}	Grain yield (kg ha^{-1})
Straw yield (t ha^{-1})	1.000	0.244	0.886**	0.725**	0.738**	0.552**	0.651**	0.674**	0.730**	0.952**
Harvest index		1.000	0.569**	0.425*	0.285	0.235	0.505**	0.427*	0.257	0.523**
Water-use efficiency (kg ha^{-1}cm^{-1})			1.000	0.719	0.650**	0.501**	0.716**	0.681**	0.634**	0.961**
Ear mass (g plant^{-1})				1.000	0.931**	0.774**	0.864**	0.894**	0.846**	0.772**
Grain mass (g plant^{-1})					1.000	0.796**	0.797**	0.849**	0.924**	0.737**
1000-grain mass (g)						1.000	0.722**	0.726**	0.555**	0.557**
Ear length (cm)							1.000	0.915**	0.702**	0.728**
Ear diameter (cm)								1.000	0.761**	0.725**
Number of grains ear^{-1}									1.000	0.722**
Grain yield (kg ha^{-1})										1.000

1. * = Significant at 5% level; ** = Significant at 1% level.

Growth indices. Postrainy season sorghum grain yield was positively and significantly correlated with LAD (0.677), LAI (0.594), AGR (0.522) and CGR (0.512) (Table 2). Correlation between grain yield and RGR and NAR was positive but not significant. The above results clearly indicated that the longer the duration of leaf greenness (fresh green leaf) the greater is its role in determining the yield. Highly significant and positive correlation was observed between AGR, CGR, RGR, grain yield and LAI with LAD (Table 2).

Yield components. The correlation results showed that grain yield is positively and significantly correlated with water-use efficiency, straw yield, harvest index and yield components (ear mass, grain mass, ear length, ear diameter, grains ear^{-1} and 1000-grain mass) (Table 3). The correlation coefficient was maximum (0.961) between water-use efficiency and grain yield, indicating the importance of higher moisture availability for better crop growth with higher dry matter partitioning to ear, and thereby increasing the grain yield. High correlation between water-use efficiency and grain yield of sorghum in Vertisols in drylands was mainly due to conservation of moisture through tillage practices and supply of nitrogen through organic and inorganic sources. The correlation coefficient between grain yield and straw yield was high (0.952) and significantly positive. Also, correlation coefficient between grain yield and other parameters (plant height, leaf area, leaf mass and dry matter production plant^{-1}) was significant and positive. This clearly indicates that grain yield is high when plant growth is good. Maximum ear size [ear length (0.728) and ear diameter (0.725)], high dry matter accumulation in ear [ear mass (0.772) and grain mass plant^{-1} (0.737)] with more number of grains ear^{-1} (0.722), ultimately determines the grain yield in postrainy season sorghum (Table 3). Hence, manipulation of the environment (management practices) that improves the above characters in postrainy season sorghum can boost the yield besides manipulation of genetic characters. These results are similar to earlier results recorded in sorghum by Pawar and Jadav (1996), Navale et al. (2000) and Veerabadhiran and Kennedy (2001).

Among the yield components, highest correlation coefficient was observed between ear mass and grain mass plant^{-1} (0.931), followed by grain mass plant^{-1} and grains ear^{-1} (0.924), ear length and ear diameter (0.915) and ear mass and ear diameter (0.894) (Table 3).

Conclusions

It was observed that high dry matter production plant^{-1} is an indication of accumulation of more carbohydrates during the vegetative phase and its subsequent translocation in reproductive parts during later stages

resulting in high grain yield. This was indicated by the high magnitude of correlation that existed between plant height, LAI, LAD, AGR, CGR, dry matter production plant^{-1} and dry matter accumulation in ear with bigger ear size, ie, ear length, ear diameter and grains ear^{-1}. The above growth and yield components ultimately determine the grain yield of postrainy season sorghum under dryland situations in Vertisols with different tillage practices (moisture conservation and moisture availability) and integrated nutrient management (nutrient supply) at different stages of crop growth. These characters must be given due importance in the breeding program to evolve drought resistant and moisture and nutrient-responsive sorghum varieties particularly for postrainy season.

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Heterosis in Postrainy Season Sorghum Under Shallow and Medium-deep Soils

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Introduction

The productivity levels of postrainy *(rabi)* season grain sorghum *(Sorghum bicolor)* in India is much lower (611 kg ha^{-1}) compared to rainy (*kharif*) season sorghum (1000 kg ha^{-1}) (Anonymous 2001). While the success of rainy season sorghum was mainly credited to the development of high-yielding grain hybrids and their commercial cultivation on large scale, lack of appropriate hybrids for different agro-ecological situations of postrainy season such as severe drought, variable depth of soil and biotic stresses are primarily responsible for low productivity level in postrainy season sorghum (Rana et al. 1996). Much of the postrainy season sorghum grown on residual and receding soil moisture on shallow and medium-deep soils in the states of Maharashtra, Karnataka, Andhra Pradesh and Gujarat are still under local cultivars or landraces. Therefore, there is a need for the development of hybrids adapted to postrainy season to enhance production and productivity levels. Heterosis studies using elite genotypes provide an insight into the genetic material available with plant breeders for improvement for both soil types, which cover 70% of the cultivated sorghum area under postrainy season (Bapat and Gujar 1990). This study was aimed at assessing the performance of hybrids under medium-deep and shallow soils, and to identify the cytoplasmic male sterile (CMS) lines and pollinators for further use in hybrid breeding for postrainy season.

Materials and Methods

This study was based on a line x tester mating design of diverse postrainy season adapted sorghum genotypes of the All India Coordinated Sorghum Improvement Project (A1CSIP). Three CMS lines (53A, 104A and 116A) were pollinated each with 12 restorers (SPV 504, SPV 783, SPV 839, SPV 913, SPV 932, SPV 1090, SPV 1102, SPV 1155, SPV 1159, SPV 1172, SPV 1173 and Sel 3) to produce 36 F_1 hybrids. All the 36 F_1s and their parents (both CMS lines and pollinators) were evaluated under two contrasting environments (medium-deep and shallow soils). The experiment was conducted during 1994/95 postrainy season at the Post Graduate Farm, Department of Botany, Mahatma Phule Krishi Vishwavidyalaya,

Table 1. Analysis of variance for sorghum parents and hybrids under medium-deep and shallow soils, postrainy season 1994–95, Rahuri, India[1].

Source	Soil[2]	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	Leaf area (cm^2)	Number of grains $panicle^{-1}$	1000-grain mass (g)	Grain yield (g $plant^{-1}$)
Replication	M	2	0.84	0.63	0.75	90.00	3696.0	0.31	0.36
	S	2	0.83	0.25	1.25	200.00	240.0	0.23	0.46
Female	M	2	5.33**	24.11**	169.82**	28750.0**	453765.0	18.52**	182.52**
	S	2	5.78**	28.78**	155.62**	45393.5**	173066.50**	11.58**	64.08**
Male	M	11	23.02**	34.02**	971.56**	102796.4**	202106.20**	46.31**	186.83**
	S	11	20.26**	33.78**	772.33**	70138.18**	81388.0**	42.88**	30.84**
Female vs Male	M	1	6.42**	21.19**	23475.0**	242768.0**	532360.0**	126.02**	108.88**
	S	1	3.37*	14.44**	14101.63**	38284.0**	262968.0**	40.41**	64.31**
Crosses	M	35	48.66**	69.04**	508.36**	52980.12**	211489.4**	40.02**	166.58**
	S	35	36.22**	53.21**	612.58**	24361.09**	916141.8**	22.09**	45.93**
Parents vs Crosses	M	1	157.37**	132.0**	7835.0**	636512.0**	161440.0**	78.81**	926.28**
	S	1	97.31**	160.12**	15402.50**	312112.0**	24180.0**	199.8**	534.55**
Error	M	100	0.40	0.71	3.39	32.44	2413.74	0.07	0.42
	S	100	0.55	0.61	4.79	169.45	59.35	0.17	0.72

1. * = Significant at 5% level; ** = Significant at 1% level.
2. M = Medium-deep; S = Shallow.

Rahuri, India following randomized complete block design with three replications. The entries were planted in 4 rows per plot of size 11.01 m^2 per replication with 45 cm x 15 cm spacing. Non-experimental rows were planted with landraces all around the experimental plots to eliminate the border effects. Observations were recorded on ten random plants from each plot per replication for days to 50% flowering, days to maturity, plant height (cm), leaf area (cm^2), number of grains per panicle, 1000-grain mass (g), and grain yield (g $plant^{-1}$). The heterosis (over mid parent) was calculated as $(F_1\text{-}MP)*100/MP$ where F_1 is hybrid performance, and MP is mid parent value.

Results and Discussion

Hybrid performance and heterosis. The analysis of variance for parents and hybrids (Table 1) revealed significant differences among females, males, female vs male crosses and parents vs crosses for all the characters. The means and ranges of per se performance and heterosis over mid parent (HMP) for hybrids evaluated under medium-deep and shallow soils for various traits are given in Table 2. Under shallow soils, the hybrids were shorter, flowered and matured early by two days compared to medium-deep soils. The mean leaf area of the hybrids under medium-deep soils was high (1723 cm^2) and average expression of grain number (1569 grains $panicle^{-1}$) and 1000-grain mass (37 g) were also noticeably better under medium-deep soils. The grain yield per plant of the hybrids was markedly high (54 g) under medium-deep soils compared to shallow soils (40 g). Higher grain and fodder yields were reported at increased soil depth of 60 cm than at 30 cm (Patil and Chavan 1989, Jadhav et al. 1996). Leaf area, grain number, grain size and grain yield showed an amplified expression of 72%, 30%, 12% and 35% respectively under medium-deep soils over shallow soils. The hybrids were superior to their parents under each soil type. They were taller (8-13%) and flowered and matured early by three days than the parents. Increased leaf area, number of grains per panicle, 1000-grain mass and grain yield per plant was observed in hybrids under both soils compared to their parents. The increase in grain number in hybrids under medium-deep soil was substantial (12%) while only 2% increase was observed under shallow soils.

The degree of HMP differed between soils and from trait to trait (Table 2). The range observed for HMP for various characters under medium-deep soils was higher compared to that under shallow soils. The mean heterosis for leaf area and number of grains per panicle was greatest under medium-deep soils and was higher by 207% and 130%, respectively over that of shallow soils. The dimension of heterotic effect for grain yields and

Table 2. Per se performance of sorghum hybrids and heterosis over mid parent of 36 F_1 hybrids evaluated under medium-deep and shallow soils during postrainy season 1994/95, Rahuri, India.

	Per se performance of hybrids				Heterosis over mid parent			
	Medium-deep soil		Shallow soil		Medium-deep soil		Shallow soil	
Trait	Mean[1]	Range	Mean	Range	Mean	Range	Mean	Range
Days to 50% flowering	72*	63-76	70	63-74	-2.70	-14.29-2.74	-2.36	-12.93-2.78
Days to maturity	118	108-124	116	106-121	-1.17	-10.66-2.50	-3.38	-87.50-4.04
Plant height (cm)	204*	185-230	196	162-260	14.83	-4.48-39.27	18.84	-3.32-57.10
Leaf area (cm^2)	1723*	1428-1947	1001	815-1164	15.81	-5.37-33.05	5.15	-12.95-27.05
Number of grains panicle^{-1}	1569*	977-1952	1209	895-1708	17.01	-25.37-235.47	7.39	-13.16-72.09
1000-grain mass (g)	37*	30-44	33	28-39	5.83	-24.05-26.98	7.09	-16.42-20.69
Grain yield (g plant"^{1})	54*	39-73	40	34-48	14.18	-19.27-80.25	14.31	-2.44-42.42

1. * = Mean difference between hybrids under medium-deep and shallow soils are significant (*P* <0.01).

yield component traits in this study is in agreement with those of other studies (Nandanwankar 1990, Salunke and Deore 1998, Prabhakar 2001).

The range of HMP for grain yield under medium-deep soil was higher (-19.27 to 80.25%) compared to that for shallow soil (-2.44 to 42.42) (Tables 2 and 3). Under medium-deep soils, the hybrids 116A x SPV 1090 (73.4 g), 104A x SPV 932 (69.4 g) and 116A x SPV 1102 (63.8 g) produced high grain yield per plant and showed 80,41 and 54% HMP, respectively. The hybrids 53A x SPV 1090 (48.33 g plant^{-1}), 116 A x SPV 932 (46.66 g plant^{-1}) and 116 A x Sel 3 (46.27 g plant^{-1}) were highest grain yielders with 29.73%, 42.42% and 33.33% superiority over their mid parents, respectively under shallow soils (Table 3). Seventy percent (25 of 36) of the hybrids manifested significant heterosis over mid parent under medium-deep and shallow soils. To identify CMS lines and pollinators suitable for medium-deep and shallow soils, superiority of mean of hybrids involving a common parent was calculated over hybrids grand mean for grain yield (Table 3). For medium-deep soils, the pollinator SPV 932, SPV 1090 and SPV 1102 performed well for grain yield. The hybrids involving these pollinators gave a grain yield superiority of 17%, 9% and 6%, respectively over grand hybrid mean. The pollinators, SPV 1090, Sel 3 and SPV 932 performed well for grain yield under shallow soils with their hybrid means exceeding the overall hybrid mean by 12%, 9% and 9%, respectively. Sel 3 has been released as drought tolerant variety for shallow soils (Gujar et al. 1995). Much faster growth rate in growth stage II, increased leaf area expansion, delayed senescence, less number of stomata and small stomatal size (Patil and Chavan 1989), higher photosynthesis rate and grain yield (Jadhav et al. 1996) were observed for cultivar Sel 3. For both soils, SPV 932 and SPV 1090 were identified as good pollinators. Among CMS lines, 116A performed well for grain yield under both medium-deep and shallow soils. Line 116A produced a greater proportion of hybrids with significant heterosis for grain yield than did 53A and 104A. The mean superiority of hybrids involving 116A was 6.5% and 4.5% under medium-deep and shallow soils, respectively. Similar observations were recorded by Salunke and Deore (1998) on hybrids involving 116A for several characters including grain yield.

This study indicated the exploitation of hybrids as a good option to enhance the productivity of postrainy season sorghum. The depth of soil profile does influence the performance of hybrids and magnitude of heterosis. Hybrids were expressed better under medium-deep than shallow soils. Pollinators SPV 932 and SPV 1090 and the line CMS 116A were good for both soils.

Table 3. Mean performance and heterosis over mid parent (HMP) of sorghum hybrids and average performance of sorghum hybrid parents over series of cross combinations for grain yield (g $plant^{-1}$) under medium-deep and shallow soils, postrainy season 1994/95, Rahuri, India[1].

		53A		104A		116A		M		S	
Testers	Description	M	S	M	S	M	S	Mean	SOGM	Mean	SOGM
SPV 504	Mean	53.8	37.2	54.27	36.13	56.87	42.73	54.98	0.88	38.68	–3.54
	HMP	3.85*	5.71*	12.5**	9.09**	14**	30.3**	10.12		15.03	
SPV 783	Mean	48.07	34.6	38.6	33.53	47.47	35.4	47.7	–12.47	34.51	–13.9
	HMP	–2.04	–	–13.33**	3.03	–15.32**	2.94**	–10.23		1.99	
SPV 839	Mean	55.07	36.13	48.4	38.6	59.4	41.8	54.29	–0.38	38.84	–3.14
	HMP	7.84**	0	2.13	14.71**	28.26**	29.23**	12.74		14.65	
SPV 913	Mean	58.13	37.4	53.67	35.66	56.4	38.26	56.06	2.86	37.1	–7.48
	HMP	19.59**	0	21.35**	2.86	20.43**	10.14*	20.46		4.33	
SPV 932	Mean	59.4	40.8	69.4	43.6	63.46	46.66	64.08	17.57	43.68	8.92
	HMP	11.32**	13.89**	4082**	29.41**	27.27**	42.42**	26.47		28.57	
SPV 1090	Mean	61.73	48.33	43.8	40.73	73.4	46	59.64	9.43	45.02	12.26
	HMP	5.98**	29.73**	–19.27**	17.14**	80.25**	31.43**	22.32**		26.10	
SPV 1102	Mean	55.73	41.73	53.93	34.6	63.8	41.07	57.82	6.09	38.8	–3.24
	HMP	14.29**	18.31**	20**	4.48	54.22**	17.65**	29.50		13.48	
SPV 1155	Mean	49.78	38.26	54.87	36.66	55.8	41.4	53.51	–1.81	38.77	–3.31
	HMP	1.01	1.33	20.88**	4.23	23.08**	7.89*	14.99		4.48	
SPV 1159	Mean	53.93	38.8	47.87	37	56.6	39.93	52.8	–3.11	38.07	–5.06
	HMP	2.86	8.33**	–1.03	8.82	14**	15.4*	5.28		10.85	
SPV 1172	Mean	44.47	42.4	50	41	43.87	43.55	46.11	–15.3	42.31	5.51
	HMP	1.15	10.53**	26.58**	13.89**	–6.38**	31.34**	7.12		18.59	
SPV 1173	Mean	48.53	38.73	53.63	44.6	63.53	41.07	55.24	1.35	41.46	3.39
	HMP	10.11**	5.41**	33.33**	28.57**	26.73**	20.59	23.39		18.19	
Sel 3	Mean	57.53	40.2	42.6	45.2	55.73	46.27	51.95	–4.67	43.89	9.45
	HMP	19.59**	–2.44**	–3.37**	15.38**	7.69**	33.33	7.97		15.42	
Mean grain yield		53.9	39.5	50.9	38.9	58.0	41.9	54.5[2]		40.1[2]	
Mean heterosis		7.96	7.57	11.72	12.63	22.85	22.72	14.18		14.31	
SOGM		–1.1	–1.49	–6.6	–2.99	6.42	4.48				

1. M = Medium-deep soil; S = Shallow soil; SOGM = Superiority of hybrids involving pollinator/cytoplasmic male sterile (CMS) line over mean.
   * = Significant at 5% level; ** = Significant at 1% level.
2. Grand mean.

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Heterobeltiosis and Combining Ability for Grain Yield and Yield Components in Postrainy Season Sorghum

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Introduction

Postrainy *(rabi)* season sorghum *(Sorghum bicolor)* in India is grown under residual moisture situations primarily in the states of Maharashtra, Karnataka and Andhra Pradesh. Since there is no alternative remunerative cereal that can be grown during this season, which receives only 8% of the annual rainfall (Garad et al. 1995), postrainy sorghum is very crucial for food and fodder security in drought-prone areas of these states (Anonymous 2001). Though efforts have been made at various sorghum breeding centers to develop hybrids adapted to postrainy season, these have not been fruitful. Much of the sorghum-growing area is still under postrainy local sorghum. Therefore, this study was undertaken to assess the heterobeltiosis (heterosis over the superior parent) for grain yield and its components in postrainy season sorghum using line x tester analysis and identify good parents and their hybrids suited for the postrainy season.

Materials and Methods

Two cytoplasmic male sterile (CMS) lines (116A and 117A) were crossed with seven restorers (M148-138-1, MI48-138-2, M148-138-3, Tandur local, RS645 x (RS71 x NL), SPV 980-2 and SPV 980-1) in line x tester mating design to produce 14 hybrids during the postrainy season 2001/02 at the National Research Centre for Sorghum in Hyderabad, Andhra Pradesh. All the 14 hybrids along with their parents were grown in a randomized block design in the postrainy season 2002/03. The entries were planted in three replications, each consisting of two rows of 4-m length with 45 cm x 15 cm plant spacing. Observations were recorded on five random plants for days to 50% flowering, plant height, panicle length, branches per panicle, grains per branch, test weight and grain yield per plant. Statistical analysis was done as outlined by Kempthorne (1957) and Arunachalam (1974). Heterobeltiosis (%) (heterosis over superior parent) was calculated by the formula:

$$[(F_1-SP)/SP] \times 100$$

where SP = mean of superior parent.

Results and Discussion

The analysis of variance (Table 1) clearly shows significant differences among the genotypes. Crosses showed significant differences for all the characters except time to flower when compared to parents; this indicates the presence of heterosis. Line mean sum of squares was significant only for test weight whereas tester mean sum of squares was significant for time to flower, plant height, grains per branch, test weight and grain yield. Line x tester mean sum of squares was significant only for branches per panicle, test weight and grain yield plant^{-1}.

The estimates of variance indicate that the specific combining ability (sca) variance was higher than general combining ability (gca) variance for all the characters studied. This shows the predominance of non-additive gene action in the inheritance of all the characters. Similar results were obtained by Badhe and Patil (1997) and Hovny et al. (2000). Rafiq et al. (2002) reported both additive and non-additive gene action for grain yield.

Table 1. Analysis of variance for grain yield and its component characters in sorghum in Hyderabad, India, postrainy season 2001/02[1].

Source[2]	Df	Time to flower (days)	Plant height (cm)	Panicle length (cm)	No. of branches panicle^{-1}	No. of grains branch^{-1}	Test weight (g)	Grain yield (g plant^{-1})
Replications	2	18.36	214.36	1.31	434.18	390.56	4.16	227.88
Treatments	22	43.65**	1206.77**	23.05**	254.67**	349.16**	3.34**	1626.98**
Parents	8	62.66**	949.48**	8.06	122.64*	82.58*	1.52**	469.33**
Lines	1	28.16	266.66	0.16	4.16	4.16	2.80**	4.16
Testers	6	71.52**	1165.65**	9.66	107.26	108.93*	1.09**	519.65**
Line x Tester	1	44.02	335.28	6.35	333.39*	2.88	2.76**	632.59*
Parent vs Crosses	1	35.22	5875.27**	185.51**	3211.48**	3425.21**	44.84**	8279.07**
Crosses	13	32.58	1005.98**	19.78**	108.43*	276.59**	1.27**	1827.69**
σ^2gca		0.60	16.13	0.45	0.19	1.25	0.04	6.98
$\sigma^2$8ca		4.51	110.35	0.64	16.27	66.20	0.08	475.31
σ^2gca / σ^2sca		0.13	0.14	0.70	0.01	0.01	0.5	0.01
Error	44	14.31	248.33	4.77	53.70	36.23	0.32	130.30

1. * Significant at 5% level; ** = Significant at 1% level.
2. gca = General combining ability; sca = Specific combining ability.

Table 2. Heterobeltiosis and combining ability of top three sorghum crosses for grain yield and its component characters in Hyderabad, India, postrainy season 2001/02[1].

Trait	116A X SPV 980-1	116A x [RS645 x (RS71 x ND]	117A X SPV 980-2
Per se performance	110.67	91.33	91.00
Heterobeltiosis (%)			
Grain yield (g plant^{-1})	238.78**	101.47**	84.46**
Time to flower (days)	-5.38**	1.43*	7.52**
Plant height (cm)	7.39	17.64*	5.61
Panicle length (cm)	19.70*	4.55	13.85
No. of branches panicle^{-1}	15.46	4.12	26.46**
No. of grains branch^{-1}	45.74**	50.96**	66.39**
Test weight (g)	87.50**	53.50**	36.07**
Combining ability[2]			
sca	23.98**	8.31	12.19
gca (P1)	10.19**	10.19**	-10.19**
(P2)	13.17*	9.5	25.67**

1. * = Significant at 5% level; ** = Significant at 1% level.
2. sca = Specific combining ability; gca = General combining ability; P = Parent.

The cross 116A x SPV 980-1 exhibited maximum per se performance for grain yield plant^{-1} with corresponding highly significant positive heterobeltiosis for grain yield plant^{-1} (238.78%), time to flower (-5.38), panicle length (19.70%) and test weight (87.50%) (Table 2). The cross 116A x [RS645 x (RS71 x NL)] is the second best cross with respect to per se performance for grain yield plant^{-1} with corresponding significant positive heterobeltiosis for grain yield plant^{-1} (101.47%) and plant height (17.64%). The cross 117A x SPV 980-2 is the third best cross with respect to per se performance for grain yield plant^{-1} with corresponding significant positive heterobeltiosis for grain yield plant^{-1} (84.46%) and grains branch^{-1} (66.39%).

The female parent 116A was a good general combiner for time to flower, test weight and grain yield. Among the male parents, SPV 980-1 was a good general combiner for days to flower, panicle length, test weight and grain yield plant^{-1}. The cross 116A x SPV 980-1 exhibited significant sca effect for days to flower and grain yield per plant in desired directions.

The results obtained in this study show that the cross 116A x SPV 980-1 not only exhibited high desirable sca effect for grain yield per plant but also had high per se performance and heterobeltiosis for this trait, indicating the association of these parameters with each other and was the most desirable hybrid. Line 116A was the most desirable female parent while SPV 980-1 and RS645 x (RS71 x NL) were the best male parents for the postrainy season sorghum.

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Providing of Plants with Water Regulates Expression of Fertility-restoring Genes for the A4 and M35 CMS-inducing Cytoplasms of Sorghum

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Diversification of types of cytoplasmic male sterility (CMS) is one of the main factors ensuring genetic variability of the F_1 hybrids. During past years a large number of new CMS-inducing cytoplasms have been revealed in sorghum (*Sorghum bicolor)* (Pring et al. 1995); however, many of them are not used in practical breeding because of the absence of reliable fertility restorers. Previously, developing early maturing CMS-lines for Volga-Region of Russia using the new types of male-sterile cytoplasms (A2, A3, A4,9E M35), we found few line-fertility restorers for the A4 and 9E cytoplasms. However, in our crosses significant instability of expression and inheritance of male fertility restoration was revealed (Elkonin et al. 1998; Elkonin and Kozhemyakin 2000).

Among numerous entries crossed to the Indian CMS-line M 35-1 A, the line KVV-97 was the only one able to produce fertile F_1 hybrids. The ratio of fertile, semi-sterile and sterile plants in the F_2 generation fitted well to segregation 9:6:1, respectively, suggesting complementary interaction of two genes controlling restoration of male fertility. The same segregation ratio was observed also in the F_2 from the cross [A4]Tx398/(KVV-97/Soriz) testifying to similarity of mechanisms of restoration of male fertility in the A4 and M35 cytoplasms (Table 1).

To obtain homozygous line-fertility restorer for the M35 cytoplasm, fertile plants from $F_2$and from subsequent generations of hybrid combination M 35-1A/KVV-97 were self-pollinated and crossed to the CMS-line [M35]Pishchevoye-614. However, four cycles of self-pollination and selection of the most fertile plants did not result in significant increase of percentage of plants with complete or partial (seed set >50%) male fertility (Table 2).

The comparison of variability of a level of male fertility in the testcrosses and in the self-pollinated progenies in different generations, with variation in these years of the sum of precipitations within 3 weeks prior to the beginning of anthesis, ie, during the period of anther and pollen formation, has allowed to find dependence of expression of fertility-restoring genes from water-providing of plants (Fig. 1). A strong positive correlation of percentage of fertile and partially fertile plants (with seed set >50%) in total sampling of the testcross hybrids, and the total sum of precipitations during 3 weeks before anthesis in these seasons (1995-2001) was found (r = 0,933±0,506; P >0,05). No influence of total sum of precipitations during the whole period from sowing to anthesis as well as of the temperature during microsporogenesis on male fertility of the testcross hybrids was observed.

Similar dependence of expression of fertility-restoring genes from artificial humidification during microsporogenesis was found in the F_1 hybrids in the A4 cytoplasm (Table 3). In a special experiment conducted in 2002, a drought year, F_1 hybrids that were obtained by crossing fertile plants from a population [A4]Tx398/(KVV-97/Soriz) with the CMS-line (A4]KVV-52 were grown at additional watering during microsporogenesis (50 L m^{-2}). In the control, the same hybrids were grown without watering. Significant augmentation of percentage of fertile and partially fertile plants under additional watering was observed.

These data testify to modifying influence of conditions of water-providing of plants during their generative development on an expression of fertility-restoring genes in the M35 and A4 CMS-inducing cytoplasms: either the expression of one of complementary

Table 1. Inheritance of male fertility restoration in the M35 and A4 CMS-inducing cytoplasms of sorghum.

Hybrid combination	Year	Number of plants[1] f	ss	s	Ratio	X^2	P
F_1M 35-1A/KVV-97	1993	2	0	12			
F_2M 35-1A/KVV-97	1994	31	25	5	9:6:1	0.955	0.50-0.25
F_1 [A4]Tx398/(KV V-97/Soriz)	1992	2	0	2			
F_2[A4]Tx398/(KVV-97/Soriz)	1997	20	11	4	9:6:1	1.856	0.25-0.10

1. f = fertile; ss = semi-sterile; and s = sterile.

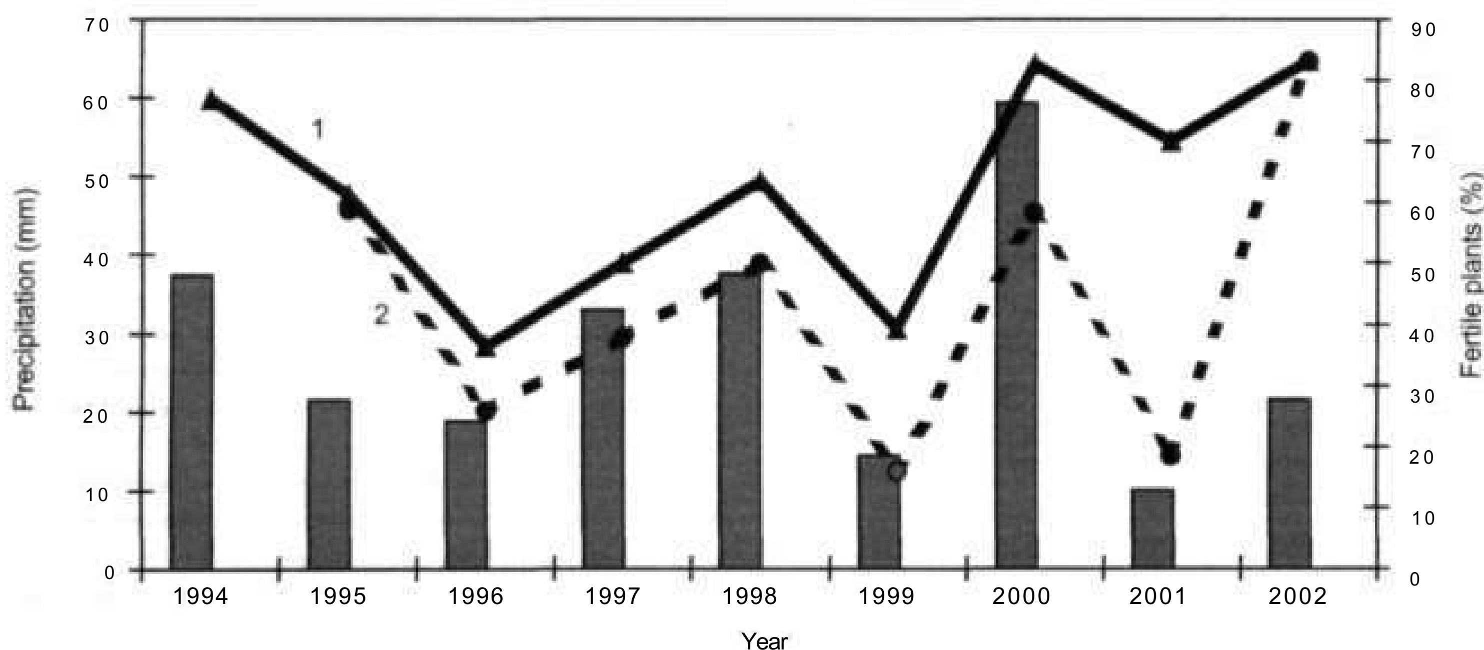

Figure 1. Variation of a level of male fertility in the self-pollinated progenies of selections on the M35 CMS-inducing cytoplasm (1) and in their testcross populations (2) and the sum of precipitations within 3 weeks prior to the beginning of anthesis in 1994-2002.

Table 2. Fertility of selections from sorghum populations M 35-1A/KVV-97 and [M 35]Pishchevoye-614/(M 35-1A/KVV-97) and its testcrosses *to* CMS-line [M35]Pishchevoye-614.

Year[1]	Hybrid combination	Number of plants	
		Total	Fertile and partially fertile[2]
Selections from population M 35-1-A/KVV-97			
1995 (-)	F_3	18	11 (61.1)
1996 (-)	F_4	13	5 (38.5)
1997 (+)	F,	13	7 (53.8)
1998 (+)	F_6	25	17 (68.0)
1999 (-)	F_7	25	14 (56.0)
Selection in the progeny of hybrid [M35]Pishchevoye-614/F_4(M 35-1A/KVV-97)			
2000 (+)	F_2	25	18 (72.0)
2001 (-)	F_3 (N 45)	19	16 (84.2)
2002 (-)	F_4(N 45-3)	10	8 (80.0)
Testcrosses of selection N 45 F_3[M 351Pishchevoye-6l4/F_4(M 35-1 A/KVV-97)			
2002 (-)	[M35]Pishchevoye-614/N 45-1	18	12 (66.7)
2002 (-)	[M35]Pishchevoye-614/N 45-2	25	23 (92.0)
2002 (-)	[M35]Pishchevoye-614/N 45-3	52	52 (100.0)
2002 (-)	[M35]Pishchevoye-614/N 45-4	8	8 (100.0)

1. Water-providing conditions during microsporogenesis: + = sufficient; and - = deficient.
2. With seed set level >50%; percentage values are given in parentheses.

Table 3. Influence of additional watering during microsporogenesis on male fertility of F_1 hybrids on the A4 cytoplasm, which were obtained by testcrossing fertile plants from population [A41Tx398/(KVV97/Soriz) (N58) to CMS-line [A4]KVV-52 in 2002[1].

Hybrid combination	Experimental variant	Number of plants	
		Total	Fertile and partially fertile[2]
F_1[A4]KVV-52/N58-1	Watering (50 L m''2)	34	6 (17.6)*
	Without watering	43	2 (4.7)
F_1[A4]KVV-52/ N 58-2	Watering (50 L m^{-2})	38	24 (63.2)*
	Without watering	48	14 (29.2)
F (experimental variants) 34.49*			
F(genotypes) 89.79*			

1. * = Significant at *P* <0.05.
2. Percentage values are given in parentheses.

genes-fertility restorers depends on action of this environmental factor, or this gene is linked to the gene-modifier changing a level of its expression in dependence from water-providing of plants. Probably, the synthesis of a product that is controlled by such a gene, which is necessary for a normal course of microsoporogenesis, considerably falls at deficiency of a moisture and thus, reduces a level of male fertility.

Assuming that expression of this modifier is most clearly observed in moisture-deficient conditions, we started selection of genotypes lacking this gene(s) during the most droughty season. In addition, to obtain such recombinants fertile selection from F_4 of M 35-1 A/KVV-97 was crossed to CMS-line [M35]Pishchevoye-614. In the progeny of this hybrid a selection N 45 has been revealed. During strict droughty conditions of 2001, 84%

of fertile plants were observed in the self-pollinated progeny of this selection (Table 2). In 2002, which was also characterized by strict drought during microsporogenesis, the percentage of fertile plants in this selection was 80%; its testcross populations with [M35]Pishchevoye-614 were also characterized by high level of male fertility.

Thus, as a result *of* genetic recombination and subsequent selection at regime of drought during microsporogenesis we could create reliable lines-fertility restorers capable for restoration of male fertility of the F_1 hybrids in the M35 cytoplasm under conditions of moisture deficiency.

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Sweet Sorghum: Characteristics and Potential

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Introduction

Sweet sorghum *(Sorghum bicolor)* is similar to common grain sorghum with a sugar-rich stalk. Sweet sorghum is characterized by wide adaptability, drought resistance, waterlogging tolerance, saline-alkali tolerance, rapid growth, high sugar accumulation, and biomass. Lengthy growing period and high water requirement are the disadvantages in sugarcane (*Saccharum officinarum*) and sugarbeet *(Beta vulgaris),* the main sources of sugar production in the world. These factors along with the comparative disadvantage of molasses (higher price, and water and air pollution) are expected to increase the interest in sweet sorghum. The water requirement of sugarcane is about 36000 m^3, which is double that of sugarbeet while that of sweet sorghum, due to its extensive root system and short growing period, is about 8000 m^3 (Soltani and Almodares 1994). Variability has been recorded in sweet sorghum for grain yield from 1.5 to 7.5 t ha^{-1}, for brix ranging from 13 to 24%, for sucrose from 7.2% to 15.5%, for stalk yield from 24 to 120 t ha^{-1} and for biomass yield from 36 to 140 t ha^{-1} (Almodares et al. 1997). Sweet sorghum has a biomass production capacity equal or superior to sugarcane in the tropics (Monk et al. 1984). Alcohol is produced at 6106 L ha^{-1} from sweet sorghum while only 4680 L ha^{-1} from sugarcane is produced. There are several advantages of using sweet sorghum instead of sugarcane for alcohol production. These are: sweet sorghum is harvested in four months (whereas, the first cut of sugarcane is 18 months after planting); sweet sorghum production can be completely mechanized; the crop can be established from seed; the grain may be used as either food or feed; the stillage from sweet sorghum has a higher biological value than the bagasse from sugarcane when used as forage for animals. Stillage obtained after extraction of juice from the stalks of sweet sorghum contains similar levels of cellulose as sugarcane bagasse; therefore, it has a good prospect as a raw material for pulp product. It could be processed as a feed for ruminant animals (Sumantri and Edi Purnomo 1997). Furthermore, it is rich in micronutrients and minerals (Seetharama et al. 2002). Singh and Singh (1986) reported that jaggery prepared from sweet sorghum juice contained 78.1% sucrose and 8.8% reducing sugars while that from sugarcane contained 84.2% sucrose and 7.5% reducing sugars. They also reported that starch in sweet sorghum juice, a major problem for sugar production, can be removed up to 93.7% with the use of flocculent truefloc S-3 (500 ppm) and by heating the juice to 55°C and adjusting its pH to 8.5. The quality of sorghum juice, sugarcane juice, and the mixed juice is given in Table 1. Cultivation of sweet sorghum will only lead to value addition and a shift in utilization and it will not hamper the grain (from panicle similar to grain sorghum) production.

Table 1. Comparative quality of juice of sweet sorghum and sugarcane[1].

Sample	Brix (%)	Purity (%)	Reducing sugar (% brix)	Starch (pprn)	Ash (%)
Sorghum juice	18.45	77.3	8.71	1685	1.26
Sugarcane juice	20.21	82.4	5.22	251	0.46
Mixed juice[2]	19.30	79.3	7.14	363	0.72

1. Adapted from Edi Purnomo and Sumantri (1997).
2. Sorghum juice and sugarcane juice mixed in the ratio of 1:5.

Programs

ICRISAT has initiated research, though limited, taking the future needs into consideration. Several programs (listed below) arc being taken up to accelerate the cultivation of sweet sorghum. Research in sweet sorghum is being carried out in several parts of the world lor different objectives as listed below:

ICRISAT:

- Development of ratoon and multicut high biomass yielding sweet sorghum lines.
- Development of ratoon and multicut dual purpose sweet sorghum lines.
- Development of ratoon and multicut sweet sorghum hybrid parental lines.

Worldwide programs:

- Breeding on grain and stalk, yield and quality characters of sweet sorghum (Romania, India, China, Indonesia, Greece, southern Italy, southern Spain, Pakistan, Argentina, Australia, Hungary, Zimbabwe).
- Exploitation of sweet sorghum in fodder sorghum breeding (China, Europe, India, Italy, Hungary).
- Studies on the effects of feeding sweet sorghum to livestock (China, India, Japan).
- Standardization of processing techniques for end products (India, China, Indonesia, Romania, Italy, Zambia, Egypt, France, Iran, London).
- Identification of cultivars desirable for development of end products (India, China, Italy, Ukraine).

Two major problems that occur during sweet sorghum production are the crop's sensitivity to chill and lodging of plants when mature. Ravi et al. (1997) reported that intermating sweet sorghum with grain sorghum having high stalk sugar content and stay green trait is likely to improve the grain productivity without affecting stalk sugar content. Sorghum stalks are ideal for ethanol production, as the ethanol from sorghum is significantly cleaner than that from sugarcane. Potable alcohol can also be produced from mold affected rainy season sorghum grain (Seetharama et al. 2002).

Products

The reasons for decline in the area under grain sorghum are: (1) progressively reducing per capita consumption of sorghum; and (2) absence of alternate demand for grain. Sweet sorghum is a multipurpose crop. Apart from grain and fodder, several alternate products such as forage/silage, syrup, jaggery, alcohol, fuel for bioenergy production, sugar, wine, vinegar, pulp and paper, sweetener and natural pigments (dark red color) can be made. Thus, it can create demand through value addition to the sorghum crop.

Potential

Sweet sorghum can produce from a single crop 3 t ha^{-1} grain, 2.03 t ha^{-1} sugar, white spirit (65% alcohol) 1.605 t ha^{-1} and vinegar 11.741 ha^{-1} (Liu Guifeng et al. 1997). Net income from sorghum is 38% higher than sugarbeet (Almodares and Sepahi 1997). Other products reported from sweet sorghum are:

Alcohol: 45.4 L of alcohol from one t of chopped stalk, 42.1 L from one t of shredded stalk, and 39.6 L from one t of juice extracted before fermentation is obtained (Charlie et al. 1983) or 2760 L ha^{-1} (Ravi et al. 1997). Somani and Pandrangi (1993) reported that 384 L of ethanol can be produced from one t of sorghum.

Sugar: 3.8 to 5.9 t ha^{-1}(Cosentino et al. 1997).

Biomass: 56.24 to 65.24 t ha^{-1} (Jingshan et al. 1997).

Wine: One hectare of sweet sorghum produces 3.24 t of malt sugar obtained after extracting crystal sugar, which produces 1.61 t of spirit (Liu Guifeng et al. 1997).

Vinegar: After refining sugar obtained from one ha of sweet sorghum, the remaining waste can be used to produce 1.74 t of vinegar (Liu Guifeng et al. 1997).

Silage: The effect of silage made of sweet sorghum is better than maize (*Zea mays):* 17.85 t ha^{-1} of silage is obtained. The output of milk is 65% more with a saving of 7% green forage compared to maize (Bolin 1997).

Energy production: Cultivation of approximately 250 ha of sweet sorghum would result in 500 kW_{el} power production (Chiaramonti and Taviani 1997).

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Grain Yield and Stover Fodder Value Relations in *Rabi* Sorghum

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Introduction

Both sorghum {Sorghum bicolor) grain and stover contribute to livelihoods of poor in India (Hall and Yogand 2000). Stover utilization as fodder can provide for up to 50% of the income from cropping (Rama Devi et al. 2000). In response to farmers' demand for sorghum stover with high fodder value new sorghum improvement programs aim at integrating stover value as an additional trait into sorghum breeding and selection. The success of this multidimensional sorghum improvement depends on two essential conditions: (1) genotypic variability for stover yield and quality is high enough to positively impact on on-farm fodder resources; and (2) relations between desirable traits, for example, grain yield and stover value (yield and quality) are clarified and traits are not, or at least not overly, competitive. These two conditions were found to hold widely true in sorghum grown in the rainy (*knarif*) season in India (Bliimmel et al. 2003) but little information is available about sorghum types grown under the more harsh conditions in the postrainy *(rabi)* season. This work investigates relationship

between grain yields and stover fodder value measurements in a total of 83 *rabi* sorghum varieties and hybrids in various stages of the All India Coordinated Sorghum Improvement Project.

Material and Methods

A total of 83 genotypes (49 varieties and 34 hybrids) of sorghum from the All India Coordinated Sorghum Improvement Project were investigated. These genotypes were grown in the *rabi* season 2002 at the University of Agricultural Sciences, Sorghum Research Scheme, Main Research Station in Dharwad, Karnataka, India using agreed standard agronomic practices for *rabi* sorghum in India. Stover quantity and quality estimates were based on five plants randomly collected from each of three field replications at harvest. Harvested net plot size per replication was 6.15 m^2 (gross plot size 18.1 m^2) and row distance was 0.45 m. Stover crude protein content and stover in vitro digestibility were investigated using combinations of conventional nutritional laboratory analysis with Near Infrared Spectroscopy (NIRS). For conventional analysis, nitrogen was determined by auto-analyzer and crude protein was calculated from nitrogen by multiplication with the factor of 6.25. In vitro digestibility was measured in rumen microbial inoculum using the in vitro gas production technique and equation described by Menke and Steingass (1988). NIRS (Instrument FOSS 5000 Forage Analyzer with WINSI II software package) blind prediction of crude protein and digestibility was based on 20 out of the 83 genotypes and the agreement between conventionally measured crude protein and in vitro digestibility and NIRS predicted values were R^2 = 0.91 [Standard Error of Prediction (SEP) = 0.66] and R^2 = 0.91 (SEP = 1.9), respectively.

Results and Discussion

Mean values of grain yield, stover yield, stover crude protein content, stover in vitro digestibility and digestible stover yield (the product of stover yield and in vitro digestibility) of sorghum genotypes in Initial Variety Trial I, Advanced Variety Trial I, Multi-Location Variety Trial I, Initial Hybrid Trial I and Multi-Location Hybrid Trials I and II are presented in Table 1. Mean grain yields in the advanced variety trial were similar to the grain yields observed in the multilocational hybrid trials indicating that varieties are not necessarily inferior to hybrids in terms of grain yield. On the other hand, varieties had a consistent advantage over hybrids in terms of stover yield, which was at least 15% above the stover yield observed in hybrids. The data suggest that currently bred *rabi* varieties have inherently better dual-purpose characteristics than currently bred *rabi* hybrids. Interestingly, the stover quality measurements crude protein and in vitro digestibility seem to decline with advancement of both varieties and hybrids in the releasing process. We therefore argue for further concerted action of sorghum breeders and animal nutritionists to include nutritional screening for stover value at a very early stage of the releasing process.

Ultimately, fodder value of stover will be a product of stover quantity and stover quality. In addition, price differences in sorghum stover trading are quality-dependent and can vary between Rs 1.30 and 2.80 kg^{-1} of stover. At the same time price of sorghum grain approximately ranged from Rs 3 to 5 kg^{-1} (Dayakar Rao 2000). Decisions about genotypes of sorghum to be released and promoted should be based on grain yield, stover yield and stover quality, and the respective income generated by these commodities in a given farming, feeding and fodder trading system.

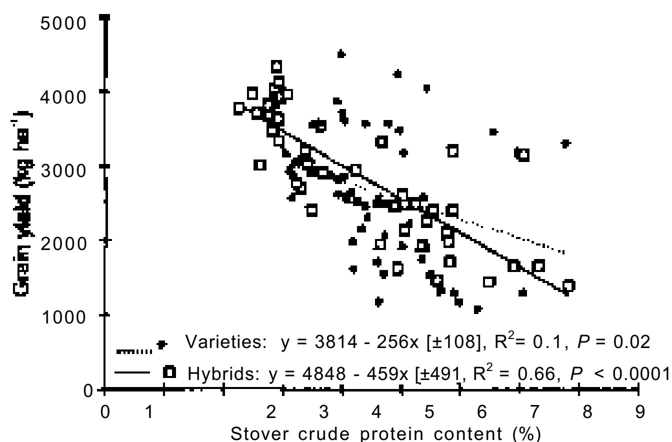

Figure 1. Relation between stover crude protein content and grain yield in 83 genotypes of rabi sorghum.

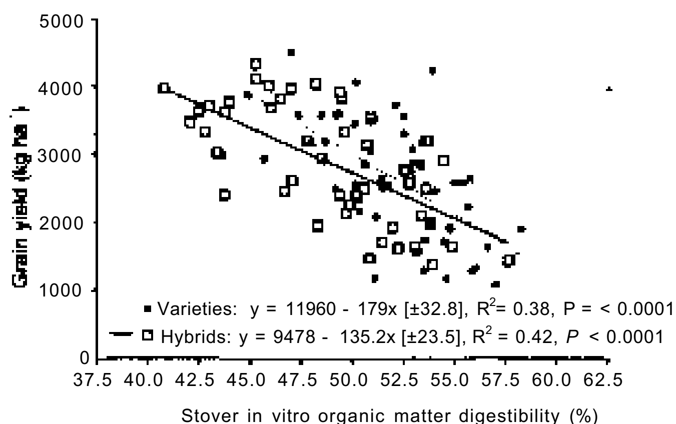

Figure 2. Relation between stover in vitro digestibility and grain yield in 83 genotypes of rabi *sorghum.*

While no trade-off effects between grain yield and stover yield and stover quality were observed for *kharif* season sorghum types (Blummel et al. 2003), in this work, stover crude protein content and in vitro digestibility were found to be significantly inversely related to grain yield in both varieties and hybrids, but with stronger associations observed for hybrids than for varieties (Figs. 1 and 2). Nevertheless, grain yields of about 4000 kg ha^{-1} could be associated with highly varying contents of crude protein (approximately 2.5 to 5.5%) and of about 14 units differences in in vitro digestibility (Figs. 1 and 2). Differences of this magnitude are highly relevant for fodder value and livestock productivity (Van Soest 1994). These findings show that considerable scope already exists for the selection of genotypes with higher stover value without sacrificing grain yields. No trade-off effects were observed between stover yield and stover crude protein content and in vitro digestibility, as these traits were positively associated (Figs. 3 and 4). It appears that seasonal effects in the postrainy season, perhaps moisture stress and associated limitations in nutrient supply, can arrest translocation of nutrients from the stem into the grain resulting in competition between grain and stover for crude protein and soluble carbohydrate. Arrested translocation of these will result in higher quality stover with the resultant reduction in grain yield.

Grain yield and stover yield were not significantly related (Fig. 5) and high grain and stover yield are not mutually exclusive traits. It is important to visualize that 1 ton of stover can be associated with an income of Rs 1300 to 2800, and stover yields in the high grain yielding genotypes (about 4000 kg ha^{-1}) could vary approximately from 3000 to 9000 kg ha^{-1} (Fig. 5). The potential revenues from these variations seem substantial. As mentioned previously, digestible stover yield is a nutritionally more meaningful measurement of stover value than total stover yield. It is encouraging that no significant competitive relationship was observed between digestible stover yield and grain yield (Fig. 6), even though the relationship approached (*P* = 0.09) significance level in the case of hybrids. At very high

Table 1. Mean grain yield (GY), stover yield (SY), stover crude protein content (CP), stover in vitro digestibility (!VD) and digestible stover yield (DSY) in sorghum varieties and hybrids in various stages of release screening[1].

Trial (n)	GY(kg ha^{-1})	SY(kg ha^{-1})	CP (%)	IVD (%)	DSY (kg ha^{-1})
Initial Variety 1 (20)	1849d(507)	6090c (1933)	5.1b (0.8)	54.1a (2.2)	3302b (1096)
Advanced Variety 1(18)	3345a (639)	8537a (2287)	4.9b (1.2)	49.9c (2.2)	4282a (1232)
Multi-Location Variety I (15)	2787b (599)	6712b (2125)	3.8c (0.7)	51.9b (2.7)	3500b (1174)
Initial Hybrid I (22)	2174c (571)	4896d (1384)	5.7a (0.9)	51.2b (2.7)	2515cd(783)
Multi-Location Hybrid 1(15)	3397a (580)	5225d (2294)	3.1d (0.5)	48.7d (3.8)	2617c(1316)
Multi-Location Hybrid II (12)	3561a (476)	5182d (2439)	3.0d(0.5)	44.7c (3.2)	2375d (1310)

1. Values followed by different letters in columns reflect significant differences (*P* <0.05).
Values in parentheses arc standard deviations.

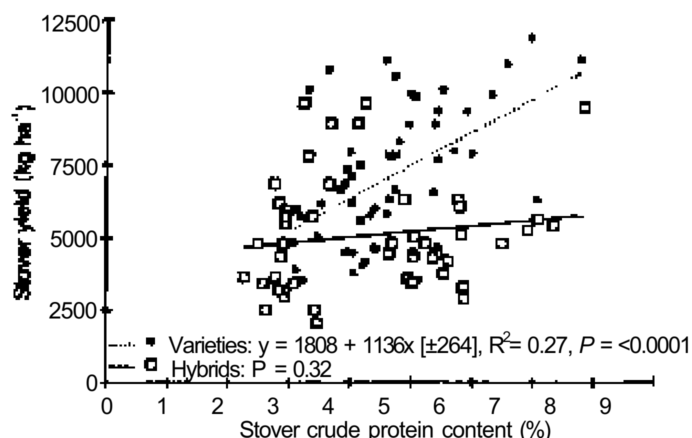

Figure 3. Relation between stover crude protein content and grain yield in 83 genotypes of rabi sorghum.

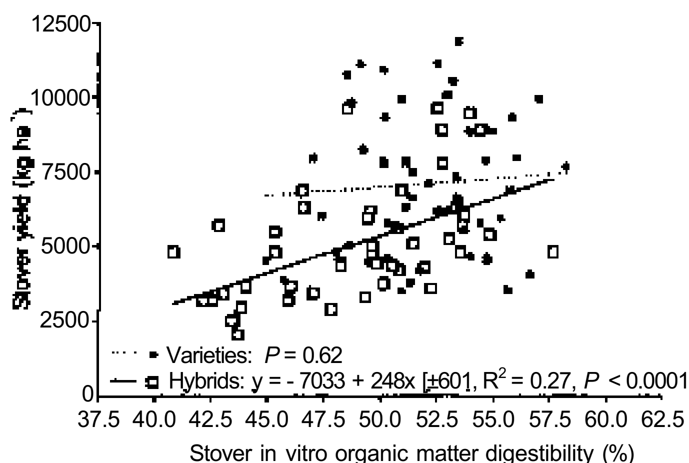

Figure 4. Relation between stover in vitro digestibility and grain stover yield in 83 genotypes of rabi sorghum.

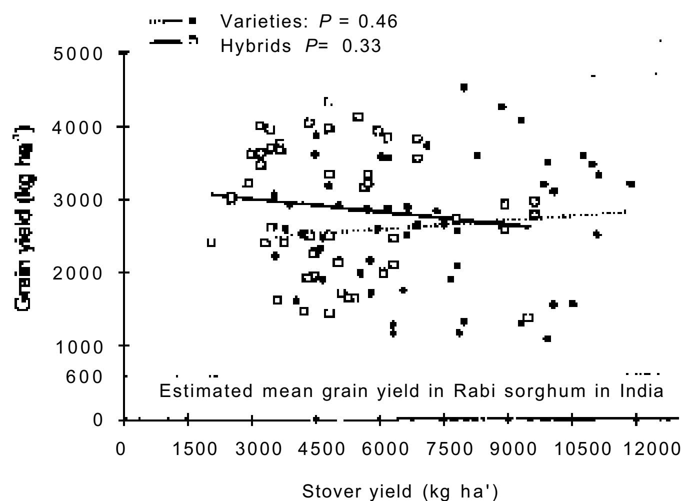

Figure 5. Relation between stover yield and grain yield in 83 genotypes of rabi *sorghum.*

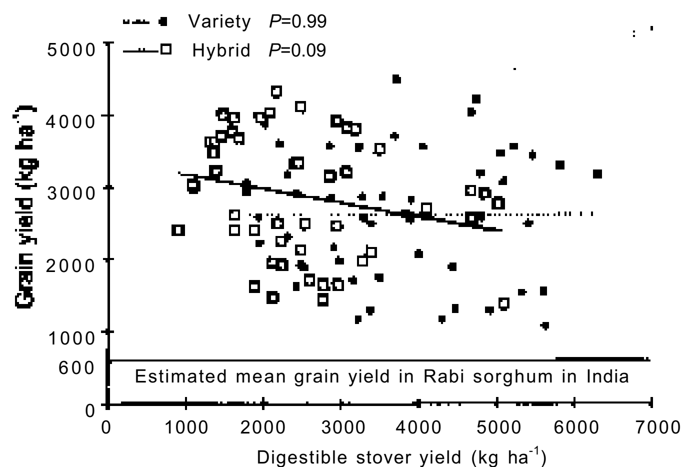

Figure 6. Relation between digestible stover yield and grain yield in 83 genotypes of rabi *sorghum.*

grain yields (about 4000 kg ha^{-1}), digestible stover yields could differ from about 2000 to 5000 kg ha^{-1} and from 1500 to 3000 kg ha^{-1} in varieties and hybrids, respectively. At low grain yields of about 1500 kg ha^{-1}, which is much closer even though still above the current average *rabi* yields of about 600 kg ha ' in India (Dayakar Rao 2000), digestible stover yields varied from approximately 2500 to 5500 kg ha^{-1} and from 2000 to 5000 kg ha^{-1} in varieties and hybrids, respectively. These findings suggest that genotypic variations in stover value may already be exploited under the lower levels of grain production often prevalent in smallholder crop-livestock systems.

Conclusions

The stover quality traits crude protein content and in vitro digestibility in *rabi* sorghum were significantly inversely associated with grain yield in varieties as well as in hybrids. The inverse associations between stover quality traits and grain yield might be due to severe competition for protein and carbohydrates under most commonly observed water stress in *rabi* season growing conditions. More work is required to investigate grain-stover relationships under on-farm conditions where water and nutrient inputs tend to be more restricted than in experimental fields of crop improvement programs. Nevertheless, genotypes do already exist that provide substantially higher digestible stover yield than others under diverse levels of grain production.

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Registration of Sorghum Cultivars, Germplasm, Genetic Stock and Parental Lines in the United States from 1936 through 2003

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The United States began registering cultivars in 1926, followed by parental lines and elite germplasm in 1966, genetic stocks in 1988 and mapping populations in 2000. The word 'cultivar' is derived from a contraction of the words cultivated variety. Cultivar can be defined as a plant that is valuable in agriculture and that is propagated with little or no genetic change in its offspring (Hartmann et al. 1981). The Crop Science Society of America further elaborates through the following statement: "The terms cultivar and variety are synonymous as applied to names of cultivated plants, but cultivar is strongly preferred, to avoid confusing cultivated variety (a term of convenience) with botanical variety (a subtaxon to species)" (ASA, CSSA, SSSA 1998). Germplasm as it is used in the registration process may be defined as any plant material that has some known genetic value. This may be a cultivar or selection from a breeding population that has been identified through observation or screening to have a unique genotype. Genetic stocks have been defined by the US National Plant Germplasm System as: "These accessions have unique mutant genes, groups of genes, or gene deletions or duplications; interchanged or translocated chromosomes, where two distinct chromosomes had broken and the parts of each were then interchanged; and chromosomes with portions that are inverted. Some of the stocks may have duplicate or deleted chromosomes or may represent genetically distinct cytoplasms" (National Research Council 1991). Finally, parental lines are defined as breeding lines from which a parent of a cross or hybrid is taken.

Since 1936, the United States has registered 1197 sorghums, broomcorns, sudangrasses and other sorghum grasses either as cultivars, germplasm, genetic stocks or parental lines. The first sorghums were registered in the Journal of American Society of Agronomy in 1936 as cultivars (Table 1). The Agronomy Journal took over responsibility of registration of sorghums in 1949 and finally Crop Science became the official journal of registration for sorghum in 1963. Beginning in 1936, 135 sorghums have been registered as cultivars, with the last registration occurring in 1998. Sorghum germplasm was first registered in 1972 and since then 609 sorghums have

Table 1. Cultivar name, registration number and year, designation and source of sorghums registered as cultivars since 1936 in USA.

Cultivar name	Registration No.	Registration Year	Designation	Source
White Durra	CV-1	1936	CIso 938	Journal of American Society of Agronomy 28(12): 1027
Dwarf White Durra	CV-2	1936	CIso 946	Journal of American Society of Agronomy 28(12): 1027
Brown Durra	CV-3	1936	NSL 3929	Journal of American Society of Agronomy 28(12): 1027
Standard Feterita	CV-4	1936	PI 19517	Journal of American Society of Agronomy 28(12): 1027
Spur Feterita	CV-5	1936	CIso 623	Journal of American Society of Agronomy 28(12): 1027
Dwarf Feterita	CV-6	1936	NSL 3932	Journal of American Society of Agronomy 28(12): 1027
Hegari	CV-7	1936	PI 61455	Journal of American Society of Agronomy 28(12): 1027
Chiltex	CV-8	1936	NSL 3934	Journal of American Society of Agronomy 28(12): 1027
Premo	CV-9	1936	NSL 3935	Journal of American Society of Agronomy 28(12): 1027
Ajax	CV-10	1936	NSL 3936	Journal of American Society of Agronomy 28(12): 1027
Wonder	CV-11	1936	NSL 3937	Journal of American Society of Agronomy 28(12): 1027
Standard Blackhull Kafir	CV-12	1936	CIso 71	Journal of American Society of Agronomy 28(12): 1027
Dwarf Blackhull Kafir	CV-13	1936	CIso 204	Journal of American Society of Agronomy 28(12): 1027
Western Blackhull Kafir	CV-14	1936	NSL 3940	Journal of American Society of Agronomy 28(12): 1027
Texas Blackhull Kafir	CV-15	1936	CIso 865	Journal of American Society of Agronomy 28(12): 1027
Sunrise Kafir	CV-16	1936	PI 32707	Journal of American Society of Agronomy 28(12): 1027
Dawn Kafir	CV-17	1936	CIso 904	Journal of American Society of Agronomy 28(12): 1027
Reed Kafir	CV-18	1936	CIso 628	Journal of American Society of Agronomy 28(12): 1027
Pearl Kafir	CV-19	1936	NSL 3945	Journal of American Society of Agronomy 28(12): 1027
Rice Kafir	CV-20	1936	NSL 3946	Journal of American Society of Agronomy 28(12): 1027

continued

Table 1. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
White Kafir	CV-21	1936	PI 48770	Journal of American Society of Agronomy 28(12): 1027
Pink Kafir	CV-22	1936	CIso 432	Journal of American Society of Agronomy 28(12): 1027
Red Kafir	CV-23	1936	CIso 957	Journal of American Society of Agronomy 28(12): 1027
Manchu Brown Kaoliang	CV-24	1936	PI 18518	Journal of American Society of Agronomy 28(12): 1027
Standard Yellow Milo	CV-25	1936	PI 24960	Journal of American Society of Agronomy 28(12): 1027
Dwarf Yellow Milo	CV-26	1936	PI 24969	Journal of American Society of Agronomy 28(12): 1027
Double Dwarf Yellow Milo	CV-27	1936	CIso 868	Journal of American Society of Agronomy 28(12): 1027
Standard White Milo	CV-28	1936	CIso 352	Journal of American Society of Agronomy 28(12): 1027
Dwarf White Milo	CV-29	1936	NSL 3955	Journal of American Society of Agronomy 28(12): 1027
Early White Milo	CV-30	1936	NSL 3956	Journal of American Society of Agronomy 28(12): 1027
Beaver	CV-31	1936	CIso 871	Journal of American Society of Agronomy 28(12): 1027
Wheatland	CV-32	1936	CIso 918	Journal of American Society of Agronomy 28(12): 1027
Fargo	CV-33	1936	CIso 809	Journal of American Society of Agronomy 28(12): 1027
Manko	CV-34	1936	NSL 3960	Journal of American Society of Agronomy 28(12):1027
Desert Bishop	CV-35	1936	CIso 870	Journal of American Society of Agronomy 28(12): 1027
Bishop	CV-36	1936	CIso 814	Journal of American Society of Agronomy 28(12): 1027
Shallu	CV-37	1936	CIso 85	Journal of American Society of Agronomy 28(12): 1027
Freed	CV-38	1936	PI 29166	Journal of American Society of Agronomy 28(12): 1027
Dwarf Freed	CV-39	1936	NSL 3965	Journal of American Society of Agronomy 28(12): 1027
Grohoma	CV-40	1936	NSL 3966	Journal of American Society of Agronomy 28(12): 1027
Darso	CV-41	1936	CIso 615	Journal of American Society of Agronomy 28(12): 1027
Schrock	CV-42	1936	CIso 616	Journal of American Society of Agronomy 28(12): 1027
Sumac	CV-43	1936	PI 35038	Journal of American Society of Agronomy 28(12): 1027
Early Sumac	CV-44	1936	NSL 3970	Journal of American Society of Agronomy 28(I2):1027
Chinese Amber	CV-45	1936	PI 22913	Journal of American Society of Agronomy 28(12): 1027
Minnesota Amber	CV-46	1936	NSL 3972	Journal of American Society of Agronomy 28(12): 1027
Waconia Amber	CV-47	1936	NSL 3973	Journal of American Society of Agronomy 28(12): 1027
Dakota Amber	CV-48	1936	NSL 3974	Journal of American Society of Agronomy 28(12): 1027
Red Amber	CV-49	1936	PI 17548	Journal of American Society of Agronomy 28(12):1027
Orange	CV-50	1936	NSL 3976	Journal of American Society of Agronomy 28(12): 1027
Kansas Orange	CV-51	1936	NSL 3977	Journal of American Society of Agronomy 28(12): 1027
Colman	CV-52	1936	NSL 3978	Journal of American Society of Agronomy 28(12): 1027
Honey	CV-53	1936	NSL 4030	Journal of American Society of Agronomy 28(12): 1027
Sourless	CV-54	1936	NSL 3979	Journal of American Society of Agronomy 28(12): 1027
Sapling	CV-55	1936	NSL 3980	Journal of American Society of Agronomy 28(12): 1027
Planter	CV-56	1936	NSL 3981	Journal of American Society of Agronomy 28(12): 1027
Gooseneck	CV-57	1936	NSL 3982	Journal of American Society of Agronomy 28(12): 1027
Leoti	CV-58	1936	NSL 3983	Journal of American Society of Agronomy 28(12): 1027
Folger	CV-59	1936	NSL 3984	Journal of American Society of Agronomy 28(12): 1027
White African	CV-60	1936	NSL 3985	Journal of American Society of Agronomy 28(12): 1027
Atlas	CV-61	1936	NSL 3986	Journal of American Society of Agronomy 28(12): 1027
Mclean	CV-62	1936	NSL 3987	Journal of American Society of Agronomy 28(12): 1027
Rex	CV-63	1936	NSL 3988	Journal of American Society of Agronomy 28(12): 1027
Collier	CV-64	1936	NSL 3989	Journal of American Society of Agronomy 28(12): 1027
Denton	CV-65	1936	NSL 3990	Journal of American Society of Agronomy 28(12): 1027
Sugar Drip	CV-66	1936	NSL 3991	Journal of American Society of Agronomy 28(12): 1027
Evergreen	CV-67	1936	CIso 556	Journal of American Society of Agronomy 28(12): 1027
Black Spanish	CV-68	1936	CIso 827	Journal of American Society of Agronomy 28(12): 1027
California Golden	CV-69	1936	CIso 580	Journal of American Society of Agronomy 28(12): 1027
Evergreen Dwarf	CV-70	1936	CIso 243	Journal of American Society of Agronomy 28(12): 1027
Scarborough	CV-71	1936	NSL 3995	Journal of American Society of Agronomy 28(12): 1027
Japanese Dwarf	CV-72	1936	PI 30204	Journal of American Society of Agronomy 28(12): 1027
Black Spanish Dwarf	CV-73	1936	CSR 213	Journal of American Society of Agronomy 28(12):1027

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Table 1. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
Club	CV-74	1938	NSL 3997	Journal of American Society of Agronomy 30(4):306
Finney Milo	CV-75	1938	NSL 3998	Journal of American Society of Agronomy 30(4):306
Early Kalo	CV-76	1938	NSL 3999	Journal of American Society of Agronomy 30(4):306
Coes	CV-77	1941	NSL 4000	Journal of American Society of Agronomy 33(3):257
Highland	CV-78	1941	NSL 4001	Journal of American Society of Agronomy 33(3):257
Norkan	CV-79	1942	NSL 4002	Journal of American Society of Agronomy 34(3):280
Westland	CV-80	1944	NSL 4003	Journal of American Society of Agronomy 36(5):453
Midland	CV-81	1949	NSL 4004	Agronomy Journal 41(11):536
Cody	CV-82	1949	NSL 4005	Agronomy Journal 41(11):536
Texas Milo	CV-83	1949	NSL 4006	Agronomy Journal 41(11):536
Sooner Milo No. 8	CV-84	1949	NSL 4007	Agronomy Journal 41(11):536
Bonita	CV-85	1949	NSL 4008	Agronomy Journal 41(11):536
Early Hegari	CV-86	1949	NSL 4009	Agronomy Journal 41(11):536
Plainsman	CV-87	1949	NSL 4010	Agronomy Journal 41(11):536
Caprock	CV-88	1949	NSL 4011	Agronomy Journal 41(11):536
Martin	CV-89	1949	NSL 4012	Agronomy Journal 41(11):536
Double Dwarf White Sooner Milo	CV-90	1949	NSL 4013	Agronomy Journal 41(11):536
Double Dwarf Yellow Sooner Milo	CV-91	1949	NSL 4014	Agronomy Journal 41(11):536
Sweet Sudan	CV-92	1949	NSL 4015	Agronomy Journal 41(11):536
Rancher	CV-93	1949	NSL 4016	Agronomy Journal 41(11):536
Ellis	CV-94	1949	NSL 4017	Agronomy Journal 41(11):536
Tift	CV-95	1951	NSL 4018	Agronomy Journal 43(5):243
Sart	CV-96	1953	NSL 4019	Agronomy Journal 45(7):322
Combine Kafir-60	CV-97	1953	NSL 4020	Agronomy Journal 45(7):322
Redbine-60	CV-98	1953	NSL 4021	Agronomy Journal 45(7):322
Redbine-66	CV-99	1953	NSL 4022	Agronomy Journal 45(7):322
Hi-hegari	CV-100	1953	NSL 4023	Agronomy Journal 45(7):322
Popsorghum	CV-101	1953	PI 584989	Agronomy Journal 45(7):322
Redlan	CV-102	1954	NSL 4025	Agronomy Journal 46(11):526
Dwarf Kafir 44-14	CV-103	1954	NSL 4026	Agronomy Journal 46(11):526
Darset	CV-104	1954	NSL 4027	Agronomy Journal 46(11):526
Greenleaf	CV-105	1955	NSL 4028	Agronomy Journal 47(11):540
Tracy	CV-106	1955	NSL 4029	Agronomy Journal 47(11):540
Wiley	CV-107	1960	NSL 40377	Agronomy Journal 52(11):666
Lahoma	CV-108	1960	CSR 214	Agronomy Journal 52(11):666
Brawley	CV-109	1960	NSL 4346	Agronomy Journal 52(11):666
Suhi-1	cv-no	1963	CSR 215	Crop Science 3(4):367
Georgia 337	CV-111	1964	NSL 4857	Crop Science 4(6):666
Meloland	CV-112	1972	PI 540514	Crop Science 12(3):395
Rio	CV-113	1972	NSL 40230	Crop Science 12(5):716
Dale	CV-114	1973	NSL 74333	Crop Science 13(6):776
Piper	CV-115	1973	NSL 4434	Crop Science 13(5):584
Brandes	CV-116	1974	NSL 29336	Crop Science 14(3):494
Theis	CV-117	1978	CSR 216	Crop Science 18(1): 165
Ramada	CV-118	1980	NSL 107377	Crop Science 20(5):672
Wray	CV-119	1981	NSL 117772	Crop Science 21(6):987
Keller	CV-120	1982	NSL 165819	Crop Science 22(6): 1263
M 81E	CV-121	1983	NSL 174431	Crop Science 23(5): 1013
Wgf	CV-122	1984	NSL 80335	Crop Science 24(3):620
Bailey	CV-123	1984	NSL 187557	Crop Science 24(5):997
Cowley	CV-124	1985	NSL 189405	Crop Science 25(1):200
ICSV 197	CV-125	1987	PI 509071	Crop Science 27(6): 1312
Grassl	CV-126	1988	PI 154844	Crop Science 28(1): 194

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Table 1. ***continued.***

	Registration			
Cultivar name	No.	Year	Designation	Source
Smith	CV-127	1988	PI 511355	Crop Science 28(1): 195
ICSV 145	CV-128	1989	PI 522247	Crop Science 29(2):488
Sureno	CV-129	1993	PI 561472	Crop Science 33(1):213
Delia	CV-130	1993	PI 566819	Crop Science 33(6): 1416
TOP 76-6	CV-131	1994	PI 583832	Crop Science 35(4): 1213
Millo Blanco	CV-132	1996	PI 550725	Crop Science 36 (5): 1406
ICSV 111	CV-133	1998	PI 601815	GRIN[1]
ICSV 400	CV-134	1998	PI 601816	GRIN[1]
S-35	CV-135	1998	PI 602982	GRIN[1]

1. USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network (GRIN). (Online Database] National *Germplasm Resources* Laboratory, *Beltsville,* Maryland, *USA. Available: http.//www.ars-grin.gov/cgi-bin/npgs/html/acchtml.pl*?1555263 (09 October 2003).

Table 2. Cultivar name, registration number and year, designation and source of sorghums registered as germplasm since 1972 in USA.

	Registration			
Germplasm name	No.	Year	Designation	Source
KS30	GP-1	1972	NSL 110183	Crop Science 12(5):719
KS41	GP-2	1972	NSL 110187	Crop Science 12(5):720
KS42	GP-3	1972	NSL 110188	Crop Science 12(5):720
KS43	GP-4	1972	NSL 110189	Crop Science 12(5):720
KS44	GP-5	1972	NSL 110190	Crop Science 12(5):720
KS31	GP-6	1972	NSL 110184	Crop Science 12(5):720
KS32	GP-7	1972	NSL 110185	Crop Science I2(5):720
KS33	GP-8	1972	NSL 110186	Crop Science 12(5):720
KS34	GP-9	1972	NSL 109740	Crop Science 12(5):720
KS35	GP-10	1972	NSL 109742	Crop Science 12(5):720
KS36	GP-11	1972	NSL 109744	Crop Science 12(5):720
KS37	GP-12	1972	NSL 109746	Crop Science 12(5):720
KS38	GP-13	1972	NSL 109748	Crop Science 12(5):720
KS39	GP-14	1972	NSL 109750	Crop Science 12(5):720
KS40	GP-15	1972	NSL 109753	Crop Science 12(5):720
NP1BR	GP-16	1973	NSL 109754	Crop Science 13(1): 132
NP2B	GP-17	1973	NSL 109755	Crop Science 13(1): 132
NP3R	GP-18	1973	NSL 109756	Crop Science 13(1): 132
SGIRL-MR-1	GP-19	1973	PI 552818	Crop Science 13(3):398
PR 1BR	GP-20	1976	CSR 217	Crop Science 16(3):447
KP6BR	GP-21	1976	CSR 218	Crop Science I6(3):448
KS58	GP-22	1977	CSR 219	Crop Science)7(3):486
KS59	GP-23	1977	CSR 220	Crop Science I7(3):486
KS60	GP-24	1977	CSR 221	Crop Science 17(3):486
KS61	GP-25	1977	CSR 222	Crop Science 17(3):486
KS62	GP-26	1977	CSR 223	Crop Science 17(3):486
KS63	GP-27	1977	CSR 224	Crop Science I7(3):486
KS64	GP-28	1977	CSR 225	Crop Science I7(3):486
TP11R	GP-29	1977	NSL 106599	Crop Science 17(4):676
A2Tx2753	GP-30	1977	NSL 92621	Crop Science 17(6):983
BTx2753	GP-31	1977	NSL 92622	Crop Science 17(6):983

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Table 2. *continued.*

Germplasm name	Registration No.	Year	Designation	Source
RP1R	GP-32	1977	NSL 109757	Crop Science 17(6):983
RP2B	GP-33	1977	NSL 109758	Crop Science 17(6):983
RSP3BR	GP-34	1979	CSR 226	Crop Science 19(2):300
N!	GP-35	1979	P1 552819	Crop Science 19(3):420
N2	GP-36	1979	PI 552820	Crop Science 19(3):420
N3	GP-37	1979	PI 552821	Crop Science 19(3):420
N4	GP-38	1979	PI 552822	Crop Science 19(3):420
N5	GP-39	1979	PI 552823	Crop Science 19(3):420
N6	GP-40	1979	PI 552824	Crop Science 19(3):420
N7	GP-41	1979	PI 552825	Crop Science 19(3):420
N8	GP-42	1979	PI 552826	Crop Science 19(3):420
N9	GP-43	1979	PI 552827	Crop Science 19(3):420
N10	GP-44	1979	PI 552828	Crop Science 19(3):420
N11	GP-45	1979	PI 552829	Crop Science 19(3):420
N12	GP-46	1979	P1 552830	Crop Science 19(3):420
N13	GP-47	1979	PI 552831	Crop Science 19(3):420
N14	GP-48	1979	PI 552832	Crop Science 19(3):420
N15	GP-49	1979	PI 552833	Crop Science 19(3):420
N16	GP-50	1979	PI 552834	Crop Science 19(3):420
N17	GP-51	1979	P1 552835	Crop Science 19(3):420
N18	GP-52	1979	P1 552836	Crop Science 19(3):420
N19	GP-53	1979	PI 552837	Crop Science 19(3):420
N20	GP-54	1979	PI 552838	Crop Science 19(3):420
N21	GP-55	1979	PI 552839	Crop Science 19(3):420
N22	GP-56	1979	PI 552840	Crop Science 19(3):420
N23	GP-57	1979	PI 552841	Crop Science 19(3):420
N24	GP-58	1979	PI 552842	Crop Science 19(3):420
N25	GP-59	1979	PI 552843	Crop Science 19(3):420
N26	GP-60	1979	PI 552844	Crop Science 19(3):420
N27	GP-61	1979	PI 552845	Crop Science 19(3):420
N28	GP-62	1979	PI 552846	Crop Science 19(3):420
N29	GP-63	1979	PI 552847	Crop Science 19(3):420
83E	GP-64	1980	NSL 107353	Crop Science 20(5):676
97E	GP-65	1980	NSL 107355	Crop Science 20(5):676
68009	GP-66	1980	NSL 107357	Crop Science 20(5):676
68027	GP-67	1980	NSL 107359	Crop Science 20(5):676
68181	GP-68	1980	NSL 107361	Crop Science 20(5):676
IAPIR(M)C4	GP-69	1980	P1 561811	Crop Science 20(5):676
A2TAM428	GP-70	1981	NSL 113820	Crop Science 21(1): 148
B2TAM428	GP-70	1981	NSL 113821	Crop Science 21(1): 148
A2Tx624	GP-71	1981	NSL 113822	Crop Science 21(1): 148
B2Tx624	GP-71	1981	NSL 113823	Crop Science 21(1): 148
A2Tx2788	GP-72	1981	NSL 113824	Crop Science 21(1): 148
B2Tx2788	GP-72	1981	NSL 113825	Crop Science 21(1): 148
GPIR	GP-73	1981	NSL 114678	Crop Science 21(4):637
IAP3BR(M)C3	GP-74	1982	PI 561812	Crop Science 22(1): 165
TAM2566	GP-75	1982	CSR 227	Crop Science 22(6): 1271
TAM2567	GP-76	1982	CSR 228	Crop Science 22(6): 1271
TAM2568	GP-77	1982	CSR 229	Crop Science 22(6): 1271
ISRI	GP-78	1982	CSR 230	Crop Science 22(6): 1271
Tx2734	GP-79	1982	CSR 231	Crop Science 22(6): 1272
Tx2735	GP-80	1982	CSR 232	Crop Science 22(6): 1272
Tx2736	GP-81	1982	CSR 233	Crop Science 22(6): 1272

continued

Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
Tx2737	GP-82	1982	CSR 234	Crop Science 22(6): 1272
Tx2738	GP-83	1982	CSR 235	Crop Science 22(6): 1272
Tx2739	GP-84	1982	CSR 236	Crop Science 22(6): 1272
Tx2740	GP-85	1982	CSR 237	Crop Science 22(6): 1272
Tx2741	GP-86	1982	CSR 238	Crop Science 22(6): 1272
Tx2742	GP-87	1982	CSR 239	Crop Science 22(6): 1272
Tx2743	GP-88	1982	CSR 240	Crop Science 22(6): 1272
Tx2744	GP-89	1982	CSR 241	Crop Science 22(6): 1272
Tx2745	GP-90	1982	CSR 242	Crop Science 22(6): 1272
Tx2746	GP-91	1982	CSR 243	Crop Science 22(6): 1272
Tx2747	GP-92	1982	CSR 244	Crop Science 22(6): 1272
Tx2748	GP-93	1982	CSR 245	Crop Science 22(6): 1272
Tx2749	GP-94	1982	CSR 246	Crop Science 22(6): 1272
Tx2750	GP-95	1982	CSR 247	Crop Science 22(6): 1272
Tx2751	GP-96	1982	CSR 248	Crop Science 22(6): 1272
Tx2752	GP-97	1982	CSR 249	Crop Science 22(6): 1272
Tx2754	GP-98	1982	CSR 250	Crop Science 22(6): 1273
Tx2755	GP-99	1982	CSR 251	Crop Science 22(6): 1273
Tx2756	GP-100	1982	CSR 252	Crop Science 22(6): 1273
Tx2757	GP-101	1982	CSR 253	Crop Science 22(6): 1273
Tx2758	GP-102	1982	CSR 254	Crop Science 22(6): 1273
Tx2759	GP-103	1982	CSR 255	Crop Science 22(6): 1273
Tx2760	GP-104	1982	CSR 256	Crop Science 22(6): 1273
Tx2761	GP-105	1982	CSR 257	Crop Science 22(6): 1273
Tx2762	GP-106	1982	CSR 258	Crop Science 22(6): 1273
Tx2763	GP-107	1982	CSR 259	Crop Science 22(6): 1273
Tx2764	GP-108	1982	CSR 260	Crop Science 22(6): 1273
Tx2765	GP-109	1982	CSR 261	Crop Science 22(6): 1273
Tx2766	GP-110	1982	CSR 262	Crop Science 22(6): 1273
Tx2767	GP-111	1982	CSR 263	Crop Science 22(6): 1273
Tx2768	GP-112	1982	CSR 264	Crop Science 22(6): 1273
Tx2769	GP-113	1982	CSR 265	Crop Science 22(6): 1273
Tx2770	GP-114	1982	CSR 266	Crop Science 22(6): 1273
Tx2771	GP-115	1982	CSR 267	Crop Science 22(6): 1273
Tx2772	GP-116	1982	CSR 268	Crop Science 22(6): 1273
Tx2773	GP-117	1982	CSR 269	Crop Science 22(6): 1273
Tx2774	GP-118	1982	CSR 270	Crop Science 22(6): 1273
Tx2775	GP-119	1982	CSR 271	Crop Science 22(6): 1273
Tx2776	GP-120	1982	CSR 272	Crop Science 22(6): 1273
Tx2777	GP-121	1982	CSR 273	Crop Science 22(6): 1273
Tx2778	GP-122	1982	CSR 274	Crop Science 22(6): 1273
Tx2779	GP-123	1982	CSR 275	Crop Science 22(6): 1273
Tx2780	GP-124	1982	CSR 276	Crop Science 22(6): 1273
Tx2781	GP-125	1982	CSR 277	Crop Science 22(6): 1273
TAM Bk 41	GP-126	1982	CSR 278	Crop Science 22(6): 1273
TAM Bk 42	GP-127	1982	CSR 279	Crop Science 22(6): 1273
TAM Bk 43	GP-128	1982	CSR 280	Crop Science 22(6): 1273
TAM Bk 44	GP-129	1982	CSR 281	Crop Science 22(6): 1273
GPT2RB	GP-130	1982	NSL 165124	Crop Science 22(6): 1274
IAP2B(M)C3	GP-131	1982	PI 561813	Crop Science 22(6): 1275
Tx2784	GP-132	1983	NSL 176214	Crop Science 23(2):405
Tx2785	GP-133	1983	CSR 282	Crop Science 23(2):405
AZ9504	GP-134	1983	NSL 74322	Crop Science 23(3):601

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Table 2. *continued.*

Germplasm name	Registration No.	Year	Designation	Source
PR5BR	GP-135	1984	PI 603812	Crop Science 24(3):627
Tx2782	GP-136	1984	NSL 183030	Crop Science 24(2):389
Tx2783	GP-137	1984	NSL 183031	Crop Science 24(2):390
NP22	GP-138	1984	NSL 180066	Crop Science 24(2):391
SGIRL-MR-2	GP-139	1984	NSL 183543	Crop Science 24(3):627
83BL2080	GP-140	1984	NSL 185477	Crop Science 24(5): 1006
83BL2089	GP-141	1984	NSL 185478	Crop Science 24(5): 1006
83BL2104	GP-I42	1984	NSL 185479	Crop Science 24(5): 1006
IAP5R(M)C3	GP-143	1984	PI 561837	Crop Science 24(6): 1219
Tx2801	GP-144	1985	CSR 283	Crop Science 25(2):372
Tx2802	GP-145	1985	CSR 284	Crop Science 25(2):372
Tx2803	GP-146	1985	CSR 285	Crop Science 25(2):372
Tx28()4	GP-147	1985	CSR 286	Crop Science 25(2):372
Tx2805	GP-148	1985	CSR 287	Crop Science 25(2):372
Tx2806	GP-149	1985	CSR 288	Crop Science 25(2):372
Tx2807	GP-150	1985	CSR 289	Crop Science 25(2):372
Tx2808	GP-151	1985	CSR 290	Crop Science 25(2):372
Tx2809	GP-152	1985	CSR 291	Crop Science 25(2):372
Tx2810	GP-153	1985	CSR 292	Crop Science 25(2):372
Tx2811	GP-154	1985	CSR 293	Crop Science 25(2):372
Tx2812	GP-155	1985	CSR 294	Crop Science 25(2):372
Tx2813	GP-156	1985	CSR 295	Crop Science 25(2):372
Tx2814	GP-157	1985	CSR 296	Crop Science 25(2):372
Tx2815	GP-158	1985	CSR 297	Crop Science 25(2):372
Tx2789	GP-159	1985	CSR 298	Crop Science 25(2):373
Tx2790	GP-160	1985	CSR 299	Crop Science 25(2):373
Tx2791	GP-161	1985	CSR 300	Crop Science 25(2):373
Tx2792	GP-162	1985	CSR 301	Crop Science 25(2):373
Tx2793	GP-163	1985	CSR 302	Crop Science 25(2):373
Tx2794	GP-164	1985	CSR 303	Crop Science 25(2):373
Tx2795	GP-165	1985	CSR 304	Crop Science 25(2):373
Tx2796	GP-166	1985	CSR 305	Crop Science 25(2):373
Tx2797	GP-167	1985	CSR 306	Crop Science 25(2):373
Tx2798	GP-168	1985	CSR 307	Crop Science 25(2):373
Tx2799	GP-169	1985	CSR 308	Crop Science 25(2):373
Tx2800	GP-170	1985	CSR 309	Crop Science 25(2):373
TAM Bks-53	GP-172	1986	CSR 310	Crop Science 26(1):208
TAM Bks-54	GP-173	1986	CSR 311	Crop Science 26(1):208
TAM Bks-55	GP-174	1986	CSR 312	Crop Science 26(1):208
TAM Bks-56	GP-175	1986	CSR 313	Crop Science 26(1):208
TAM Bks-57	GP-176	1986	CSR 314	Crop Science 26(1):208
TAM Bks-58	GP-177	1986	CSR 315	Crop Science 26(1):208
NP23	GP-178	1986	NSL 195190	Crop Science 26(1):212
NP24	GP-179	1986	NSL 195191	Crop Science 26(1):212
NP25	GP-180	1986	NSL 195192	Crop Science 26(1):212
IAP4R(S1)C3	GP-181	1986	PI 561840	Crop Science 26(2):39l
OK GP-11	GP-182	1986	NSL 199468	Crop Science 26(4): 840
OK GP-12	GP-183	1986	NSL 199469	Crop Science 26(4):840
OK GP-13	GP-184	1986	NSL 199470	Crop Science 26(4):840
OK GP-14	GP-185	1986	NSL 199471	Crop Science 26(4): 840
OK GP-15	GP-186	1986	NSL 199472	Crop Science 26(4).840
OK GP-16	GP-187	1986	NSL 199473	Crop Science 26(4):840
OK GP-17	GP-188	1986	NSL 199474	Crop Science 26(4):840

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Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
OK GP-18	GP-189	1986	NSL 199475	Crop Science 26(4):840
OK GP-19	GP-190	1986	NSL 199476	Crop Science 26(4):840
OK GP-20	GP-I91	1986	NSL 199477	Crop Science 26(4):840
OK GP-21	GP-192	1986	NSL 199478	Crop Science 26(4):840
OK GP-22	GP-193	1986	NSL 199479	Crop Science 26(4):840
OK GP-23	GP-194	1986	NSL 199480	Crop Science 26(4):840
OK GP-24	GP-195	1986	NSL 199481	Crop Science 26(4):840
OK GP-25	GP-196	1986	NSL 199482	Crop Science 26(4):840
OK GP-26	GP-197	1986	NSL 199483	Crop Science 26(4):840
IAP6B(M)C3	GP-198	1986	PI 561841	Crop Science 26(6): 1263
N41	GP-199	1987	NSL 202109	Crop Science 27(1): 154
N42	GP-200	1987	NSL 202110	Crop Science 27(1): 154
N43	GP-201	1987	NSL 202111	Crop Science 27(1): 154
NP3R(S1)C4	GP-202	1987	NSL 197089	Crop Science 27(3):614
NP5R(S1)C4	GP-203	1987	NSL 197090	Crop Science 27(3):614
NP12B(S1)C2	GP-204	1987	NSL 197091	Crop Science 27(3):614
NP18B(S1)C2	GP-205	1987	NSL 197092	Crop Science 27(3):614
NP20BR(M/S1)C2	GP-206	1987	NSL 197093	Crop Science 27(3):614
NP21R(M)C4	GP-207	1987	NSL 197094	Crop Science 27(3):614
RP2B(S1)C3(ECB)	GP-208	1987	PI 561838	Crop Science 27(3):614
RP4BR(S1)C3(ECB)	GP-209	1987	PI 561839	Crop Science 27(3):614
GPTM3BR(H)C4	GP-210	1987	PI 509050	Crop Science 27(6): 1321
SGIRL-MR-3	GP-211	1988	PI 510688	Crop Science 28(1):202
SGIRL-MR-4	GP-212	1988	PI 510689	Crop Science 28(1):202
N49	GP-213	1988	PI 511319	Crop Science 28(1):203
N50	GP-214	1988	PI 511320	Crop Science 28(1):203
N51	GP-215	1988	PI 511321	Crop Science 28(1):203
N52	GP-216	1988	PI 511322	Crop Science 28(1):203
N53	GP-217	1988	PI 511323	Crop Science 28(1):203
N54	GP-218	1988	PI 511324	Crop Science 28(1):203
N55	GP-219	1988	PI 511325	Crop Science 28(1): 203
N56	GP-220	1988	PI 511326	Crop Science 28(1):203
N57	GP-221	1988	PI 511327	Crop Science 28(1):203
N58	GP-222	1988	PI 511328	Crop Science 28(1):203
N59	GP-223	1988	PI 511329	Crop Science 28(1):203
N60	GP-224	1988	PI 511330	Crop Science 28(1):203
N6 1	GP-225	1988	PI 511331	Crop Science 28(I):203
N62	GP-226	1988	PI 511332	Crop Science 28(1):203
N63	GP-227	1988	PI 511333	Crop Science 28(1):203
N64	GP-228	1988	PI 511334	Crop Science 28(1):203
N65	GP-229	1988	PI 511335	Crop Science 28(1):203
N66	GP-230	1988	PI 511336	Crop Science 28(1):203
N67	GP-231	1988	PI 511337	Crop Science 28(1):203
87BL2598	GP-232	1988	PI 518657	Crop Science 28(6): 1037
TIFT MR88	GP-233	1989	PI 520602	Crop Science 29(1):245
GPP4BR(H)C5	GP-234	1989	PI 531231	Crop Science 29(6): 1581
GTPP7R(H)C5	GP-235	1990	PI 533653	Crop Science 30(1):239
NP28	GP-236	1990	PI 535772	Crop Science 30(3):758
NP29	GP-237	1990	PI 535773	Crop Science 30(3):758
NP30	GP-238	1990	PI 535774	Crop Science 30(3):759
NP31	GP-239	1990	PI 535775	Crop Science 30(3):759
NP32	GP-240	1990	PI 535776	Crop Science 30(3):759
NP33	GP-241	1990	PI 535777	Crop Science 30(3):760

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Table *2. continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
NP34	GP-242	1990	PI 535778	Crop Science 30(3):760
NP35	GP-243	1990	PI 535779	Crop Science 30(3):760
NP36	GP-244	1990	PI 535780	Crop Science 30(3):761
NP37	GP-245	1990	PI 535781	Crop Science 30(3):761
N97	GP-246	1990	PI 535782	Crop Science 30(3):762
N98	GP-247	1990	PI 535783	Crop Science 30(3):762
N99	GP-248	1990	PI 535784	Crop Science 30(3):762
N100	GP-249	1990	PI 535785	Crop Science 30(3): 762
N101	GP-250	1990	PI 535786	Crop Science 30(3):762
N102	GP-251	1990	PI 535787	Crop Science 30(3):762
N103	GP-252	1990	PI 535788	Crop Science 30(3):762
NI04	GP-253	1990	PI 535789	Crop Science 30(3):762
N105	GP-254	1990	PI 535790	Crop Science 30(3):762
N106	GP-255	1990	PI 535791	Crop Science 30(3):762
N107	GP-256	1990	PI 535792	Crop Science 30(3): 762
N108	GP-257	1990	PI 535793	Crop Science 30(3): 762
N109	GP-258	1990	PI 535794	Crop Science 30(3):762
N110	GP-259	1990	PI 535795	Crop Science 30(3):762
N111	GP-260	1990	PI 535796	Crop Science 30(3):762
N112	GP-261	1990	PI 535797	Crop Science 30(3):763
N113	GP-262	1990	PI 535798	Crop Science 30(3):763
N114	GP-263	1990	PI 535799	Crop Science 30(3):763
N115	GP-264	1990	PI 535800	Crop Science 30(3):763
N116	GP-265	1990	PI 535801	Crop Science 30(3):763
N117	GP-266	1990	PI 535802	Crop Science 30(3):763
N118	GP-267	1990	PI 535803	Crop Science 30(3):763
N119	GP-268	1990	PI 535804	Crop Science 30(3):763
N120	GP-269	1990	PI 535805	Crop Science 30(3):763
N121	GP-270	1990	PI 535806	Crop Science 30(3):763
RTx2858	GP-271	1990	PI 536016	Crop Science 30(3):764
Tx2818	GP-272	1990	PI 537395	Crop Science 30(5): 1168
Tx2819	GP-273	1990	PI 537396	Crop Science 30(5): 1168
Tx2820	GP-274	1990	PI 537397	Crop Science 30(5): 1168
Tx2821	GP-275	1990	PI 537398	Crop Science 30(5): 1168
Tx2822	GP-276	1990	PI 537399	Crop Science 30(5): 1168
Tx2823	GP-277	1990	PI 537400	Crop Science 30(5): 1168
Tx2824	GP-278	1990	PI 537401	Crop Science 30(5): 1168
Tx2825	GP-279	1990	PI 537402	Crop Science 30(5): 1168
Tx2826	GP-280	1990	PI 537403	Crop Science 30(5): 1168
Tx2827	GP-281	1990	PI 537404	Crop Science 30(5): 1168
Tx2828	GP-282	1990	PI 537405	Crop Science 30(5): 1168
Tx2829	GP-283	1990	PI 537406	Crop Science 30(5): 1168
Tx2830	GP-284	1990	PI 537407	Crop Science 30(5): 1168
Tx2831	GP-285	1990	PI 537408	Crop Science 30(5): 1168
Tx2832	GP-286	1990	PI 537409	Crop Science 30(5): 1168
Tx2833	GP-287	1990	PI 537410	Crop Science 30(5): 1168
Tx2834	GP-288	1990	PI 537411	Crop Science 30(5): 1168
Tx2835	GP-289	1990	PI 537412	Crop Science 30(5): 1168
Tx2836	GP-290	1990	PI 537413	Crop Science 30(5): 1168
Tx2837	GP-291	1990	PI 537414	Crop Science 30(5): 1168
Tx2838	GP-292	1990	PI 537415	Crop Science 30(5): 1168
Tx2839	GP-293	1990	PI 537416	Crop Science 30(5): 1168
Tx2840	GP-294	1990	PI 537417	Crop Science 30(5): 1168

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Table 2. *continued.*

Germplasm name	Registration		Designation	Source
	No.	Year		
Tx2841	GP-295	1990	PI 537418	Crop Science 30(5): 1168
Tx2842	GP-296	1990	PI 537419	Crop Science 30(5): 1168
Tx2843	GP-297	1990	PI 537420	Crop Science 30(5): 1168
Tx2844	GP-298	1990	PI 537421	Crop Science 30(5): 1168
Tx2845	GP-299	1990	PI 537422	Crop Science 30(5): 1168
Tx2846	GP-300	1990	PI 537423	Crop Science 30(5): 1168
Tx2847	GP-301	1990	PI 537424	Crop Science 30(5): 1168
Tx2848	GP-302	1990	PI 537425	Crop Science 30(5): 1168
Tx2849	GP-303	1990	PI 537426	Crop Science 30(5): 1168
Tx2850	GP-304	1990	PI 537427	Crop Science 30(5): 1168
Tx2851	GP-305	1990	PI 537428	Crop Science 30(5): 1168
Tx2852	GP-306	1990	PI 537429	Crop Science 30(5): 1168
Tx2853	GP-307	1990	PI 537430	Crop Science 30(5): 1168
Tx2854	GP-308	1990	PI 537431	Crop Science 30(5): 1168
Tx2855	GP-309	1990	PI 537432	Crop Science 30(5): 1168
Tx2856	GP-310	1990	PI 537433	Crop Science 30(5): 1168
Tx2857	GP-311	1990	PI 537434	Crop Science 30(5): 1168
GATCCP 100	GP-312	1991	PI 537308	Crop Science 31(1):242
GATCCP 101	GP-313	1991	PI 537309	Crop Science 31(1):242
GP9BR	GP-314	1991	PI 540313	Crop Science 31 (1):244
GPP5BR(M/H/F)C3	GP-315	1991	PI 538245	Crop Science 31(1):241
Tx2859	GP-316	1991	PI 540793	Crop Science 31(2):499
Tx2860	GP-317	1991	PI 540794	Crop Science 31(2):499
Tx2861	GP-318	1991	PI 540795	Crop Science 31(2):499
Tx2862	GP-319	1991	PI 540796	Crop Science 31(2):499
Tx2863	GP-320	1991	PI 540797	Crop Science 31(2):499
Tx2864	GP-321	1991	PI 540798	Crop Science 31(2):499
Tx2865	GP-322	1991	PI 540799	Crop Science 31(2):499
Tx2866	GP-323	1991	PI 540800	Crop Science 31 (2):499
Tx2867	GP-324	1991	PI 540801	Crop Science 31(2):499
Tx2868	GP-325	1991	PI 540802	Crop Science 31(2):499
Tx2869	GP-326	1991	PI 540803	Crop Science 31(2):498
Tx2870	GP-327	1991	PI 540804	Crop Science 31(2):498
Tx2871	GP-328	1991	PI 540805	Crop Science 31 (2):498
Tx2872	GP-329	1991	PI 540806	Crop Science 31(2):498
Tx2873	GP-330	1991	PI 540807	Crop Science 31(2):498
Tx2874	GP-331	1991	PI 540808	Crop Science 31 (2):498
Tx2875	GP-332	1991	PI 540809	Crop Science 31(2):498
Tx2876	GP-333	1991	PI 540810	Crop Science 31(2):498
Tx2877	GP-334	1991	PI 540811	Crop Science 31(2):498
Tx2878	GP-335	1991	PI 540812	Crop Science 31 (2):498
Tx2879	GP-336	1991	PI 540813	Crop Science 31 (2):498
Tx2880	GP-337	1991	PI 540814	Crop Science 31(2):498
Tx2881	GP-338	1991	PI 540815	Crop Science 31(2):498
Tx2882	GP-339	1991	PI 540816	Crop Science 31(2):498
Tx2883	GP-340	1991	PI 540817	Crop Science 31(2):498
Tx2884	GP-341	1991	PI 540818	Crop Science 31(2):498
Tx2885	GP-342	1991	PI 540819	Crop Science 31(2):498
Tx2886	GP-343	1991	PI 540820	Crop Science 31(2):498
Tx2887	GP-344	1991	PI 540821	Crop Science 31(2):498
Tx2888	GP-345	1991	PI 540822	Crop Science 31(2):498
Tx2889	GP-346	1991	PI 540823	Crop Science 31(2):498
Tx2890	GP-347	1991	PI 540824	Crop Science 31(2):498

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Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
KS 84R	GP-348	1991	PI 542985	Crop Science 31(4): 1099
KS 85R	GP-349	1991	PI 542986	Crop Science 31(4): 1099
KS 86R	GP-350	1991	PI 542987	Crop Science 31(4): 1099
KS 87R	GP-351	1991	PI 542988	Crop Science 31(4): 1099
KS 88R	GP-352	1991	PI 542989	Crop Science 31(4): 1099
KS 89R	GP-353	1991	PI 542990	Crop Science 31(4): 1099
KS 90R	GP-354	1991	PI 542991	Crop Science 31(4): 1099
KS 91R	GP-355	1991	PI 542992	Crop Science 31(4): 1099
KS 92R	GP-356	1991	PI 542993	Crop Science 31(4): 1099
KS 93R	GP-357	1991	PI 542994	Crop Science 31(4): 1099
GAC 102	GP-358	1991	PI 546350	Crop Science 31(5): 1396
GC 103	GP-359	1992	PI 559482	Crop Science 32(4): 1076
GC104	GP-360	1992	PI 559483	Crop Science 32(4): 1076
N82	GP-361	1992	PI 559723	Crop Science 32(4): 1077
N83	GP-362	1992	PI 559724	Crop Science 32(4): 1077
N84	GP-363	1992	PI 559725	Crop Science 32(4): 1077
N85	GP-364	1992	PI 559726	Crop Science 32(4): 1077
N86	GP-365	1992	PI 559727	Crop Science 32(4): 1077
N87	GP-366	1992	PI 559728	Crop Science 32(4): 1077
N88	GP-367	1992	PI 559729	Crop Science 32(4): 1077
N89	GP-368	1992	PI 559730	Crop Science 32(4): 1077
N90	GP-369	1992	PI 559731	Crop Science 32(4): 1077
Tx2891	GP-370	1993	PI 548797	Crop Science 33(5): 1109
TIFT MR9110	GP-371	1993	PI 564512	Crop Science 33(5): 1118
TIFT MR9115	GP-372	1993	PI 564513	Crop Science 33(5): 1118
TIFT MR9120	GP-373	1993	PI 564514	Crop Science 33(5): 1118
ICSV 692	GP-374	1994	PI 576123	Crop Science 34(5): 1425
ICSV 729	GP-375	1994	PI 576124	Crop Science 34(5): 1425
ICSV 730	GP-376	1994	PI 576125	Crop Science 34(5): 1425
ICSV 731	GP-377	1994	PI 576126	Crop Science 34(5): 1425
ICSV 736	GP-378	1994	PI 576127	Crop Science 34(5): 1425
ICSV 739	GP-379	1994	PI 576128	Crop Science 34(5): 1425
ICSV 744	GP-380	1994	PI 576129	Crop Science 34(5): 1425
ICSV 745	GP-381	1994	PI 576130	Crop Science 34(5): 1425
ICSV 748	GP-382	1994	PI 576131	Crop Science 34(5): 1425
NP26 Sorghum Population	GP-383	1994	PI 583834	Crop Science 35(3):946
Tx2908	GP-384	1996	PI 585279	Crop Science 36(2):476
Tx2892	GP-385	1996	PI 585280	Crop Science 36(2):476
Tx2893	GP-386	1996	PI 585281	Crop Science 36(2):476
Tx2894	GP-387	1996	PI 585282	Crop Science 36(2):476
Tx2895	GP-388	1996	PI 585283	Crop Science 36(2):476
Tx2896	GP-389	1996	PI 585284	Crop Science 36(2):476
Tx2897	GP-390	1996	PI 585285	Crop Science 36(2):476
Tx2898	GP-391	1996	PI 585286	Crop Science 36(2):476
Tx2899	GP-392	1996	PI 585287	Crop Science 36(2):476
Tx2900	GP-393	1996	PI 585288	Crop Science 36(2):476
Tx2901	GP-394	1996	PI 585289	Crop Science 36(2):476
Tx2902	GP-395	1996	PI 585290	Crop Science 36(2):476
Tx2903	GP-396	1996	PI 585291	Crop Science 36(2):476
Tx2904	GP-397	1996	PI 585292	Crop Science 36(2):476
Tx2905	GP-398	1996	PI 585293	Crop Science 36(2):476
Tx2906	GP-399	1996	PI 585294	Crop Science 36(2):476
AD9B(MS1)C2	GP-401	1997	PI 595205	Crop Science 37(3): 1036

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Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
AD11B(MS1)C2	GP-402	1997	PI 595206	Crop Science 37(3): 1036
AD12R(MS1)C2	GP-403	1997	PI 595207	Crop Science 37(3): 1036
AD13R(MS1)C2	GP-404	1997	PI 595208	Crop Science 37(3): 1036
IS 1029C	GP-405	1997	PI 595699	Crop Science 37(4): 1397
IS 1530C	GP-406	1997	PI 595700	Crop Science 37(4): 1397
IS 2377C	GP-407	1997	PI 595701	Crop Science 37(4): 1397
MN 4592 (preconverted)	GP-408	1997	PI 595702	Crop Science 37(4): 1397
IS 4308C	GP-409	1997	PI 595703	Crop Science 37(4): 1397
IS 4540C	GP-410	1997	PI 595704	Crop Science 37(4): 1397
IS 4870C	GP-411	1997	PI 595705	Crop Science 37(4): 1397
IS 4902C	GP-412	1997	PI 595706	Crop Science 37(4): 1397
IS 5792C	GP-413	1997	PI 595707	Crop Science 37(4): 1397
IS 6026C	GP-414	1997	PI 595708	Crop Science 37(4): 1397
IS 6991C	GP-415	1997	PI 595709	Crop Science 37(4): 1397
IS 7344C	GP-416	1997	PI 595710	Crop Science 37(4): 1397
IS 7380C	GP-417	1997	PI 595711	Crop Science 37(4): 1397
IS 7528C	GP-418	1997	PI 595712	Crop Science 37(4): 1397
IS 8104C	GP-419	1997	PI 595713	Crop Science 37(4): 1397
IS 9290C	GP-420	1997	PI 595714	Crop Science 37(4): 1397
IS 9738C	GP-421	1997	PI 595715	Crop Science 37(4): 1397
IS 9784C	GP-422	1997	PI 595716	Crop Science 37(4): 1397
IS 9796C	GP-423	1997	PI 595717	Crop Science 37(4): 1397
IS 10759C	GP-424	1997	PI 595718	Crop Science 37(4): 1397
IS 11424C	GP-425	1997	PI 595719	Crop Science 37(4): 1397
IS 11814C	GP-426	1997	PI 595720	Crop Science 37(4): 1397
IS 11818C	GP-427	1997	PI 595721	Crop Science 37(4): 1397
IS 11822C	GP-428	1997	PI 595722	Crop Science 37(4): 1397
IS 11971C	GP-429	1997	PI 595723	Crop Science 37(4): 1397
IS 12181C	GP-430	1997	PI 595724	Crop Science 37(4): 1397
MN 1230 (preconverted)	GP-431	1997	PI 595725	Crop Science 37(4): 1397
MN 1524 (preconverted)	GP-432	1997	PI 595726	Crop Science 37(4): 1397
MN 1562 (preconverted)	GP-433	1997	PI 595727	Crop Science 37(4): 1397
IS 12652C	GP-434	1997	PI 595728	Crop Science 37(4): 1397
IS 17220C	GP-435	1997	PI 595729	Crop Science 37(4): 1397
IS 17221C	GP-436	1997	PI 595730	Crop Science 37(4): 1397
IS 17547C	GP-437	1997	PI 595731	Crop Science 37(4): 1397
IS 23490C	GP-438	1997	PI 595732	Crop Science 37(4): 1397
IS 23520C	GP-439	1997	PI 595733	Crop Science 37(4): 1397
IS 23533C	GP-440	1997	PI 595734	Crop Science 37(4): 1397
IS 23573C	GP-441	1997	PI 595735	Crop Science 37(4): 1397
IS 23587C	GP-442	1997	PI 595736	Crop Science 37(4): 1397
IS 23590C	GP-443	1997	PI 595737	Crop Science 37(4): 1397
IS 23595C	GP-444	1997	PI 595738	Crop Science 37(4): 1397
MN 1056 (preconverted)	GP-445	1997	PI 595739	Crop Science 37(4): 1397
MN 1500 (preconverted)	GP-446	1997	PI 595740	Crop Science 37(4): 1397
SC 1063C	GP-447	1997	PI 595741	Crop Science 37(4): 1397
SC 1177C	GP-448	1997	PI 595742	Crop Science 37(4): 1397
SC 1201C	GP-449	1997	PI 595743	Crop Science 37(4): 1397
SC 1211C	GP-450	1997	PI 595744	Crop Science 37(4): 1397
SC 1214C	GP-451	1997	PI 595745	Crop Science 37(4): 1397
SC 1287C	GP-452	1997	PI 595746	Crop Science 37(4): 1397
SC 1293C	GP-453	1997	PI 595747	Crop Science 37(4): 1397
SC 1338C	GP-454	1997	PI 595748	Crop Science 37(4): 1397

continued

Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
IC4258(T.3)	GP-455	1997	PI 533745	Crop Science 37(4): 1399
C.10-2	GP-456	1997	PI 533746	Crop Science 37(4): 1399
Nilwa	GP-457	1997	PI 533747	Crop Science 37(4): 1399
Nauhatta	GP-458	1997	PI 533748	Crop Science 37(4): 1399
AS9117	GP-459	1997	PI 533749	Crop Science 37(4): 1399
K.3 Perimanjial Irungu Cholam	GP-460	1997	PI 533750	Crop Science 37(4): 1399
Birgalli Ahmar	GP-461	1997	PI 533751	Crop Science 37(4): 1399
54.K.94 Witchweed Resistant	GP-462	1997	PI 533752	Crop Science 37(4): 1399
MN 732 (preconverted)	GP-463	1997	PI 533753	Crop Science 37(4): 1399
MN 733 (preconverted)	GP-464	1997	PI 533754	Crop Science 37(4): 1399
Feterita Gondal	GP-465	1997	PI 533755	Crop Science 37(4): 1399
Hegari Makwar	GP-466	1997	PI 533756	Crop Science 37(4): 1399
Monshal	GP-467	1997	PI 533757	Crop Science 37(4): 1399
MN 879 (preconverted)	GP-468	1997	PI 533758	Crop Science 37(4): 1399
Mugbash 56/56	GP-469	1997	PI 533759	Crop Science 37(4): 1399
Zcra Zera White	GP-470	1997	PI 533760	Crop Science 37(4): 1399
SC 333	GP-471	1997	PI 533761	Crop Science 37(4): 1399
Tambroro 7	GP-472	1997	PI 533762	Crop Science 37(4): 1399
BE 13	GP-473	1997	PI 533763	Crop Science 37(4): 1399
Roxi Barikel	GP-474	1997	PI 533764	Crop Science 37(4): 1399
Deori Badri	GP-475	1997	PI 533765	Crop Science 37(4): 1399
No. 4 Hadoui	GP-476	1997	PI 533766	Crop Science 37(4): 1399
105 Nazongliala	GP-477	1997	PI 533767	Crop Science 37(4): 1399
428 El Safra	GP-478	1997	PI 533768	Crop Science 37(4): 1399
290 Feterita Shendi 2	GP-479	1997	PI 533769	Crop Science 37(4): 1399
FC Standard	GP-480	1997	PI 533770	Crop Science 37(4): 1399
Agyou	GP-481	1997	PI 533771	Crop Science 37(4): 1399
AD 9	GP-482	1997	PI 533772	Crop Science 37(4): 1399
AD 10	GP-483	1997	PI 533773	Crop Science 37(4): 1399
BA 26	GP-484	1997	PI 533774	Crop Science 37(4): 1399
BA 29	GP-485	1997	PI 533775	Crop Science 37(4): 1399
KA 3	GP-486	1997	PI 533776	Crop Science 37(4): 1399
KO 15	GP-487	1997	PI 533777	Crop Science 37(4): 1399
KO 19	GP-488	1997	PI 533778	Crop Science 37(4): 1399
KO 23	GP-489	1997	PI 533779	Crop Science 37(4): 1399
KO 58	GP-490	1997	PI 533780	Crop Science 37(4): 1399
ZA2	GP-491	1997	PI 533781	Crop Science 37(4): 1399
ZA 16	GP-492	1997	PI 533782	Crop Science 37(4): 1399
ZA 77	GP-493	1997	PI 533783	Crop Science 37(4): 1399
S03	GP-494	1997	PI 533784	Crop Science 37(4): 1399
SO 16	GP-495	1997	PI 533785	Crop Science 37(4): 1399
SO 101	GP-496	1997	PI 533786	Crop Science 37(4): 1399
Belig White	GP-497	1997	PI 533787	Crop Science 37(4): 1399
MN 775 (preconverted)	GP-498	1997	PI 533788	Crop Science 37(4): 1399
Kodilib	GP-499	1997	PI 533789	Crop Science 37(4): 1399
Mori Red Glume	GP-500	1997	PI 533790	Crop Science 37(4): 1399
Mur Ban	GP-501	1997	PI 533791	Crop Science 37(4): 1399
No. 1 Gambela	GP-502	1997	PI 533792	Crop Science 37(4): 1399
No. 4 Gambela	GP-503	1997	PI 533793	Crop Science 37(4): 1399
No. 5 Gambela	GP-504	1997	PI 533794	Crop Science 37(4): 1399
SC 126	GP-505	1997	PI 533795	Crop Science 37(4): 1399
SC 131	GP-506	1997	PI 533796	Crop Science 37(4): 1399
SC 154	GP-507	1997	PI 533797	Crop Science 37(4): 1399

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Table 2. *continued.*

Germplasm name	Registration No.	Year	Designation	Source
SC 171	GP-508	1997	PI 533798	Crop Science 37(4): 1399
SC 173	GP-509	1997	PI 533799	Crop Science 37(4): 1399
IS 12666C	GP-510	1997	PI 533800	Crop Science 37(4): 1399
Ethiopian Sel. #3	GP-511	1997	PI 533801	Crop Science 37(4): 1399
BO 41	GP-512	1997	PI 533802	Crop Science 37(4): 1399
K0 8	GP-513	1997	PI 533803	Crop Science 37(4): 1399
K0 25	GP-514	1997	PI 533804	Crop Science 37(4): 1399
SC 220	GP-515	1997	PI 533805	Crop Science 37(4): 1399
SC 221	GP-516	1997	PI 533806	Crop Science 37(4): 1399
SC 223	GP-517	1997	PI 533807	Crop Science 37(4): 1399
Tx2909	GP-518	1998	PI 598069	Crop Science 38(2):566
Tx2910	GP-519	1998	PI 598070	Crop Science 38(2):566
IS 1117C	GP-520	1998	PI 597943	Crop Science 38(2):564
IS 2680C	GP-521	1998	PI 597944	Crop Science 38(2):564
IS 2871C	GP-522	1998	PI 597945	Crop Science 38(2):564
IS 3106C	GP-523	1998	PI 597946	Crop Science 38(2):564
Segaolane 16	GP-524	1998	PI 597947	Crop Science 38(2):564
IS 4832C	GP-525	1998	PI 597948	Crop Science 38(2):564
IS 5168C	GP-526	1998	PI 597949	Crop Science 38(2):564
SC 449	GP-527	1998	PI 597950	Crop Science 38(2):564
IS 6733C	GP-528	1998	PI 597951	Crop Science 38(2):564
IS 6960C	GP-529	1998	PI 597952	Crop Science 38(2):564
IS 7436C	GP-530	1998	PI 597953	Crop Science 38(2):564
IS 77I4C	GP-531	1998	PI 597954	Crop Science 38(2):564
IS 8898C	GP-532	1998	PI 597955	Crop Science 38(2):564
IS 11885C	GP-533	1998	PI 597956	Crop Science 38(2):564
IS 1I930C	GP-534	1998	PI 597957	Crop S.cience 38(2):564
IS 12675C	GP-535	1998	PI 597958	Crop Science 38(2):564
IS 17204C	GP-536	1998	PI 597959	Crop Science 38(2):564
IS 17215C	GP-537	1998	PI 597960	Crop Science 38(2):564
IS 17216C	GP-538	1998	PI 597961	Crop Science 38(2):564
IS 23492C	GP-539	1998	PI 597962	Crop Science 38(2):564
IS 23601C	GP-540	1998	PI 597963	Crop Science 38(2):564
IS 23607C	GP-541	1998	PI 597964	Crop Science 38(2):564
SC 1205C	GP-542	1998	PI 597965	Crop Science 38(2):564
SC 1212C	GP-543	1998	PI 597966	Crop Science 38(2):564
SC 1320C	GP-544	1998	PI 597967	Crop Science 38(2):564
SC 1321C	GP-545	1998	PI 597968	Crop Science 38(2):564
SC 1322C	GP-546	1998	PI 597969	Crop Science 38(2):564
SC 1325C	GP-547	1998	PI 597970	Crop Science 38(2):564
SC 1328C	GP-548	1998	PI 597971	Crop Science 38(2):564
SC 1329C	GP-549	1998	PI 597972	Crop Science 38(2):564
SC 1330C	GP-550	1998	PI 597973	Crop Science 38(2):564
SC 1332C	GP-551	1998	PI 597974	Crop Science 38(2):564
SC 1333C	GP-552	1998	PI 597975	Crop Science 38(2):564
SC 1337C	GP-553	1998	PI 597976	Crop Science 38(2):564
SC 1339C	GP-554	1998	PI 597977	Crop Science 38(2):564
SC 1341C	GP-555	1998	PI 597978	Crop Science 38(2):564
SC 1342C	GP-556	1998	PI 597979	Crop Science 38(2):564
SC 1345C	GP-557	1998	PI 597980	Crop Science 38(2):564
SC 1351C	GP-558	1998	PI 597981	Crop Science 38(2):564
SC 1356C	GP-559	1998	PI 597982	Crop Science 38(2):564
GT-IR6	GP-560	1998	PI 602444	Crop Science 38(5): 1410

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Table 2. *continued.*

Germplasm name	Registration No.	Registration Year	Designation	Source
GT-IR7	GP-561	1998	PI 602445	Crop Science 38(5): 1410
GT-IR8	GP-562	1998	PI 602446	Crop Science 38(5): 1410
N244	GP-563	1999	PI 606744	Crop Science 39(4): 1263
N245	GP-564	1999	PI 606745	Crop Science 39(4): 1263
N246	GP-565	1999	PI 606746	Crop Science 39(4): 1263
N247	GP-566	1999	PI 606747	Crop Science 39(4): 1263
Tx2911	GP-567	2000	PI 607931	Crop Science 40(2):584
TAM Bk-59	GP-568	2000	PI 607932	Crop Science 40(2):585
KS 97	GP-569	2000	PI 607900	Crop Science 40(3):866
KS 98	GP-570	2000	PI 607901	Crop Science 40(3):867
KS 99B	GP-571	2000	PI 612396	Crop Science 40(5): 1509
KS 99A	GP-571 cms	2000	PI 612395	Crop Science 40(5): 1509
KS 100B	GP-572	2000	PI 612398	Crop Science 40(5): 1509
KS 100 A	GP-572cms	2000	PI 612397	Crop Science 40(5): 1509
KS 101B	GP-573	2000	PI 612400	Crop Science 40(5): 1509
KS 101A	GP-573cms	2000	PI 612399	Crop Science 40(5): 1509
KS 102B	GP-574	2000	PI 612402	Crop Science 40(5): 1509
KS 102 A	GP-574cms	2000	PI 612401	Crop Science 40(5): 1509
KS 103B	GP-575	2000	PI 612404	Crop Science 40(5): 1509
KS 103A	GP-575cms	2000	PI 612403	Crop Science 40(5): 1509
KS 104B	GP-576	2000	PI 612406	Crop Science 40(5): 1509
KS 104A	GP-576cms	2000	PI 612405	Crop Science 40(5): 1509
KS 105B	GP-577	2000	PI 612408	Crop Science 40(5): 1509
KS 105 A	GP-577cms	2000	PI 612407	Crop Science 40(5): 1509
KS 106B	GP-578	2000	PI 612410	Crop Science 40(5): 1509
KS 106 A	GP-578cms	2000	PI 612409	Crop Science 40(5): 1509
KS 107B	GP-579	2000	PI 612412	Crop Science 40(5): 1509
KS 107 A	GP-579cms	2000	PI 612411	Crop Science 40(5): 1509
KS 108R	GP-580	2000	PI 612413	Crop Science 40(5): 1510
KS 109R	GP-581	2000	PI 612414	Crop Science 40(5): 1510
KS 110R	GP-582	2000	PI 612415	Crop Science 40(5): 1510
KS 111R	GP-583	2000	PI 612416	Crop Science 40(5): 1510
KS 112R	GP-584	2000	PI 612417	Crop Science 40(5): 1510
KS 113R	GP-585	2000	PI 612418	Crop Science 40(5). 1510
KS 114R	GP-586	2000	PI 612419	Crop Science 40(5): 1510
N313	GP-587	2001	PI 612984	Crop Science 41(2):600
N314	GP-588	2001	PI 612985	Crop Science 41(2):600
N315	GP-589	2001	PI 612986	Crop Science 41(2):600
KS 115	GP-590	2001	PI 613536	Crop Science 41(3):932
RN582	GP-591	2003	PI 628277	Crop Science 43(1):441
Tx2912	GP-592	2003	PI 629035	Crop Science 43(1):442
Tx2913	GP-593	2003	PI 629036	Crop Science 43(1):442
Tx2914	GP-594	2003	PI 629037	Crop Science 43(1):442
Tx2915	GP-595	2003	PI 629038	Crop Science 43(1):442
Tx2916	GP-596	2003	PI 629039	Crop Science 43(1):442
Tx2917	GP-597	2003	PI 629040	Crop Science 43(1):442
Tx2918	GP-598	2003	PI 629041	Crop Science 43(1):442
Tx2919	GP-599	2003	PI 629042	Crop Science 43(1) :442
Tx2920	GP-600	2003	PI 629043	Crop Science 43(1):442
B.Tx2921	GP-601	2003	PI 629045	Crop Science 43(1):443
A.Tx2921	GP-601cms	2003	PI 629044	Crop Science 43(1):443
B.Tx2922	GP-602	2003	PI 629047	Crop Science 43(1):443
A.Tx2922	GP-602cms	2003	PI 629046	Crop Science 43(1):443

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Table 2. ***continued.***

Germplasm name	Registration No.	Registration Year	Designation	Source
B.Tx2923	GP-603	2003	PI 629049	Crop Science 43(1):443
A.Tx2923	GP-603cms	2003	PI 629048	Crop Science 43(1):443
B.Tx2924	GP-604	2003	PI 629051	Crop Science 43(1):443
A.Tx2924	GP-604cms	2003	PI 629050	Crop Science 43(1):443
B.Tx2925	GP-605	2003	PI 629053	Crop Science 43(1):443
A.Tx2925	GP-605cms	2003	PI 629052	Crop Science 43(1):443
B.Tx2926	GP-606	2003	PI 629055	Crop Science 43(1):443
A.Tx2926	GP-606cms	2003	PI 629054	Crop Science 43(1):443
B.Tx2927	GP-607	2003	PI 629057	Crop Science 43(1):443
A.Tx2927	GP-607cms	2003	PI 629056	Crop Science 43(1):443
B.Tx2928	GP-608	2003	PI 629059	Crop Science 43(1):443
A.Tx2928	GP-608cms	2003	PI 629058	Crop Science 43(1):443
RN583	GP-609	2003	PI 632253	GRIN[1]

1. USDA, ARS. National Genetic Resources Program. Germplasm Resources Information Network (GRIN). [Online Database] National Germplasm Resources Laboratory, Beltsville, Maryland, USA. Available: http://www.ars-grin.gov/cgi-bin/npgs/html/acchtml.pl71555263 (09 October 2003).

Table 3. Cultivar name, registration number and year, designation and source of sorghums registered as genetic stock since 1990 in USA.

Genetic stock name	Registration No.	Registration Year	Designation	Source
A3Tx430	GS-1	1990	PI 536632	Crop Science 30(5): 1163
A3Tx7000	GS-2	1990	PI 536633	Crop Science 30(5): 1163
A3N 149	GS-3	1997	PI 595222	Crop Science 37(4): 1408
A3N 150	GS-4	1997	PI 595223	Crop Science 37(4): 1408
A3N151	GS-5	1997	PI 595224	Crop Science 37(4): 1408
A3N 152	GS-6	1997	PI 595225	Crop Science 37(4): 1408
A3N 153	GS-7	1997	PI 595226	Crop Science 37(4): 1408
A3N 154	GS-8	1997	PI 595227	Crop Science 37(4): 1408
A3N 155	GS-9	1997	PI 595228	Crop Science 37(4): 1408
A3N 156	GS-10	1997	PI 595229	Crop Science 37(4): 1408
A3N 157	GS-11	1997	PI 595230	Crop Science 37(4): 1408
A3N158	GS-12	1997	PI 595231	Crop Science 37(4): 1408
A3N 159	GS-13	1997	PI 595232	Crop Science 37(4): 1408
A3N 160	GS-14	1997	PI 595233	Crop Science 37(4): 1408
A3N 161	GS-15	1997	PI 595234	Crop Science 37(4): 1408
A3N 162	GS-16	1997	PI 595235	Crop Science 37(4): 1408
A3N 163	GS-17	1997	PI 595236	Crop Science 37(4): 1408
A3N 164	GS-18	1997	PI 595237	Crop Science 37(4): 1408
A3N 165	GS-19	1997	PI 595238	Crop Science 37(4): 1408
A3N 166	GS-20	1997	PI 595239	Crop Science 37(4): 1408
A3N 167	GS-21	1997	PI 595240	Crop Science 37(4): 1408
A3N 168	GS-22	1997	PI 595241	Crop Science 37(4): 1408
A3N 169	GS-23	1997	PI 595242	Crop Science 37(4): 1408
A3N 170	GS-24	1997	PI 595243	Crop Science 37(4): 1408
A3N171	GS-25	1997	PI 595244	Crop Science 37(4): 1408
A3N 172	GS-26	1997	PI 595245	Crop Science 37(4): 1408

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Table 3. *continued.*

Genetic stock name	Registration No.	Year	Designation	Source
A3N 173	GS-27	1997	PI 595246	Crop Science 37(4): 1408
A3N 174	GS-28	1997	PI 595247	Crop Science 37(4): 1408
A3N 175	GS-29	1997	PI 595248	Crop Science 37(4): 1408
A3N 176	GS-30	1997	PI 595249	Crop Science 37(4): 1408
A3N 177	GS-31	1997	PI 595250	Crop Science 37(4): 1408
N221ms3ms3	GS-32	1997	PI 595251	Crop Science 37(4): 1411
N222ms3ms3	GS-33	1997	PI 595252	Crop Science 37(4): 1411
N223ms3ms3	GS-34	1997	PI 595253	Crop Science 37(4): 1411
N224ms3ms3	GS-35	1997	PI 595254	Crop Science 37(4): 1411
N225ms3ms3	GS-36	1997	PI 595255	Crop Science 37(4): 1411
N226ms3ms3	GS-37	1997	PI 595256	Crop Science 37(4): 1411
N227ms3ms3	GS-38	1997	PI 595257	Crop Science 37(4): 1411
N228ms3ms3	GS-39	1997	PI 595258	Crop Science 37(4): 1411
N229ms3ms3	GS-40	1997	PI 595259	Crop Science 37(4): 1411
N230ms3ms3	GS-41	1997	PI 595260	Crop Science 37(4): 1411
N231ms3ms3	GS-42	1997	PI 595261	Crop Science 37(4): 1411
N232ms3ms3	GS-43	1997	PI 595262	Crop Science 37(4): 1411
N233ms3ms3	GS-44	1997	PI 595263	Crop Science 37(4): 1411
N234ms3ms3	GS-45	1997	PI 595264	Crop Science 37(4): 1411
N235ms3ms3	GS-46	1997	PI 595265	Crop Science 37(4): 1411
N236ms3ms3	GS-47	1997	PI 595266	Crop Science 37(4): 1411
N237ms3ms3	GS-48	1997	PI 595267	Crop Science 37(4): 1411
N238ms3ms3	GS-49	1997	PI 595268	Crop Science 37(4): 1411
N239ms3ms3	GS-50	1997	PI 595269	Crop Science 37(4): 1411
N240ms3ms3	GS-51	1997	PI 595270	Crop Science 37(4): 1411
N241ms3ms3	GS-52	1997	PI 595271	Crop Science 37(4): 1411
A2N 178	GS-53	1997	PI 595272	Crop Science 37(4): 1412
A3N 179	GS-54	1997	PI 595273	Crop Science 37(4): 1412
A4N 180	GS-55	1997	PI 595274	Crop Science 37(4): 1412
A2N 181	GS-56	1997	PI 595275	Crop Science 37(4): 1412
A3N 182	GS-57	1997	PI 595276	Crop Science 37(4): 1412
A4N 183	GS-58	1997	PI 595277	Crop Science 37(4): 1412
A2N 184	GS-59	1997	PI 595278	Crop Science 37(4): 1412
A3N 185	GS-60	1997	PI 595279	Crop Science 37(4): 1412
A4N 186	GS-61	1997	PI 595280	Crop Science 37(4): 1412
A2N 187	GS-62	1997	PI 595281	Crop Science 37(4): 1412
A3N 188	GS-63	1997	PI 595282	Crop Science 37(4): 1412
A4N 189	GS-64	1997	PI 595283	Crop Science 37(4): 1412
A2N 190	GS-65	1997	PI 595284	Crop Science 37(4): 1412
A3N191	GS-66	1997	PI 595285	Crop Science 37(4): 1412
A2N 192	GS-67	1997	PI 595286	Crop Science 37(4): 1412
A3N 193	GS-68	1997	PI 595287	Crop Science 37(4): 1412
A3N 194	GS-69	1997	PI 595288	Crop Science 37(4): 1412
A3N 195	GS-70	1997	PI 595289	Crop Science 37(4): 1412
A3N196	GS-71	1997	PI 595290	Crop Science 37(4): 1412
A3N 197	GS-72	1997	PI 595291	Crop Science 37(4): 1412
A3N 198	GS-73	1997	PI 595292	Crop Science 37(4): 1412
A3N 199	GS-74	1997	PI 595293	Crop Science 37(4): 1412
A3N200	GS-75	1997	PI 595294	Crop Science 37(4): 1412
A3N201	GS-76	1997	PI 595295	Crop Science 37(4): 1412
A3N202	GS-77	1997	PI 595296	Crop Science 37(4): 1412
A3N203	GS-78	1997	PI 595297	Crop Science 37(4): 1412
A3N204	GS-79	1997	PI 595298	Crop Science 37(4): 1412

continued

Table 3. *continued.*

Genetic stock name	Registration No.	Registration Year	Designation	Source
A3N205	GS-80	1997	PI 595299	Crop Science 37(4): 1412
A3N206	GS-81	1997	PI 595300	Crop Science 37(4): 1412
A3N207	GS-82	1997	PI 595301	Crop Science 37(4): 1412
A3N208	GS-83	1997	PI 595302	Crop Science 37(4): 1412
A3N209	GS-84	1997	PI 595303	Crop Science 37(4): 1412
A3N210	GS-85	1997	PI 595304	Crop Science 37(4): 1412
A3N 211	GS-86	1997	PI 595305	Crop Science 37(4): 1412
A2N212	GS-87	1997	PI 595306	Crop Science 37(4): 1412
A3N213	GS-88	1997	PI 595307	Crop Science 37(4): 1412
A3N2I4	GS-89	1997	PI 595308	Crop Science 37(4): 1412
A3N215	GS-90	1997	PI 595309	Crop Science 37(4): 1412
A2N216	GS-91	1997	PI 595310	Crop Science 37(4): 1412
A3N217	GS-92	1997	PI 595311	Crop Science 37(4): 1412
A3N218	GS-93	1997	PI 595312	Crop Science 37(4): 1412
A3N219	GS-94	1997	PI 595313	Crop Science 37(4): 1412
A2N220	GS-95	1997	PI 595314	Crop Science 37(4): 1412
N316	GS-96	2001	PI 612987	Crop Science 41(2):607
N317	GS-97	2001	PI 612988	Crop Science 41(2):607
N318	GS-98	2001	PI 612989	Crop Science 41(2):607
N319	GS-99	2001	PI 612990	Crop Science 41(2):607
N320	GS-100	2001	PI 612991	Crop Science 41(2):607
N321	GS-101	2001	PI 612992	Crop Science 41(2):607
N322	GS-102	2001	PI 612993	Crop Science 41(2):607
N323	GS-103	2001	PI 612994	Crop Science 41(2):607
N324	GS-104	2001	PI 612995	Crop Science 41(2):607
N325	GS-105	2001	PI 612996	Crop Science 41 (2):607
N326	GS-106	2001	PI 612997	Crop Science 41 (2):607
N327	GS-107	2001	PI 612998	Crop Science 41 (2):607
N328	GS-108	2001	PI 612999	Crop Science 41(2):607
N329	GS-109	2001	PI 613000	Crop Science 41(2):607
N330	GS-110	2001	PI 613001	Crop Science 41(2):607
N331	OS-111	2001	PI 613002	Crop Science 41(2):607
N332	GS-112	2001	PI 613003	Crop Science 41(2):607
N333	GS-113	2001	PI 613004	Crop Science 41(2):607
N334	GS-114	2001	PI 613005	Crop Science 41(2):607
N335	GS-115	2001	PI 613006	Crop Science 41(2):607
N336	GS-116	2001	PI 613007	Crop Science 41(2):607
N337	GS-I17	2001	PI 613008	Crop Science 41(2):607
N338	GS-118	2001	PI 613009	Crop Science 41(2): 607
N339	GS-119	2001	PI 613010	Crop Science 41(2):607
N340	GS-120	2001	PI 613011	Crop Science 41(2):607

Table 4. Cultivar name, registration number and year, designation and source of sorghums registered as parental lines since 1972 in USA.

Cultivar name	Registration No.	Registration Year	Designation	Source
KS1	PL-1	1972	NSL 20635	Crop Science 12(5): 722
KS2	PL-2	1972	NSL 20636	Crop Science 12(5):722
KS3	PL-3	1972	NSL 20637	Crop Science 12(5):722
KS4	PL-4	1972	NSL 54011	Crop Science 12(5):722
KS5	PL-5	1972	NSL 34229	Crop Science 12(5):722
KS6	PL-6	1972	NSL 40326	Crop Science 12(5):722
KS7	PL-7	1972	NSL 54012	Crop Science 12(5):722
KS8	PL-8	1972	NSL 43593	Crop Science 12(5):722
KS9	PL-9	1972	NSL 73231	Crop Science 12(5):722
KS10	PL-10	1972	NSL 73232	Crop Science 12(5):722
KS11	PL-11	1972	NSL 73233	Crop Science 12(5): 722
KS12	PL-12	1972	NSL 73234	Crop Science 12(5): 722
KS13	PL-13	1972	NSL 73235	Crop Science 12(5):722
KS14	PL-14	1972	NSL 73236	Crop Science 12(5):722
KS15	PL-15	1972	NSL 73237	Crop Science 12(5):722
KS16	PL-16	1972	NSL 73238	Crop Science 12(5):722
KS17	PL-17	1972	NSL 73239	Crop Science 12(5):722
KS18	PL-18	1972	NSL 73240	Crop Science 12(5): 722
KS19	PL-19	1972	NSL 110174	Crop Science 12(5):722
KS20	PL-20	1972	NSL 110175	Crop Science 12(5):722
KS21	PL-21	1972	NSL 110176	Crop Science 12(5): 722
KS22	PL-22	1972	NSL 110178	Crop Science 12(5): 722
KS23	PL-23	1972	NSL 110180	Crop Science 12(5):722
KS24	PL-24	1972	NSL 110182	Crop Science 12(5):722
KS25	PL-25	1972	NSL 67381	Crop Science 12(5):722
KS26	PL-26	1972	NSL 67382	Crop Science 12(5):722
KS27	PL-27	1972	NSL 67383	Crop Science 12(5):722
KS28	PL-28	1972	NSL 67384	Crop Science 12(5):722
KS29	PL-29	1972	NSL 67385	Crop Science 12(5):722
KS45	PL-30	1972	NSL 110192	Crop Science 12(5):722
KS46	PL-31	1972	NSL 110194	Crop Science 12(5):722
KS47	PL-32	1972	NSL 110196	Crop Science 12(5):722
KS48	PL-33	1972	NSL 110198	Crop Science 12(5):722
KS49	PL-34	1972	NSL 110200	Crop Science 12(5):722
KS50	PL-35	1972	NSL 110202	Crop Science 12(5):722
KS51	PL-36	1972	NSL 110204	Crop Science 12(5):722
KS52	PL-37	1972	NSL 110206	Crop Science 12(5):722
KS53	PL-38	1972	NSL 110207	Crop Science 12(5):722
KS54	PL-39	1972	NSL 110208	Crop Science 12(5):722
KS55	PL-40	1974	NSL 110209	Crop Science 14(2):343
DA3494	PL-41	1977	PI 552848	Crop Science 17(1): 191
HA4692	PL-42	1977	PI 552849	Crop Science 17(1): 191
PM4917	PL-43	1977	PI 552850	Crop Science 17(1): 191
7035S	PL-44	1977	PI 552851	Crop Science 17(1): 191
WBH-DAY4610	PL-45	1977	PI 552852	Crop Science 17(1): 191
NB6250	PL-46	1977	PI 552853	Crop Science 17(1): 191
NB6229	PL-47	1977	PI 552854	Crop Science 17(1): 191
NB9040	PL-48	1977	PI 552855	Crop Science 17(1):191
N30	PL-49	1980	NSL 109760	Crop Science 20(6):834
N31	PL-50	1980	NSL 109762	Crop Science 20(6):834
N32	PL-51	1980	NSL 109764	Crop Science 20(6):834
N34	PL-52	1980	NSL 109766	Crop Science 20(6):834

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Table 4. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
N35	PL-53	1980	NSL 109768	Crop Science 20(6): 834
N36	PL-54	1980	NSL 109770	Crop Science 20(6):834
N38	PL-55	1980	NSL 109772	Crop Science 20(6):834
N39	PL-56	1980	NSL 109774	Crop Science 20(6):834
N40	PL-57	1980	NSL 109776	Crop Science 20(6):834
N48	PL-58	1980	NSL 109778	Crop Science 20(6):834
TAM2551	PL-59	1982	CSR 316	Crop Science 22(6): 1280
TAM2552	PL-60	1982	CSR 317	Crop Science 22(6): 1280
TAM2553	PL-61	1982	CSR 318	Crop Science 22(6): 1280
TAM2554	PL-62	1982	CSR 319	Crop Science 22(6): 1280
TAM2555	PL-63	1982	CSR 320	Crop Science 22(6): 1280
TAM2556	PL-64	1982	CSR 321	Crop Science 22(6): 1280
TAM2557	PL-65	1982	CSR 322	Crop Science 22(6): 1280
TAM2558	PL-66	1982	CSR 323	Crop Science 22(6): 1280
TAM2559	PL-67	1982	CSR 324	Crop Science 22(6): 1280
TAM2560	PL-68	1982	CSR 325	Crop Science 22(6): 1280
TAM2561	PL-69	1982	CSR 326	Crop Science 22(6): 1280
TAM2562	PL-70	1982	CSR 327	Crop Science 22(6): 1280
TAM2563	PL-71	1982	CSR 328	Crop Science 22(6): 1280
TAM2564	PL-72	1982	CSR 329	Crop Science 22(6): 1280
TAM2565	PL-73	1982	CSR 330	Crop Science 22(6): 1280
IA1	PL-74	1982	PI 532875	Crop Science 22(6): 1280
IA2	PL-75	1982	PI 532876	Crop Science 22(6): 1280
1A3	PL-76	1982	PI 532877	Crop Science 22(6): 1280
IA4	PL-77	1982	PI 532878	Crop Science 22(6): 1280
IA5	PL-78	1982	PI 532879	Crop Science 22(6): 1280
IA6	PL-79	1982	PI 532880	Crop Science 22(6): 1280
IA7	PL-80	1982	PI 532881	Crop Science 22(6): 1280
IAS	PL-81	1982	PI 532882	Crop Science 22(6): 1280
IA9	PL-82	1982	PI 532883	Crop Science 22(6): 1280
IA10	PL-83	1982	PI 532884	Crop Science 22(6): 1280
IA11	PL-84	1982	PI 532885	Crop Science 22(6): 1280
IA12	PL-85	1982	PI 532886	Crop Science 22(6): 1280
IA13	PL-86	1982	PI 532887	Crop Science 22(6): 1280
IA14	PL-87	1982	PI 532888	Crop Science 22(6): 1280
IA15	PL-88	1982	PI 532889	Crop Science 22(6): 1280
IA16	PL-89	1982	PI 532890	Crop Science 22(6): 1280
IA17 (R-line)	PL-90	1983	PI 561814	Crop Science 23(6): 1229
IA 18 (R-line)	PL-91	1983	PI 561815	Crop Science 23(6): 1229
IA19(R-line)	PL-92	1983	PI 561816	Crop Science 23(6): 1229
IA20(R-line)	PL-93	1983	PI 561817	Crop Science 23(6): 1229
IA21 (R-line)	PL-94	1983	PI 561818	Crop Science 23(6): 1229
IA22 (R-line)	PL-95	1983	PI 561819	Crop Science 23(6): 1229
IA23	PL-96	1983	PI 561820	Crop Science 23(6): 1229
1A24 (R-line)	PL-97	1983	PI 561821	Crop Science 23(6): 1229
IA25 (R-line)	PL-98	1983	PI 561822	Crop Science 23(6): 1229
IA26 (R-line)	PL-99	1983	PI 561823	Crop Science 23(6): 1229
IA27 (R-line)	PL-100	1983	PI 561824	Crop Science 23(6): 1229
IA28 (R-line)	PL-101	1983	PI 561825	Crop Science 23(6): 1229
RTx432	PL-102	1984	NSL 182307	Crop Science 24(2):392
ROKY3	PL-103	1984	NSL 185339	Crop Science 24(3):628
ROKY7	PL-104	1984	NSL 185340	Crop Science 24(3):628
ROKY8	PL-105	1984	NSL 185341	Crop Science 24(3):628

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Table 4. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
ROKY10	PL-106	1984	NSL 185342	Crop Science 24(3):628
ROKY12	PL-107	1984	NSL 185343	Crop Science 24(3):628
ROKY15	PL-108	1984	NSL 185344	Crop Science 24(3):628
ROKY16	PL-109	1984	NSL 185345	Crop Science 24(3):628
RWDY6	PL-110	1984	NSL 185346	Crop Science 24(3):628
ROK27	PL-111	1984	NSL 185347	Crop Science 24(3):628
BOK8	PL-112	1984	NSL 185349	Crop Science 24(3):628
BOK11	PL-113	1984	NSL 185351	Crop Science 24(3):628
BOK12	PL-114	1984	NSL 185353	Crop Science 24(3):628
BOK24	PL-115	1984	NSL 185355	Crop Science 24(3):628
BDwarf Redlan	PL-116	1984	NSL 185357	Crop Science 24(3):628
A3Tx398	PL-117	1984	NSL 184381	Crop Science 24(4):833
ROKY31	PL-118	1984	NSL 187802	Crop Science 24(6): 1224
ROKY33	PL-119	1984	NSL 187803	Crop Science 24(6): 1224
ROKY34	PL-120	1984	NSL 187804	Crop Science 24(6): 1224
ROKY35	PL-121	1984	NSL 187805	Crop Science 24(6): 1224
ROKY39	PL-122	1984	NSL 187806	Crop Science 24(6): 1224
ROKY40	PL-123	1984	NSL 187807	Crop Science 24(6): 1224
ROKY43	PL-124	1984	NSL 187808	Crop Science 24(6): 1224
ROKY46	PL-125	1984	NSL 187809	Crop Science 24(6): 1224
ROKY47	PL-126	1984	NSL 187810	Crop Science 24(6): 1224
ROKY62	PL-127	1984	NSL 187811	Crop Science 24(6): 1224
ROKY76	PL-128	1984	NSL 187812	Crop Science 24(6): 1224
ROKY78	PL-129	1984	NSL 187813	Crop Science 24(6): 1224
RWDY10	PL-130	1984	NSL 187814	Crop Science 24(6): 1224
RWDY13	PL-131	1984	NSL 187815	Crop Science 24(6): 1224
RWDY14	PL-132	1984	NSL 187816	Crop Science 24(6): 1224
RWD16	PL-133	1984	NSL 187817	Crop Science 24(6): 1224
RWDY53	PL-134	1984	NSL 187818	Crop Science 24(6): 1224
RWDY65	PL-135	1984	NSL 187819	Crop Science 24(6): 1224
BWD4	PL-136	1984	NSL 187820	Crop Science 24(6): 1224
BWDY18	PL-137	1984	NSL 187821	Crop Science 24(6): 1224
BOKY54	PL-138	1984	NSL 187822	Crop Science 24(6): 1224
BOKY55	PL-139	1984	NSL 187823	Crop Science 24(6): 1224
RTx430	PL-140	1984	NSL 92562	Crop Science 24(6): 1224
RTx433	PL-141	1984	PI 564164	Crop Science 24(6): 1225
RTx434	PL-142	1984	PI 564165	Crop Science 24(6): 1226
RTx435	PL-143	1986	NSL 199893	Crop Science 26(1):215
IA29	PL-144	1984	PI 561826	Crop Science 24(6): 1227
IA30	PL-145	1984	PI 561827	Crop Science 24(6): 1227
IA31	PL-146	1984	PI 561828	Crop Science 24(6): 1227
IA32	PL-147	1984	PI 561829	Crop Science 24(6): 1227
IA33	PL-148	1984	PI 561830	Crop Science 24(6): 1227
1A34	PL-149	1984	PI 561831	Crop Science 24(6): 1227
1A35	PL-150	1984	PI 561832	Crop Science 24(6): 1227
IA36	PL-151	1984	PI 561833	Crop Science 24(6): 1227
IA37	PL-152	1984	PI 561834	Crop Science 24(6): 1227
IA38	PL-153	1984	PI 561835	Crop Science 24(6): 1227
IA39	PL-154	1984	PI 561836	Crop Science 24(6): 1227
A/BTx626	PL-155	1986	PI 552856	Crop Science 26(1):216
A/BTx627	PL-156	1986	PI 552857	Crop Science 26(1):216
A/BTx628	PL-157	1986	PI 552858	Crop Science 26(1):216
A/BTx629	PL-158	1986	PI 552859	Crop Science 26(1):216

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Table 4. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
A/BTx630	PL-159	1986	PI 552860	Crop Science 26(1):216
A/BTx631	PL-160	1986	PI 552861	Crop Science 26(1):216
A/BTx632	PL-161	1986	PI 552862	Crop Science 26(1):216
AOK8 BM	PL-162	1986	NSL 199460	Crop Science 26(4):842
BOK8 BM	PL-163	1986	NSL 199461	Crop Science 26(4):842
AOK11 BM	PL-164	1986	NSL 199462	Crop Science 26(4):842
BOK11 BM	PL-165	1986	NSL 199463	Crop Science 26(4):842
AWheatland bm	PL-166	1986	NSL 199464	Crop Science 26(4):842
BWheatland bm	PL-167	1986	NSL 199465	Crop Science 26(4):842
ARedlan bm	PL-168	1986	NSL 199466	Crop Science 26(4):842
BRedlan bm	PL-169	1986	NSL 199467	Crop Science 26(4):842
IA40	PL-170	1988	PI 511785	Crop Science 28(2):387
IA41	PL-171	1988	PI 511786	Crop Science 28(2):387
IA42	PL-172	1988	PI 511787	Crop Science 28(2):387
IA43	PL-173	1988	PI 511788	Crop Science 28(2):387
IA44	PL-174	1988	PI 511789	Crop Science 28(2):387
IA45	PL-175	1988	PI 511790	Crop Science 28(2):387
IA46	PL-176	1988	PI 511791	Crop Science 28(2):387
IA47	PL-177	1988	PI 511792	Crop Science 28(2):387
IA48	PL-178	1988	PI 511793	Crop Science 28(2):387
IA49	PL-179	1988	PI 511794	Crop Science 28(2):387
IA50	PL-180	1988	PI 511795	Crop Science 28(2):387
IA51	PL-181	1988	PI 511796	Crop Science 28(2):387
1A52	PL-182	1988	PI 511797	Crop Science 28(2):387
IA53	PL-183	1988	PI 511798	Crop Science 28(2):387
IA54	PL-184	1988	PI 511799	Crop Science 28(2):387
IA55	PL-185	1988	PI 511800	Crop Science 28(2):387
IA56	PL-186	1988	PI 511801	Crop Science 28(2):387
IA57	PL-187	1988	PI 511802	Crop Science 28(2):387
IA58	PL-188	1988	PI 511803	Crop Science 28(2):387
1A59	PL-189	1990	PI 533606	Crop Science 30(1):243
IA60	PL-190	1990	PI 533607	Crop Science 30(1):243
IA61	PL-191	1990	PI 533608	Crop Science 30(1):243
IA62	PL-192	1990	PI 533609	Crop Science 30(1):243
IA63	PL-193	1990	PI 533610	Crop Science 30(1):243
1A64	PL-194	1990	PI 533611	Crop Science 30(1):243
1A65	PL-195	1990	PI 533612	Crop Science 30(1):243
1A66	PL-196	1990	PI 533613	Crop Science 30(1):243
IA67	PL-197	1990	PI 533614	Crop Science 30(1):243
IA68	PL-198	1990	PI 533615	Crop Science 30(1):243
IA69	PL-199	1990	PI 533616	Crop Science 30(1):243
IA70	PL-200	1990	PI 533617	Crop Science 30(1):243
1A71	PL-201	1990	PI 533618	Crop Science 30(1):243
IA72	PL-202	1990	PI 533619	Crop Science 30(1):243
IA73	PL-203	1990	PI 533620	Crop Science 30(1):243
IA74	PL-204	1990	PI 533621	Crop Science 30(1):243
IA75	PL-205	1990	PI 533622	Crop Science 30(1):243
IA76	PL-206	1990	PI 533623	Crop Science 30(1):243
N122	PL-207	1990	PI 537455	Crop Science 30(6): 1379
IA77	PL-208	1990	PI 538360	Crop Science 30(6): 1377
IA78	PL-209	1990	PI 538361	Crop Science 30(6): 1377
IA79	PL-210	1990	PI 538362	Crop Science 30(6): 1377
IA80	PL-211	1990	PI 538363	Crop Science 30(6): 1377

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Table 4. *continued.*

Cultivar name	Registration No.	Year	Designation	Source
IA81	PL-212	1990	PI 538364	Crop Science 30(6): 1377
IA82	PL-213	1990	PI 538365	Crop Science 30(6): 1377
IA83	PL-214	1990	PI 538366	Crop Science 30(6): 1377
IA84	PL-215	1990	PI 538367	Crop Science 30(6): 1377
IA85	PL-216	1990	PI 538368	Crop Science 30(6): 1377
IA86	PL-217	1990	PI 538369	Crop Science 30(6): 1377
IA87	PL-218	1990	PI 538370	Crop Science 30(6): 1377
IA88	PL-219	1990	PI 538371	Crop Science 30(6): 1377
IA89	PL-220	1990	PI 538372	Crop Science 30(6): 1377
IA90	PL-221	1990	PI 538373	Crop Science 30(6): 1377
IA9!	PL-222	1990	PI 538374	Crop Science 30(6): 1377
R LINE AR 1000	PL-223	1991	PI 542407	Crop Science 31(5): 1400
R LINE AR2200	PL-224	1991	PI 542408	Crop Science 31(5): 1400
R LINE AR2400	PL-225	1991	PI 542409	Crop Science 31(5): 1400
R LINE AK2401	PL-226	1991	PI 542410	Crop Science 31(5): 1400
R LINE AR2402	PL-227	1991	PI 542411	Crop Science 31(5): 1400
R LINE AR2403	PL-228	1991	PI 542412	Crop Science 31(5): 1400
R LINE AR2404	PL-229	1991	PI 542413	Crop Science 31(5): 1400
R LINE AR2405	PL-230	1991	PI 542414	Crop Science 31 (5): 1400
R LINE AR2406	PL-231	1991	PI 542415	Crop Science 31(5): 1400
A2/B2Tx636	PL-232	1992	PI 552527	Crop Science 32(2):511
A2/B2Tx637	PL-233	1992	PI 552528	Crop Science 32(2):511
A/BTx635	PL-234	1992	PI 561073	Crop Science 32(6): 1517
A/BTxARG-1	PL-235	1992	PI 561072	Crop Science 32(6): 1517
RTx436	PL-236	1992	PI 561071	Crop Science 32(6): 1518
P89001	PL-237	1993	PI 561846	Crop Science 33(1):222
P89002	PL-238	1993	PI 561847	Crop Science 33(1):222
P89003	PL-239	1993	PI 561848	Crop Science 33(1):222
P89004	PL-240	1993	PI 561849	Crop Science 33(1):222
P89005	PL-241	1993	PI 561850	Crop Science 33(1):222
P89006	PL-242	1993	PI 561851	Crop Science 33(1):222
P89007	PL-243	1993	PI 561852	Crop Science 33(1):222
P89008	PL-244	1993	PI 561853	Crop Science 33(1):222
P89009	PL-245	1993	PI 561854	Crop Science 33(1):222
P89010	PL-246	1993	PI 561855	Crop Science 33(1):222
NJ27	PL-247	1993	PI 562605	Crop *Science* 33(6): 1427
N128	PL-248	1993	PI 562606	Crop Science 33(6): 1427
N129	PL-249	1993	PI 562607	Crop Science 33(6): 1427
N130	PL-250	1993	PI 562608	Crop Science 33(6): 1427
N131	PL-251	1993	PI 562609	Crop Science 33(6): 1427
N132	PL-252	1993	PI 562610	Crop Science 33(6): 1427
Tx2907	PL-253	1996	PI 585295	Crop Science 36(2):479
1CSB 88019	PL-254	1996	PI 592505	Crop Science 36(3):825
ICSB 88020	PL-255	1996	PI 592506	Crop Science 36(3):825
1CSB 38	PL-256	1999	PI 602979	Crop Science 39(2):599
ICSA 38	PL-256cms	1999	PI 602989	Crop Science 39(2):599
ICSB 39	PL-257	1999	PI 602980	Crop Science 39(2):599
ICSA 39	PL-257cms	1999	PI 602990	Crop Science 39(2):599
ICSV 247	PL-258	1999	PI 602983	Crop Science 39(2):599
ICSR 101	PL-259	1999	PI 602981	Crop Science 39(2):599
B3 I00M	PL-260	1999	PI 598085	Crop Science 39(1):306
A3 100M	PL-260cms	1999	PI 598084	Crop Science 39(1):306
B3 90M	PL-261	1999	PI 598087	Crop Science 39(I):306

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Table 4. *continued.*

Cultivar name	Registration No.	Registration Year	Designation	Source
A3 90M	PL-261cms	1999	PI 598086	Crop Science 39(1):306
B3 80M	PL-262	1999	PI 598089	Crop Science 39(1):306
A3 80M	PL-262cms	1999	PI 598088	Crop Science 39(1):306
B3 60M	PL-263	1999	PI 598091	Crop Science 39(1):306
A3 60M	PL-263cms	1999	PI 598090	Crop Science 39(1):306
B3 58M	PL-264	1999	PI 598093	Crop Science 39(1):306
A3 58M	PL-264cms	1999	PI 598092	Crop Science 39(1):306
B3 44M	PL-265	1999	PI 598095	Crop Science 39(1):306
A3 44M	PL-265cms	1999	PI 598094	Crop Science 39(1):306
B3 38M	PL-266	1999	PI 598097	Crop Science 39(1):306
A3 38M	PL-266cms	1999	PI 598096	Crop Science 39(1) :306
B3 Hegari	PL-267	1999	PI 598099	Crop Science 39(1):306
A3 Hegari	PL-267cms	1999	PI 598098	Crop Science 39(1):306
B3 Early Hegari	PL-268	1999	PI 598101	Crop Science 39(1):306
A3 Early Hegari	PL-268cms	1999	PI 598100	Crop Science 39(1):306
B3 SM100	PL-269	1999	PI 598103	Crop Science 39(1):306
A3 SM100	PL-269cms	1999	PI 598102	Crop Science 39(1):306
B3 SM90	PL-270	1999	PI 598105	Crop Science 39(1):306
A3 SM90	PL-270cms	1999	PI 598104	Crop Science 39(1):306
B3 SM80	PL-271	1999	PI 598107	Crop Science 39(1):306
A3 SM80	PL-271cms	1999	PI 598106	Crop Science 39(1):306
B3 SM60	PL-272	1999	PI 598109	Crop Science 39(1):306
A3 SM60	PL-272cms	1999	PI 598108	Crop Science 39(1):306
B3 SA1170 (Tall Western)	PL-273	1999	PI 598111	Crop Science 39(1):306
A3 SA1170 (Tall Western)	PL-273cms	1999	PI 598110	Crop Science 39(1):306
B3 FC8962 (Texas Blackhull Kafir)	PL-274	1999	PI 598113	Crop Science 39(1):306
A3 FC8962 (Texas Blackhull Kafir)	PL-274cms	1999	PI 598112	Crop Science 39(1):306
B3 WSM100 (White Sooner Milo)	PL-275	1999	PI 598115	Crop Science 39(1):306
A3 WSM 100 (White Sooner Milo)	PL-275cms	1999	PI 598114	Crop Science 39(1):306
B3 CI243 (Acme Broomcorn)	PL-276	1999	PI 598117	Crop Science 39(1):306
A3 CI243 (Acme Broomcorn)	PL-276cms	1999	PI 598116	Crop Science 39(1):306
B3 Jap. Dwarf Broomcorn	PL-277	1999	PI 598119	Crop Science 39(1):306
A3 Jap. Dwarf Broomcorn	PL-277cms	1999	PI 598118	Crop Science 39(1):306
B3 BTx3197 (Combine Kafir 60)	PL-278	1999	PI 598121	Crop Science 39(1):306
A3 BTx3197 (Combine Kafir 60)	PL-278cms	1999	PI 598120	Crop Science 39(1):306
B3 BTx616 (4-dwarf Kafir)	PL-279	1999	PI 598123	Crop Science 39(1):306
A3 BTx616(4-dwarf Kafir)	PL-279cms	1999	PI 598122	Crop Science 39(1):306
TIFT 98bmrA1	PL-280cms	2000	PI 606705	Crop Science 40(2):592
TIFT 98bmrB 1	PL-281	2000	PI 606706	Crop Science 40(2):592
RTx437	PL-282	2003	PI 629034	Crop Science 43(1):445

Table 5. Cultivar name, registration number and year, designation and source of sudangrass registered as genetic stock and parental lines in USA.

Genetic stock/parental line name	Registration		Designation	Source
	No.	Year		
A3N242	GS-1	1998	PI 598139	Crop Science 38(2):555
A3N243	GS-2	1998	PI 598140	Crop Science 38(2):555
TAM-GA S-1A	PL-1	1969	CSR 388	Crop Science 9(3):398
TAM-GA S-1B	PL-2	1969	CSR 389	Crop Science 9(3):398
R LINE AR2001	PL-3	1991	PI 542405	Crop Science 31(5): 1402
R LINE AR2002	PL-4	1991	PI 542406	Crop Science 31(5): 1402

Table 6. Cultivar name, registration number and year, designation and source of broomcorn and other grass registered as cultivars in USA.

Cultivar name	Registration		Designation	Source
	No.	Year		
Broomcorn				
Plains 1	CV-1	1971	NSL 67945	Crop Science 11(4):601
Plains 2	CV-2	1971	NSL 67946	Crop Science 1 l(4):60l
Dex	CV-3	1977	NSL 42871	Crop Science 17(2):345
Deer	CV-4	1977	NSL 70792	Crop Science 17(2):345
Other grass				
Cumberland	CV-13	1968	NSL 96466	Crop Science 8(1): 130

been registered in Crop Science (Table 2.). Registration of genetic stocks of sorghum began in 1990 with a total of 120 sorghums currently registered (Table 3). Kansas registered the first parental line, KSI, in 1972 and since then 282 lines have been registered with Crop Science (Table 4). Tables 5 and 6 present information on sudangrass, broomcorn and other grass.

These tables are to be used as reference material for those requesting these sorghums, for reviewing cultivar names to ensure that names are not duplicated, and for general knowledge. Additional information on each registered sorghum can be found at http://www.ars-grin.gov/npgs/searchgrin.html.

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Release of 49 Converted Sorghum Germplasm Lines from the Sorghum Conversion Program

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The Texas Agricultural Experiment Station of the Texas A & M University System and the Agricultural Research Service (ARS), United States Department of Agriculture (USDA) announce the release of 49 combine height, early-maturing converted exotic sorghum (*Sorghum bicolor*) lines for use as genetic stocks and germplasm source materials by sorghum breeders. These 49 converted lines were developed in a research program, known as the Sorghum Conversion Program, conducted cooperatively by the USDA, ARS, at Mayaguez, Puerto Rico and the Texas Agricultural Experiment Station, Texas, USA.

The converted lines were developed through a backcross procedure in which tall, late-maturing tropical sorghum varieties or cultivars were converted to early-maturing, combine-height sorghums. Conversion is accomplished by a crossing and backcrossing program using favorable short-day pholoperiods during the winter in Puerto Rico, with selection for early, short genotypes within segregating populations under long-day, summer conditions at Chillicothe, Texas (Stephens et al. 1967). All converted lines, except five, for release (see Table 1) have received four backcrosses to the original exotic variety. The non-recurrent parent used in all cases except three was an early-maturing, 4-dwarf Martin B line, BTx406, of US origin. Three lines used BTx3121 as the non-recurrent parent. The exotic varieties are used as male parents in all crosses and backcrosses until the third backcross when they are used as the females to recover the original cytoplasm in the converted line.

The converted lines are non-sensitive to photoperiod, will mature normally in USA, and are short statured, generally 3- or 4-dwarf in height, but occasionally 2-dwarf in height. They represent new sources of germplasm from the World Sorghum Collection and are of a height and maturity to make them readily usable in the United States and other temperate zone areas of the world. These materials should contain new sources of desirable traits such as disease and insect resistance, drought resistance and improved grain quality, and should be useful to breeders and other sorghum researchers as germplasm sources in developing improved sorghum lines and hybrids. Table 1 gives the designation of the converted lines and information on the original exotic varieties.

Seed will be maintained and distributed by the Texas Agricultural Experiment Station at the Texas A & M University Agricultural Research and Extension Center at Lubbock, Route 3, Box 219, Lubbock, TX 79401-9757, USA. It will be available in germplasm quantities only. Genetic material of this release will be deposited with the National Plant Germplasm System, where it will be available for research purposes including development and commercialization of new varieties/cultivars. Those receiving seed are asked to agree to supply, upon request, information about breeding behavior, desirability and usefulness of the material and to cite it as the origin of useful derived lines.

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Table 1. Forty-nine converted line releases in 2003 and information on original exotic cultivars.

Designation[1]	Registration/PI no.[2]	SC no[3]	Local name[4]	Country of origin	Classification[5] R	Classification[5] WG	Reason for conversion[6]	Fertility reaction[7]
IS 956C	PI 570984	1251	FC 4544, Tarrano, SU 33	Sudan	C	37: Zerazera	Elite Zerazera	
IS 1596C	PI 291238	616 (BC$_3$E)	K I Irungu Cholam	India	B	11: Dochna	Mod Nur	PR
IS 2144C	PI 221552	741	Jan Dawa	Nigeria	C	36: Caud-Kaura	Mod Nur	R
IS 2267C	PI 608864	1426	CSM-205	Mali	G	20: Guineense	Elite Var	
IS 2319C	PI 217837, No. 189	706	Lwalli White	Sudan	C	30: Caudatum	Mod Nur	R
IS 2484C	PI 152595, MN 734	49*	Ankolib-Red	Sudan	G	21: Conspicuum	Div/Elite/IES	R
IS 2499C	MN 751	1218	MN 751	(through USA)	CG	100: Caud-Guin	Midge Res.	
IS 3128C	PI 213901	823		Mozambique	DB	92-93: Doc-Sub	Mod Nur	R
IS 3485C	PI 570802, SU 162	702	Fanda 128	Sudan	C	30: Caudatum	Mod Nur	
IS 3703C	NSL 55832	505	No. 42 Iecama Alemaya	Ethiopia	DB	93: Subglabrescens	Mod Nur	R
IS 3830C	NSL 50465	263 (BC$_3$E)	Gountina Chioningue	Mali	G	20: Guineense	Mod Nur	R
IS 4404C	NSL 54761	860	Ram Niwas, Etawah	India	D	50: Durra	Mod Nur	PR
IS 4929C	NSL 55497	878 (BC$_3$B)	Karjiot	India	D	50: Durra	Mod Nur	B
IS 5456C	NSL 55658	582	Cholam Mohamma	India	DB	92: D-Doc	Mod Nur	R
IS 5590C	NSL 54617	888	Kempu Jola Malkhaid	India	D	50: Durra	Mod Nur	R
IS 5900C	NSL 50376	249	LAL Bedra Seja	India	G	23: Roxburghii	Mod Nur	R
IS 6403C	NSL 55729	479	Jowar Kalgundi	India	D	51: Nandyal	Mod Nur	R
IS 6408C	NSL 55734	480	Jowar Kalgundi	India	D	51: Nandyal	Mod Nur	R
IS 7151C	NSL 51991	720	Matama	Kenya	C	31: Caud-Nig	Mod Nur	R
IS 7369C	NSL 50570	276	BA 12	Nigeria	G	21: Conspicuum	Mod Nur	PB
IS 7427C	NSL 50601	295	BE 34	Nigeria	G	21: Conspicuum	Mod Nur	R
IS 7551C	NSL 54237	409	PL 16	Nigeria	C	100: Caud-Guin	Mod Nur	R
IS 7832C	NSL 50771	551 (-B)	ZA125	Nigeria	G	21: Conspicuum	Mod Nur	R
IS 7876C	NSL 50805	542 (BC$_3$B)	IN48	Nigeria	G	21: Conspicuum	Mod Nur	B
IS 11080C	PI 329323	999	Col. No. 127-B	Ethiopia	DB	93: Subglabrescens	High Altitude	R
IS 11455C	PI 329719	1015	Col. No. R-85	Ethiopia	D-B	92-93: Sub-D-Doc	High Altitude	R
IS 11569C	PI 329836	1019	Col. No. R-251	Ethiopia	C	31: Caud-Nig	High Altitude	B
IS 12584C	PI 153852, MN 1258	75 (BC$_3$E)	Mzekwa 2 No.748	Kenya	C	31: Caud-Nig	Div/Elite/IES	R
IS 12607C	PI 248238	106	Glumes glossy	Ethiopia	B	11: Dochna	Div/Elite/JCS	PB
IS 12641C	PI 276806, SA 2324	150*	Unnamed-R2.43	Ethiopia	DB	92: D-Doc	Div/Elite/JCS	R
IS 12647C	PI 276817, SA 2335	156	Unnamed-R3,81	Ethiopia	B	11: Dochna	Div/Elite/JCS	B
IS 12650C	PI 276820, SA 2338	159	Unnamed-R3,84	Ethiopia	D-DB	50-93: D-Sub	Div/Elite/JCS	R
IS 12663C	PI 276839, SA 2357	172	Unnamed-R4,B3	Ethiopia	C	37: Zerazera	Div/Elite/JCS	R
IS 12669C	PI 276850, SA 2368	178*	Dongomogof	Ethiopia	D-DB	50-93: D-Sub	Div/Elite/JCS	PR

continued

Table 1. *continued.*

Designation[1]	Registration/PI no.[2]	SC no[3]	Local name[4]	Country of origin	Classification[5] R	Classification[5] WG	Reason for conversion[6]	Fertility reaction[7]
IS 14384C		1429	From ICRISAT Grain Mold Nur.	Zimbabwe	G	20: Guineense	Grain Mold Res.	
IS 26836C	570380	1494	Aduholio, MBKB 13, SU 2242	Sudan	GC	100: Caudatum-Guinea	Elite/RAF	
SC 968C	287660	968	S-50-74	Zimbabwe	DB	93: Subglabrescens	Anthracnose Res. (HBH)	R
SC 971C	550725	971	Millo Blanco, Local variety	Puerto Rico	DB	93: Subglabrescens	Forage/Acid Soil Tol	B
SC 1215C	NSL 365720	1215	A4 D4	Niger	KG	110: Caffrorum-Roxburghii	Sandy land variety	
SC 1277C		1277	Bargon Warni	India	D	50: Durra	Sugary Endo	
SC 1416C		1416	Col#279	Niger	DB	90: Durra-Bicolor	Div	
SC 1424C	609612	1424	CSM-932, Hamba Biba	Mali	D	150: Durra-Kafir	Hambo (Canoe Har) type	
SC 1439C	522129	1439	RC 049, FAO 36, Kitte Wuleng	Gambia	C	31: Caud-Nig	Acid Soil Tol	
SC 1440C	522160	1440	RC 092, FAO 69, Bachara	Gambia	C	31: Caud-Nig	Acid Soil Tol	
SC 1451C	525059	1451	MW 719	Malawi	C	30: Caudatum	Acid Soil Tol	
SC 1463C	NSL 360537	1463	No. Kordofan, Bautingay	Sudan	C	31: Caud-Nig	Sandy/Div/TB	
SC 1471C		1471	No. Kordofan, Beit Eltour	Sudan	DB	90: Durra-Bicolor	Sandy/Div/TB	
SC 1476C	NSL 365799	1476	No. Kordofan, Eish Jabal	Sudan	CK	130: Caudatum-Kafir	Sandy/Div/TB	
SC 1489C	NSL 360549	1489	SS58	Somalia	D	50: Durra	Elite/Div/Drought Res./HP	

1. Designation of converted lines was obtained by adding C to the IS number used in the World Sorghum Collection and in some cases C to the SC number.
2. Registration and PI (plant identification) numbers identify the converted accession in the US National Plant Germplasm System.
3. The SC number is the serial number given to the exotic variety when entered into the Sorghum Conversion Program and used during conversion. The non recurrent parent was BTx406, a 4-dwarf Martin B-line, except in lines followed by * in which BTx3121 was the parent. All convereted lines have four backcrosses to the exotic unless indicated. All are in original exotic cytoplasm unless indicated differently by "B".
4. The local name, number, code, or description of the exotic variety.
5. Classification of exotic line. R = Race, based on Harlan and de Wet (1972), where B = Bicolor, G = Guinea, C = Caudatum, K = Kafir and D = Durra. WG = Working Group number and name, where Doc = Dochna, Caud = Caudatum, Guin = Guinea, Sub = Subglabrescens and Nig = Nigricans and they are based on a revised Working Group classification by Dahlberg (2000).
6. General reasons for conversion. Elite Zerazera = Elite germplasm selected from the Sudan collection; Mod Nur = Modified Nursery selected by KO Rachie, former Rockefeller Foundation sorghum researcher and coworkers, from World Sorghum Collection, 1963–64; Elite Var = Elite variety from the Mali collection; Elite/IES = Elite material selected by JE Stokes, former USDA-ARS sorghum researcher at Meridian, MS, USA; Elite/JCS = Elite material selected by JC Stephens, former USDA-ARS sorghum researcher at Chillicothe, Texas; Elite/RAF = Elite material selected by RA Frederiksen, former sorghum researcher from Texas A&M University; High Altitude = Germplasm from the highlands of Ethiopia; Acid Soil Tol = Acid soil tolerance as reported by RR Duncan, former sorghum researcher from University of Georgia; Sandy = Represents reported drought tolerant material from dry, sandy areas in Northern Kordofan area of Sudan; Sugary Endo = Sugary endosperm sorghum from India; Div = Diversity; HBH = Resistance reported by HB Harris, former sorghum researcher from University of Georgia; TB = T Berhe (former contractor from Kansas State University) in Sudan; HP = H Porter (former contractor from University of Wyoming) in Somalia.
7. Determined from crosses between a milo-kafir cytoplasmic-genetic male sterile (A1) and the exotic line: R = restorer (progeny all male fertile); B = maintainer (progeny all male sterile); PR = partial restorer; PB = partial maintainer.

Release of 44 Grain Sorghum Seed Parents (A-lines) and their Respective Maintainers (B-lines) (N341 A-B to N384 A-B)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 44 grain sorghum *(Sorghum bicolor)* seed parents in the medium to full season maturity class for Southeast Nebraska and similar environments. These lines are male sterile in the A_1 cytoplasmic male sterility system (milo cytoplasm). These provide new genetic diversity for making full season sorghum grain hybrids.

These seed parent germplasm lines (N341 A and B to N384 A and B) were developed via the introgression of tropically adapted food quality grain sorghums into sorghum seed parents adapted to the US high plains. These lines resulted from emasculation crosses made from 1988 to 1992 between an array of parents (Table 1). Derivatives of many of the US adapted germplasm lines used as parents in this series of crosses were released as seed parents in 1998 (N250 to N311). Generally pedigree selection was followed from F_2 to F_{10} at the Agricultural Research Division Center (ARDC) experimental farm in Mead, Nebraska including 3 to 4 generation advances in

Table 1. Characteristics of 44 full season sorghum seed parent germplasm lines released by the University of Nebraska-Lincoln, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
341B	9004	99P1092-1	(JDE2300 x N122B)-2	82	96	P	W
341A	9005	99P1093 x 1092-1		81	90	P	W
342B	9006	99P1094-1	(JDE2300 x N122B)-2	78	114	P	W
342A	9008	99P 1095 x 1094-1		78	112	P	W
343B	9009	99P 1096-1	JDE2533-I x N122B	76	140	T	W
343A	9010	99P 1097 x 1096-1		74	126	T	W
344B	9011	98M9386-2	88CJDE2300 x N122B	81	104	P	W
344A	9012	99P 1099 x 1098-1		82	106	P	W
345B	9013	99P 1166-1	88CJDE2300 x N122B	80	98	P	YE
345A	9014	99P1167 x 1166-1		79	98	P	YE
346B	9015	99P1168-2	88CJDE2300 x N122B	73	120	P	YE
346A	9016	99P1169X 1168-1		71	118	P	YE
347B	9017	99P 1102-1	Dorado x 348	77	116	T	W
347A	9018	99P1103 x 1102-1		77	104	T	W
348B	9019	99P1104-1	Dorado x 348	77	102	T	W
348A	9020	99P1105 x 1104-1		79	100	T	W
349B	9023	99P1114-1	(TX623 x MB 12) x (CK60 x IS89)	79	120	T	w
349A	9024	99P1115 x 1114-1		78	118	T	w
350B	9025	99P1121-2	(TX623 x MB12) x N122B	81	116	P	W
350A	9026	99P1122 x 1121-2		81	108	P	w
35 1B	9027	99P1123-1	SRB x Dial346	81	122	P	w
351A	9028	99P1124 x 1123-1		83	112	P	w
352B	9029	99P1123-2	SRB x Dial346	80	118	P	W
352A	9030	99P1124 x 1123-2		82	116	P	w
353B	9031	99P1125	(TX623 x MB 12) x (TX623 x IS89-2B)	83	142	T	YE
353A	9032	98M9434 x 9433-1		84	122	T	YE
354B	9038	99P1127-2	(TX623 x MB 12) x (TX623 x IS89-2B)	81	120	T	YE
354A	9039	98M9438 x 9437-2	(TX623 x MB 12) x (TX623 x IS89-2B)	82	124	T	YE

continued

Table 1. *continued.*

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
355B	9040	99P1129-1	(TX623 x MB 12) x (TX623 x IS89-2B)	84	98	T	W
355A	9041	98P1241 x 1240	(TX623 x MB 12) x (TX623 x IS89-2B)	80	108	T	W
356B	9042	99P1131	(CSV-4 x GG370-1) x (SRB x Dial-346)	72	120	T	YE
356A	9043	99P1132 x 1131		71	110	T	YE
357B	9044	99P1133	(CSV-4 x GG370-1) x (SRB x Dial-346)	72	116	T	YE
357A	9045	99P1134 x 1133		71	120	T	YE
358B	9046	99P1135	(CSV-4 x GG370-1) x (SRB x Dial-346)	76	118	T	YE
358A	9047	99P1136 x 1135		76	120	T	YE
359B	9059	99P1156	063B = (SRB x MB5)	80	94	T	R
359A	9060	98M9761 x 9762-1	063A	81	94	T	R
360B	9068	99P1160-2	98M044B=(BULK-Y-398 x 348)	75	96	P	W
360A	9069	99P1161 x 1160-1	93M044A	76	100	P	W
36 1B	9070	99P1164-1	95M036B (4965 x TX6318)	80	108	P	W/YE
361A	9072	99P1165 x 1164-1	98M036A	84	100	P	W/YE
362B	9079	99P1183-2	SRB x Dial-346	80	118	P	YE
362A	9080	99P1184 x 1183-1		81	114	P	YE
363B	9081	99P1185-1	(BULK-Y-398 x 348) x PBCF2	70	116	T	W
363A	9082	99P1186 x 1185-1		70	116	T	W
364B	9083	99P1185-2	(BULK-Y-398 x 348) x PBCF2	74	116	T	W
364A	9084	99P1186 x 1185-2		74	114	T	W
365B	9085	99P1187-1	(BULK-Y-398 x 348) x PBCF2	80	116	T	W
365A	9086	99P1188X 1187-1		83	118	T/P	W
366B	9123	99P1208-1	(CK60 x SEGOASPL20) x (TX623 x MB 12)	76	106	T	YE
366A	9124	99P1209 x 1208-1		72	120	T	YE
367B	9125	99P1210-1	(CK60 x SEGOVSPL20) x (TX623 x MB 12)	82	108	T	YE
367A	9126	99P1211 x 1210-1		81	102	T	YE
368B	9132	99P1212-1	(CK60 x SEGO\SPL20) x (TX623 x MB 12)	76	104	T	YE
368A	9133	99P1213 x 1212-1		78	108	T	YE
369B	9134	99P1212-2	(CK60 x SEGOVSPL20) x (TX623 x MB 12)	81	106	T	YE
369A	9135	99P1213 x 1212-2		80	104	T	YE
370B	9137	99P1214-1	(CK60 x SEGO\SPL20) x (TX623 x MB 12)	82	104	T	YE
370A	9138	99P1215 x 1214-1		82	108	T	YE
371B	9144	98M9174-3	SRB x Dial-346	80	116	T	YE
371A	9145	98M9175 x 9174-1		80	112	T	YE
372B	9149	98M9184	(TX623 x MB9) x (TX623 x IS89-2B)	84	130	T	W
372A	9150	97M8096 x 8095-1	(TX623 x MB9) x (TX623 x IS89-2B)	83	130	T	W
373B	9154	98M8007-1	(BULK-Y-398 x 348) x PBCF2)	84	122	T	YE
373A	9155	98M8008 x 8007-1		83	120	T	YE.
374B	8004	99P1219-1	(CK60 x N122B) x (TX623 x MB 12)	79	106	T	YE
374A	8005	99P1221 X 1219-1		75	102	T	YE
375B	8006	99P1219-2	(CK60 x N122B) x (TX623 x MB 12)	78	106	T	YE
375A	8007	99P1221 x 1219-2		76	104	T	YE
376B	8008	99P1219-3	(CK60 x N122B) x (TX623 x MB 12)	79	106	T	YE
376A	8009	99P1221 x 1219-3		76	108	T	YE
377B	8013	99P1220-2	(CK60 x N122B) x (TX623 x MB 12)	79	104	T	W
377A	8014	99P1221 x 1220-2		76	94	T	W
378B	8031	98M6152-2	(CK60B x N122B)x(311B)	74	108	T	YE

continued

Table 1. *continued.*

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
378A	8032	98M6151 x 6152-2		74	110	T	YE
379B	8037	98M6157-1	(CK60B x N122B) x (SRB x RS/B-162) x SPL11	82	108	T	W
379A	8038	98M6158 x 6157-1		80	112	T	W
380B	8041	98M6165-3	(CK60 x N122B) x (TX623 x MB 12)	84	106	T	YE
380A	8040	98M6166 x 6165-2		82	106	T	YE
381B	8043	98M6173-1	(CK60 x N122B) x (TX623 x MB 12)	82	108	T	YE
381A	8044	98M6174 x 6173-1		80	110	T	YE
382B	8045	98M6173-2	(CK60 x N122B) x (TX623 x MB 12)	78	106	T	W
382A	8046	98M6174 x 6173-2		74	106	T	W
383B	8047	98M6175-1	(CK60 x N122B) x (493B(SRB x SEGO))	88	104	T	YE
383A	8048	98M6176 x 6175-1		80	108	T	YE
384B	8049	98M6179-2	(CK60 x N122B) x (TX623 x IS39-2B)	81	108	T	YE
384A	8050	98M6180 x 6179-1		79	110	T	YE
	6010	CK60A (check)		76	96	P	W

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
P = purple; T = tan; W = white; YE = yellow endosperm; R = red.

winter nurseries. Testcrosses were made at F_4 to F_6 to $CK60A_1$ (milo cytoplasm). Where testcrosses included completely male sterile plants, 4-6 generations of plant to plant backcrosses were made concurrently while selecting only within those B-lines that continued to perfectly maintain male sterility. Backcrossing is complete in the A-B pairs in Table 1 commencing with number 9 in the 1999 row number. Those pairs with a row number beginning with number 8 may require an additional backcross to attain uniformity between A and B lines. Frequently several sister A-B pairs have been developed from the same cross. These have either obvious phenotypic differences or were judged desirable separately.

Days to flowering, plant height, and plant and grain color of each germplasm line are shown in Table 1. All A lines have consistently shown good male sterility over the years. In general, these seed parents are average to short in height and medium early to medium late in maturity. All but two lines have white or pale yellow grain. Pest and disease reactions of these lines have not been determined.

Because of their parentage these seed parent germplasm lines contribute new genetic diversity for sorghum hybrid development. White or pale yellow grain lines will permit the development of white grain hybrids. Also, food quality hybrids can be made with tan plant white grain restorer lines.

Ten g of seed of individual A-B line pairs are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 49 Grain Sorghum A, CMS Male Fertility Restorer Germplasm Lines (N385R to N433R)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 49 grain sorghum *(Sorghum bi color)* lines which restore male fertility in hybrids made with A, cytoplasmic male sterile (CMS) (milo cytoplasm) seed parents. These provide new genetic diversity for making full season sorghum grain hybrids.

These restorer lines (N385R to N433R) were developed from a program to introgress grain sorghum food quality

Table 1. Characteristics of 49 full season sorghum restorer germplasm lines released by the University of Nebraska-Lincoln, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
385R	7004	99P1238-1	(PL1 x (KS4 x NP3-C1)) x NB9040 x SEGO	82	92	P	YE
386R	7006	99P1239-1	(PL1 x (KS4 x NP3-C1)) x NB9040 x SEGO	86	100	P	YE
387R	7009	99P1240-2	(PL1 x (KS4 x NP3-C1)) x (CE151-262 x 8505)	85	104	P	YE
388R	7013	99P1241-1	(PL1 x KS4 x NP3-C1)) x 9032R	82	100	T	R
389R	7015	99P1241-2(1)	(PL1 x KS4 x NP3-C1)) x 9032R	72	102	T	R
390R	7017	99P1241-3	(PL1 x KS4 x NP3-C1)) x 9032R	71	102	T	R
391R	7024	99P1244-1	9032 x (NB9040 x SEGO))	86	104	T	W
392R	7026	99P1250-1	9032 x MR732	84	120	T	R
393R	7028	99P1253-2	95PPBC23 x (SRB x MB5)	87	114	T	YE
394R	7030	99P1253-3	95PPBC23 x (SRB x MB5)	84	110	T	YE
395R	7047	99P1261-1	NB9040 (3541 x BKY-D121)=7089RSeln	80	104	T	R
396R	7057	99P1265-1	NB9040 (3541 x BKY-D121)=7089RSeln	87	112	T	YE
397R	7060	99P1266-1	NB9040 (3541 x BKY-D121)=7089RSeln	82	114	T	YE
398R	7062	99P1268 1	NB9040 (3541 x BKY-D121)=7089RScln	81	114	T	YE
399R	7068	99P1272-1	NB9040 (3541 x BKY-D121)=7089RSeln	84	120	T	YE
400R	7070	99P1278-2	NB9040 (3541 x BKY-D121)=7089RSeln	88	116	T	YE
401R	7073	99P1278-3	NB9040 (3541 x BKY-D121)=7089RSeln	79	120	T	YE
402R	7077	99P1280-1	KP9 x (SEGO x IS 1894025-1)	66	94	P	W
403R	7086	99P1284-2	PL1 x(KS4xNP3-CI)	80	116	P	YE
404R	7092	99P1287-1	PLI x (KS4 x NP3-C1) x (CE151-262) x 8505)	84	116	P	YE
405R	7096	99P1290-1	PL1 x (KS4 x NP3-C1) x (CE151-262) x 8505)	80	100	P/T	W
406R	7098	99P1290-2	PL1 x (KS4 x NP3-C1) x (CE151-262) x 8505)	86	114	P	W
407R	7100	99P1291-1	PI.I x (KS4 x NP3-C1) x (OKI51-262) x 8505)	78	106	P	W
408R	7102	99P1292-1	PL1 x (KS4 x NP3-C1) x (CE151-262) x 8505)	81	116	T	W
409R	7104	99P1292-3	PL1 x (KS4 x NP3-C1) x (CE151-262) x 8505)	81	106	PAT	W
410R	7121	99P1295-2	PL1 x (KS4 x NP3-C1) x (CE151-262) x 8505)	79	96	P	YE
411R	7137	98M7014-2	(KS4 x NP3-CI)xTX430	84	102	P	W
412R	7146	98M7021-2	CE151-262 x 8505	71	104	T	W
413R	7150	98M7031-2	NB9040 x (3541 x BKY-D121)	82	108	T	YE
414R	7154	98M7034-1	NB9040 x (3541 x BKY-D121)	81	112	T	YE
415R	7157	96M7150-1	NB9040 x SEGO	81	114	P	YE
416R	7159	98M7069-1	(KS4 x NP3-CI) x TX430	80	108	P	YE
417R	7161	98M7075-1	(KS4 x NP3-CI) x 2721	77	116	P	W
418R	7168	98M7111-1	PL1 x(KS4 x NP3-CI)	84	110	T	YE
419R	7171	98M7113-1	(KS4 x NP3-CI) x TX430	77	114	P	YE
420R	7172	98M7115-1	(KS4 x NP3-CT) x (IA28 x TX8505)	76	106	T	W
421R	7183	98M7143-1	(PL1 x (KS4 x NP3-C1)) x NB9040 x (3541 x BKY-121)	84	96	P	YE-
422R	7186	98M7143-2	(PL1 x (KS4 x NP3-C1)) x NB9040 x (3541 x BKY-121)	86	106	P	YE
423R	7195	98M7150-2	(PLI x(KS4 x NP3-CI)) x NB9040 x (3541 x BKY-121)	86	98	P	YE
424R	7200	98M7152-2	(PL 1 x (KS4 x NP3-C1)) x NB9040 x (3541 x BKY-121)	82	108	P	W
425R	7204	98M7156-2	(PL1 x (KS4 x NP3-C1)) x (CE151-262 x 8505R)	86	120	P	YE
426R	7207	98M7159-1	(PL1 x (KS4 x NP3-C1)) x (CE151-262 x 8505R)	85	108	P/T	YE
427R	7209	98M7165-1	(PL1 x (KS4 x NP3-C1)) x (CE151-262 x 8505R)	84	110	P	W
428R	7211	98M7165-3	(PL1 x (KS4 x NP3-CI)) x (CE151-262 x 8505R)	86	98	P	YE
429R	7213	98M7169-1	(PL1 x (KS4 x NP3-C1)) x (CE151-262 x 8505R)	80	100	P	YE

continued

Table 1. ***continued.***

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
430R	7216	98M7172-1	9032 x (NB9040 x SEGO)	87	122	T	YE
431R	7218	98P1420-2	9032 x (NB9040 x SEGO)	87	116	T	YE
432R	7219	98M7179-1	9032 x MR732	84	138	T	YE
433R	7220	98M7180-1	9032 x MR732	83	144	T	YE
			TX2737R (check)	79	115	P	YE

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
P = purple, T = tan; W = white; YE = yellow endosperm; R = red.

germplasm from tropical breeding programs into parental lines adapted to the high plains region of USA. Emasculation crosses were made between 1987 and 1994 and pedigree selection continued from F_2 to F_7 and up to F_{12} at the Agricultural Research Division Center (ARDC) experimental farm in Mead, Nebraska, and in winter nurseries in Mexico. The parentage of each germplasm line is shown in Table 1. Single plant testcrosses using one to several common A, CMS seed parent testers were commenced at F_4 to F_6 and selection and further testcrossing continued only in progenies that were agronomically desirable and gave visually productive hybrids where male fertility was completely restored. Frequently several lines have been developed from the same cross. These have obvious phenotypic differences or were separately judged worthy of release.

The days to flowering, plant height, and plant and grain *color of* each *restorer* germplasm are shown in Table 1. All the lines have consistently restored male fertility in all testcrosses grown. In general, these germplasm lines are average to short in height and medium early to medium late in maturity. All but 4 lines have white or pale yellow grain and 16 have tan plant color. Pest and disease reactions of these lines have not been determined.

Because of their parentage and ability to make good male fertile hybrids, these restorer germplasm lines offer new genetic diversity for the development of new hybrids. White or pale yellow grain lines will permit the development of white grain hybrids. Where the lines also have tan plant color, food quality hybrids can be made with tan plant white grain restorer lines.

Ten g of seed of individual lines is available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 27 Grain Sorghum Maintainer (B-lines) (N434B to N457B) or Restorer (R-lines) (N458R to N460R) Germplasms

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The sorghum breeding program. Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL) and the Agricultural Experiment Station, Kansas State University (KSU), Kansas, USA released 27 grain sorghum *(Sorghum bicolor)* germplasm lines on 24 February 2000. These lines either completely maintain (B-lines) male sterility or will restore male fertility (R-lines) in the A, cytoplasmic male sterility system (milo cytoplasm). These lines provide new genetic diversity for making full season sorghum grain hybrids.

This germplasm was selected in Nebraska from segregating S_3 and S_4 families provided by Dr Paula Bramel-Cox to the UNL sorghum program in 1996. Lines with 1999 row number commencing with 9, 8, 7 or 6 were selected at the UNL Agronomy Farm at Mead from later maturing S_4 families, while those commencing with 38 or 36 were derived from earlier maturing S_3 families grown at the High Plains Agricultural Laboratory at Sidney, Western Nebraska. This material originated in the study of introgression methods in sorghum at KSU involving crosses of adapted, unadapted and wild donor sources with lines or random mating populations (using ms_3) as recurrent parents. Table 1 shows the parents involved and the number of backcrosses made prior to pedigree selection commencing in Nebraska. Pedigree selection,

Table 1. Characteristics of 27 sorghum maintainer (B-lines) or restorer (R-lines) germplasm released by the University of Nebraska-Lincoln and Kansas State University, Kansas, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
B germplasm and male sterile backcrosses							
434B	9088	99P1191-1	KP9B/3/KP7B//SC279/M35-1	83	112	P	W
434A	9089	99P1192 x 1191-1		82	98	P	W
435B	9090	99P1191-3	KP9B/3/KP7B//SC279/M35-1	83	96	P	W
435A	9091	99P1192 x 1191-3		84	100	P	W
436B	9103	99P1193-3	KP7B/3/KP7B//KP7B/P850029-1	85	92	P	W
437B	9104	99P1224-1	KP7B/3/KP7B//KP7B/P850029-1	86	88	P	W
437A	9105	99P1225 x 1224-1		85	90	P	W
438B	9106	99P1224-2	KP7B/3/KP7B//KP7B/P850029-1	86	90	P	W
438A	9107	99P1225 x 1224-2		85	90	P	W
439B	9121	99P1201-1	12-26/KP9B//KP9B/3/KP9B-571/4270032	73	100	T	W
439A	9122	98P1370 x 1369-2		71	104	T	w
440B	8015	99P1222-1	KP9B/KS94-2//KP7B-296	74	92	T	w
440A	8016	99PI223 x 1222-1		70	96	T	w
441B	8017	99P1222-2	KP9B/KS94-2//KP7B-296	78	96	T	w
442B	8018	99P1222-3	KP9B/KS94-2//KP7B-296	78	96	T	w
443B	8029	98M6131-4	12-26/KP9B//KP9B/3/KP9B-571/4270032	78	104	T	w
443A	8030	98M6132 x 6131-1		74	104	T	w
444B	8064	98M6033-1	KP9B/KS94-2//KP7B-296	80	106	T	w
445B	8066	98M6037-2	KP9B/3/KP7B//SC279/M35-1	81	96	P	w
445A	8067	98M6038 x 6037-2		79	106	P	w
446B	8077	98M6073-1	12-26/KP9B//KP9B/3/KP9B-571/4270032	72	98	T	w
446A	8078	98M6074 x 6073-1		71	98	T	w
447B	8079	98M6073-2	12-26/KP9B//KP9B/3/KP9B-571/4270032	72	92	T	w
447A	8080	98M6074 x 6073-2		71	100	T	w
448B	8081	98M6077-2	12-26/KP9B//KP9B/3/KP9B-549/4/KP7B-9	76	98	P	w
448A	8082	CK60A x 97M5181-1	12-26/KP9B//KP9B/3/KP9B-549/4/KP7B-9	76	94	P	w
449B	6011	98M7121-1	KP9B/3/KP7B//SC279/M35-1	81	82	T	w
449A	6012	98M7122 x 7121-1	KP9B/3/KP7B//SC279/M35-1	80	100	T	w
450B	38018	99P1050-1	KP7B//KP913/P1308465	71	92	T	w
451B	38020	99P1050-2	KP7B//KP913/P1308465	71	104	T	w
452B	38025	99P1055-2	260022/4/CK60/3/CK60//CK60/12-26-482	81	100	T	R
453B	36014	98M35007-1	KP7B//P1550686A/KP7RS-3	67	100	P	w
453A	36015	98M35046 x 008	N250AxKP7B//P 1550686A/KP7RS-3)	65	100	P	w
454B	36017	98M35009-1	KP7B-3/4/CK60/3/CK60//CK60/12-26-443	97	130	T	YE
455B	36025	98M35027-2	KP7B-3/4/CK60/3/CK60//12-26-443	67	96	P	YE
456B	36026	98M35027-3	KP7B-3/4/CK60/3/CK60//12-26-443	68	98	P	YE
457B	36055	98M35045-1	260022/4/CK60/3/CK60//CK60/12-26-482	69	105	T	R
R germplasm							
458R	7128	99P1304-1	12-26/KP9B//KP9B/3/KP9B-549/4/KP7B-9	84	108	T	W
459R	7130	99P1304-2	12-26/KP9B//KP9B/3/KP9B-549/4/KP7B-9	81	108	T	W
460R	7182	98M7135-1	12-26/KP9B//KP9B/3/KP9B-549/4/KP7B-9	67	98	P	W

1. Lines were planted on 28 May 1999 at Mead, Nebraska. USA.
P = purple; T = tan; W = white; YE = yellow endosperm; R = red.

using only male fertile plants continued for four generations at Mead in the later maturing families and for two generations at Sidney followed by two generations at Mead in the early families. Rows were inspected at flowering and genetic male sterile plants marked for avoidance. Most selections were retained from families where random mating populations had been used as recurrent parents. Testcrossing to cytoplasmic male sterile (CMS) $CK60A_1$ for the later maturing group was commenced in 1996 and 1997. Where testcrosses included completely male sterile plants, 2 or 3 additional backcrosses were made concurrently while selecting only in those B-lines that continued to perfectly maintain male sterility. Where testcrosses were predominantly fertile, selection for restoration was continued by evaluating single plants in further testcrosses resulting in the three R-lines, N458R, N459R and N460R (Table 1). Frequently sister lines have been retained from the same cross. These either have obvious phenotypic differences or were judged desirable separately.

The days to flowering, plant height, and plant and grain color of each germplasm line are shown in Table 1. Germplasm lines in the nurseries 9, 8,7 and 6 are average in height and medium early to late in maturity. Those in the nurseries 38 and 36 are short in stature and early in maturity. The grain color in all but two lines is strong white to yellow endosperm. The pest and disease reactions of these germplasm lines have not been determined.

Because of their unique parentage, these germplasm lines contribute new genetic diversity for the development of new hybrids. White or pale yellow grain lines will permit the development of white grain hybrids. Where the lines also have tan plant color, food quality hybrids can be made with tan plant white grain restorer lines.

Ten g of seed of individual germplasm lines are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 28 Grain Sorghum F_4 to F_6 Germplasm Families (N461 to N488)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 28 grain sorghum *(Sorghum bicolor)* F_4 to F_6 germplasm families (N461 to N488) in the medium to full season maturity class for Southeast Nebraska and similar environments. These lines provide new genetic diversity for the development of full season sorghum grain hybrids.

These germplasm lines were developed via the introgression of tropically adapted food quality grain sorghums into sorghum hybrid parents adapted to the US high plains. These germplasm lines resulted from emasculation crosses made from 1992 to 1995 between introductions from tropical sorghum breeding programs, and UNL lines. Pedigree selection was followed to the F_4 or up to the F_6 generation at the Agronomy Farm, Mead, Nebraska, with emphasis on white or yellow endosperm grain, and tan plant color. The fertility restoration status of each germplasm was determined using A, cytoplasmic male sterile (CMS) testers (Table 1). Some germplasm lines which had not been testcrossed were selected.

The days to flowering, plant height, plant and grain color, testcross reaction and parentage of each germplasm are shown in Table 1. These germplasm lines are generally short to medium height and medium to full season in maturity in Eastern Nebraska. Many have white or yellow endosperm grain, and tan plant color. Pest and disease reactions of these germplasm lines have not been determined.

Because of their parentage, these germplasm families provide new genetic diversity for the selection of new parental lines for hybrid development. Testcross reactions or parentage indicate germplasm lines that have potential as seed parents or male parents. White or pale yellow grain lines will permit the development of white grain hybrids. Where the lines are also tan plant, food

Table 1. Characteristics of 28 full season grain sorghum F_4 to F_6 germplasm families released by the University of Nebraska-Lincoln, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color	restcross reaction[2]
N461	7036	99P1258-1	N250B x IC-3	74	100	T	W	(S)
N462	7043	99P1260-1	IC-2 x N249R	68	86	T	W	(F)
N463	7045	99P1260-2	IC-2 x N249R	76	102	T	YE	(F)
N464	6001	98M5025-1	94P746 x [(SRB x RS/B-162) x SPL1]	78	85	T	YE	S
	6005	98M5038 x 5037-1	94P746 x (TX623 x MB12)	76	106	T	YE	
N465	6007	98M5037-3	94P746 x (TX623 x MB12)	82	110	T	YE	s
N466	6008	98M5040-1	94P746 x (TX623 x MB 12)	84	96	T	YE	s
	6009	98MCK60 x 5040-1	94P746 x (TX623 x MB12)	74	120	P	W	
N467	5006	98M4056-1	(PL1 x (KS4 x NP3-C1)) x 9032R	78	100	P	R	F
N468	5013	98M4057-1	9032 x P316R	84	114	P/T	YE	F
N469	5020	98M4059-1	9032 x P316R	78	122	T	R	F
N470	5026	98M4060-1	9032 x P316R	81	120	T	R	F
N471	5031	98M4065-1	9032 x P316R	84	110	T	YE	F
N472	5038	98M4068-1	9032 x MR732	84	124	T	R	F
N473	5040	98M4068-3	9032 x MR732	86	115	T	R	F
N474	5046	98M4068-2	9032 x MR732	83	122	T	R	F
N475	5050	98M4071-1	95PPBC23 x (SRB x MB5)	82	100	P	R	S
N476	5054	98M4072-1	95PPBC23 x (SRB x MB5)	84	110	T	YE	S
N477	5061	98M4074-3	95PPBC23 x (SRB x MB5)	78	110	P	YE	S
N478	5062	98M4075-1	95PPBC23 x (SRB x MB5)	81	120	P	R	S
N479	5064	98M4078-1	95PPBC39 x [PL1 x (KS4 x NP3-C1)]	84	104	P	YE	F
N480	5076	98M4086-1	95PPBC39 x (NB9040 x SEGO)	85	102	P	YE	(F)
N481	5083	98M4090-1	95PPBC39 x 9032R	84	116	T	YE	F
N482	5092	98M4100-1	N122B x 95PBC34	81	104	P	W	F
N483	3001	98M2005-4	N248R x Bagoba	76	95	P	W/YE	(F)
N484	3003	98M2006-2	N250B x IC-3	68	80	T	W/YE	(S)
N485	3004	98M2006-3	N250B x IC-3	68	85	T	W	(S)
N486	3005	98M2007-1	N250B x IC-3	72	100	T	YE	(S)
N487	3006	98M2007-2	N250B x IC-3	72	90	T	YE	(S)
N488	3008	98M2007-4	N250B x IC-3	74	105	T	W	(S)
			CK60A (check)	76	96	P	W	S

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
   P = purple; T = tan; W = white; YE = yellow endosperm; R = red.
2. Reaction on A, seed parent: F = male fertile, S = male sterile (F) and (S) = probable reaction inferred from parentage or sister line testcrosses.

quality hybrids can be made with tan plant white grain restorer lines.

Ten g of seed of individual germplasm lines are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 15 Early-maturing Grain Sorghum Maintainer Parent Germplasms (B-lines) and Partially Backcrossed Seed Parents (A-lines) (N489B to N503B)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 15-early maturing grain sorghum *(Sorghum bicolor)* B-lines (maintainers) (N489B to N503B) with three of these lines partially backcrossed. These lines are maintainers of the A_1 cytoplasmic male sterility system (milo cytoplasm). These provide new genetic diversity for making early-maturing sorghum grain hybrids.

These B-lines were developed in the program conducted at the High Plains Agricultural Laboratory (HPAL), Sidney, Nebraska to produce early-maturing seed parents for Western Nebraska. These germplasm lines resulted from emasculation crosses made in 1994 between N250B (an early-maturing, tan plant, white grain seed parent subsequently released in 1998) and the parents shown in Table 1. Generally pedigree selection from F_2 to F_5 or F_6 was conducted at HPAL, Sidney with alternate generations in the 1998 and 1999 winter nurseries in Mexico. Selecting material at HPAL, Sidney ensures lines are sufficiently early to mature in Western Nebraska and have adequate lodging resistance. From F_3 onwards, duplicate nurseries were grown at Mead, Nebraska. Where testcrosses were made, cytoplasmic male sterile (CMS) $N250A_1$ was used as the milo cytoplasm source. Several sister lines were retained from the cross N269B x N250B. These have either obvious phenotypic differences or were judged desirable separately.

The days to flowering, plant height, and plant and grain color of each germplasm line are shown in Table 1. In general, these lines are average to short in height and

Table 1. Characteristics of 15 early-maturing sorghum B-lines released by the University of Nebraska-Lincoln, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color	Testcross reaction[2]
N489B	34002	98M33001-1	(618B x 144-3B) = (N269B x N250B)	69	105	T	W	(S)
N490B	34003	98M33001-2	(618B x 144-3B) = (N269B x N250B)	70	95	T	R	(S)
N491B	34005	98M33002-1	(618B x 144-3B) = (N269B x N250B)	68	100	T	YE	(S)
N492B	34009	98M3 3003-1	(618B x 144-3B) = (N269B x N250B)	67	85	T	R	(S)
N493B	340! 1	98M33004-1	(618B x 144-3B) = (N269B x N250B)	66	100	T	R	(S)
N494B	34013	98M33004-2	(618B x 144-3B) = (N269B x N250B)	69	90	T	R	(S)
N495B	34015	98M33004-3	(618B x 144-3B) = (N269B x N250B)	69	100	T	R	(S)
N496B	34019	98M33005-3	(618B x 144-3B) = (N269B x N250B)	66	100	T	R	(S)
N497B	34022	98M33010-1	N250B x (623 x IS89-2B)	67	90	T	R	(S)
N497A[3]	34023	98M33046 x 33010-1		64	94	T	R	-
N498B	38011	99P1009-2	(F1#8 x NGB1) x (SRB x TX625)	67	102	T	W	S
N499B	38031	99P1079-4	(618B x 144-3B) = (N269B x N250B)	81	112	T/P	YE	S
N500B	38037	99P1080-2	(618B x 144-3B) = (N269B x N250B)	81	102	T	R	S
N500A[1]	38038	99P1070X 1080-2	N250Ax	76	92	T	R	-
N501B	38039	99P1080-3	(618B x 144-3B) = (N269B x N250B)	74	88	T	R	S
N501A[3]	38040	99P1071 x 1080-3	N252Ax	71	94	T	R	-
N502B	38043	99P1081-1	P1550666 x N250B	74	96	P	R	(S)
N503B	38046	99P1083-1	N250B x San Chi San	70	116	P	W	(S)
	-	-	N250B (check)	68	86	T	W	S

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
   P = purple; T = tan; W = white; YE = yellow endosperm; R = red.
2. Reaction on A, seed parent: S = male sterile, (S) = probable reaction inferred from parentage or sister line testcrosses.
3. Partially backcrossed.

early in maturity. Pest and disease reactions of these lines have not been determined.

Because of their parentage these seed parents contribute new genetic diversity for the development of very early-maturing hybrids. Tan plant, white grain lines will permit the development of tan plant food quality hybrids. Tan plant, red grain lines will permit the development of attractive bronze grain hybrids.

Ten g of seed of individual germplasm lines are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 48 Early-maturing Grain Sorghum Male Fertility Restorer Germplasms (R-lines) (N504R to N551R)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 48 early-maturing grain sorghum *(Sorghum bicolor)* restorer germplasm lines, which restore male fertility in the A, cytoplasmic male sterility system (milo cytoplasm). These provide new genetic diversity for making early-maturing sorghum grain hybrids.

These R-lines (N504R to N551R) were developed in the program conducted at the High Plains Agricultural Laboratory (HPAL), Sidney, Nebraska to produce early-maturing hybrid parents for Western Nebraska. These germplasm lines resulted from emasculation crosses made in 1992 to 1994 between early-maturing R-lines under development at Sidney, from Dr Paul Nordquist's program at West Central Research and Extension Center, North Platte, Nebraska and some tropical food quality introductions. Generally pedigree selection was conducted from F_2 to F_6 or F_{10} at HPAL, Sidney, with alternate generations in the winter nursery in Mexico. Exposure at Sidney ensured that plants sufficiently early and lodging resistant for Western Nebraska were selected. From F_3 onwards duplicate nurseries were grown at Mead, Nebraska where testcrosses could be made. Usually CMS $N123A_1$ or CMS $N250A_1$ were used as testers to evaluate combining ability, hybrid phenotype and male fertility restoration. Frequently, sister lines developed from the same cross have been retained. These have either obvious phenotypic differences or were judged desirable separately.

The days to flowering, plant height, and plant and grain color of each germplasm are shown in Table 1. All lines with a prefix of 40 xxx and 37 xxx have given visually productive A_1 testcross hybrids with male fertility fully restored. The remaining germplasm lines have also either given fertile testcrosses, were sister lines of proven restorers, or were derived from crosses where both parents were R-lines. In general these germplasm lines are average to short in height, and early flowering. Grain color of all but 3 lines is while or pale yellow. Pest and disease reactions of these lines have not been determined.

Table 1. Characteristics of 48 early-maturing grain sorghum male fertility restorer germplasm lines released by the University of Nebraska-Lincoln, USA in 2000[1].

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color	Testcross reaction[2]
504R	40007	98M40036-2	3080 x Dorado	68	88	T	W	(F)
505R	40021	98M40113-1	IS7333 x SD106B	72	92	P	W	F
506R	40030	97M40067-1	CEI51-262 x 8505R	84	96	T	W	F
507R	40040	97M40084-2	3080 x TX414	66	88	P	R	F
508R	38051	99P1038	1038R Bulk (see 37025 et seq.)	71	82	T	YE	F
509R	37004	99P1018-1	IS7333 xSD106B	67	102	T	W	F
510R	37008	99P1020-1	3080 x Dorado	68	104	P	W	F

continued

Table 1. ***continued.***

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color	Testcross reaction[2]
511R	37012	99P1263	(KS4 x NP-3Cl) x TX430	84	88	P	W	F
512R	37021	99P1025-3	NQR1 x TX2727	57	92	P	YE	F
513R	37025	99P1038-1	(SD106B x MR748) x (NQRgms x 4143)	61	84	P	W	F
514R	37027	99P1038-2	(SD106B x MR748) x (NQRgms x 4143)	72	90	T/P	W	F
515R	37032	99P1038-3	(SD106B x MR748) x (NQRgms x 4143)	71	84	T	W	F
516R	37034	99P1039-1	(SD106B x MR748) x (NQRgms x 4143)	72	96	T	YE	F
5I7R	37036	99P1039-2	(SD106B x MR748) x (NQRgms x 4143)	67	86	T	YE	F
518R	37038	99P1041-1	(SD106B x MR748) x (NQRgms x 4143)	68	94	T	YE	F
519R	37040	99P1041-2	(SD106B x MR748) x (NQRgms x 4143)	66	90	T	W	F
520R	37053	99P1056-1	(IS7333 x SD106B) x (PI550658)	56	84	T	W	F/S
521R	37061	99P1059-1	N248 x 9032R	64	90	P	W	F
522R	37066	99P1059-2	N248 x 9032R	67	94	T	W	F
523R	37071	99P1062-1	684R x TX9032R	65	90	P	W	F
524R	37079	99P1065-1	(IS7333 x SD106B) x (CE151-262 x 8505R)	68	80	P	W	F
525R	37083	99P1072-1	(IS7333 x SD106B) x (CE151-262 x 8505R)	68	102	P	W	F
526R	37085	99P1073-1	(SBM x MR748) x [1R204 x (FLR266 x CSV4)]	70	90	T	W	F
527R	37088	99P1075-1	(IS7333 x SD106B) x (NB9040 x SEGO)	72	106	P	YE	F
528R	37091	99P1075-3	(IS7333 x SD106B) x (NB9040 x SEGO)	69	92	T	YE	F
529R	37098	99P1077-2	(IS7333 x SD106B) x (NB9040 x SEGO)	72	102	T/P	W/YE	F
530R	37100	99P1303-1	[(KS4 x NP-3C1) x 1 A28] x 8505	68	94	P	W	(F)
531R	37108	98M37024	IS7333 x SD106B	67	84	T	YE	F
532R	37116	98M37042-1	3080 x Dorado	64	88	P	W	F
533R	36002	98M35003-1	(SD106B x MR748) x (NQRgms x 4143)	67	90	T	YE	F
534R	36004	98M35003-2	(SD106B x MR748) x (NQRgms x 4143)	64	92	T	YE	(F)
535R	36006	98M35003-4	(SD106B x MR748) x (NQRgms x 4143)	69	96	T	YE	(F)
536R	36007	98M35003-5	(SD106B x MR748) x (NQRgms x 4143)	68	90	T	YE	(F)
537R	36008	98M35004-1	(SD106B x MR748) x (NQRgms x 4143)	68	124	T	R	(F)
538R	36056	98M40048-1	[(SRB x 625) x SRB] x (F1#8 x NQB1)	70	115	T	YE	S
539R	35018	98M34017-1	N248 x 9032R	68	98	T	W	(F)
540R	35019	98M34019-1	N248 x 9032R	69	110	T	R	F
541R	35025	98M34023-2	9032 x N248R	66	96	P	W	F
542R	35028	98M34025-2	9032X x N248	68	105	T	W	(F)
543R	35031	98M34026-1	9032 x 684R	69	85	P	W	(F)
544R	35034	98M34030-2	(1S7333 x SD106B) x (CE151-262 x 8505R)	66	70	T	W	(F)
545R	35046	98M34035-1	(1S7333 x SD106B) x (CE151-262 x 8505R)	67	100	T	W	(F)
546R	35047	98M34036-2	(IS7333 x SD106B) x (CE151-262 x 8505R)	65	90	T	W	F
547R	35052	98M34037-3	(IS7333 x SD106B) x (CE151-262 x 8505R)	67	108	T	W	(F)
548R	35053	98M34039-1	(SRM x MR748) x [IR204 x (FLR266 x CSV)]	65	108	T	W	F
549R	35055	98M34039-2	(SRM x MR748) x |1R204 x (FLR266 x CSV)]	64	90	P/T	YE	(F)
550R	35057	98M34042-1	(1S7333 x SD106B) x (NB9040 x SEGO)	67	116	P	YE	F
551R	35064	98M34049-1	(IS7330 x SD106B) x (NB9040 x SEGO)	67	104	P	YE	(F)
	38014		N249R (Check)	67	88	T	YE	F

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
   P = purple; T = tan; W = white; YE = yellow endosperm; R = red.
2. F = male fertile; S = male sterile; (F) = presumed fertile from sister line reaction or parentage.

Because of their parentage, early maturity and various plant and grain color combinations, these R-lines offer new genetic diversity for the development of very early-maturing hybrids. Germplasm with tan plant and white or yellow endosperm grain can be used to make food quality hybrids with seed parents having the same traits.

Ten g of seed of individual germplasm lines are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln. PO Box 830817, Lincoln, NE 68583-0817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Release of 7 Late-maturing Grain Sorghum Seed Parents (A-B Lines) (N552 A-B to N558 A-B) and 21 Tall Restorer Germplasms (N559R to N579R)

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The sorghum breeding program, Department of Agronomy and Horticulture, Institute for Agriculture and Natural Resources, University of Nebraska-Lincoln (UNL), USA, on 24 February 2000, released 7 grain sorghum *(Sorghum bicolor)* seed parents and 20 tall restorer germplasm lines based on their reaction in A, cytoplasmic male sterility system in the late or extra late maturity class for Southeast Nebraska and similar environments. These seed parents provide new genetic diversity for late grain hybrids or for forage hybrids. The restorer parents provide new diversity for forage hybrids.

These gennplasm lines were developed in the UNL sorghum breeding program supported by an INTSORMIL grant for conducting collaborative genetic research with tropical sorghum breeding programs. Very late-maturing or tall progenies with food quality grain generated at UNL from crosses between US sorghums and leading tropically adapted food sorghums were provided to tropical collaborating programs, and further selected in Nebraska. Those progenies that matured at the Agronomy Farm in Mead, Nebraska were developed by pedigree selection and were testcrossed both at Mead and in winter nurseries into the seed parents and R-lines listed in this release.

The days to flowering, plant height, and plant and grain color of each germplasm are shown in Table 1. All but five lines have tan plant color and all but two lines have food quality grain, white or pale yellow in color. Most lines are late to very late in maturity in Southeast Nebraska conditions. Pest and disease reactions of these germplasm lines have not been determined.

Because of their parentage, late maturity, grain color and vigor of their testcrosses. these germplasm lines provide new genetic diversity for the development of

Table 1. Characteristics of 7 late-maturing sorghum seed parents and 21 restorer germplasm lines released by the University of Nebraska-Lincoln, LISA in 2000'.

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
A-B lines							
N552A	9501	98M9514	330B (TX623 x MB9)	91	120	T	W
N552B	9502	98M9515 x 9514	330A	90	112	T	W
N553A	9503	97M9518	363B(TX623 x MB12)	89	92	T	YE
N553B	9504	97M9517 x 9518	363A	87	102	T	YE
N554B	9505	97M95020	223-B(TX623 x MB12)	88	114	T	W
N554A	9506	97M95019 x 95020	223A	86	112	T	W
N555B	9513	99P1330	Z9504-B	87	128	T	YE
N555A	9514	99P1329 x 1330	Z9504-A	85	132	T	YE
N556B	9515	99P1337	Z9528-B	89	124	T	YE
N556A	9516	99P1336 x 1337	Z9528-A	88	132	T	YE
N557B	9520	98M8507-1	(Sego x Dorado) x Sego	77	140	T	W
N557A	9521	98M8509 x 8507		80	136	T	W
N558B	9522	98M8508-1	(Sego x Dorado) x Sego	77	140	T	W
N558A	9523	98M8509 x 8508-1		79	140	T	W

continued

Table 1. *continued.*

N no.	1999 row	Source row	Parentage	Days to flowering	Plant height (cm)	Plant color	Grain color
R-lines							
N559R	9517	99P1342	7112-R = (WSV387 x TX430)	82	168	T	YE
N560R	8503	98M6526-1	(SEGO x Dorado) x Town	82	158	P	R
N561R	8505	98M6526-2	(SEGO x Dorado) x Town	79	154	P	R
N562R	7504	99P1347	CE196-7 x WSV387	99	204	T	W
N563R	7510	99P1349	SEGO x WSV387	90	212	T	YE
N564R	7512	99P1350	SEGO x WSV387	96	196	T	YE
N565R	7514	99P1352	CE196-7-2 x WSV387	97	196	T	W
N566R	7516	99P1354-2	(CE145-66 x DR2990) x (CE152-262 x 8505)	89	98	T	YE
N567R	7518	99P1356-1	9032 x MR732	82	136	T	W
N568R	7523	99P1357-1	9032 x MR732	80	134	T	W
N569R	7524	99P1357-2	9032 x MR732	74	132	T	W
N570R	7528	99P1367	CE151-262 x SuCr36	77	150	T	YE
N571R	7532	98M7501-1	CE151-262 x TX2721R	80	128	T	W
N572R	7533	98M7505-1	CE145-66BC3CF4 x DR290	80	112	T	W
N573R	7536	98M7513-1	CE145-66BC3CF4 x DR290	74	132	T	W
N574R	7539	98M7542-1	WSV387 x TX430	84	139	T	YE
N575R	7542	98M7554-1	SEGO x WSV387	89	186	T	W
N576R	7545	98M7614-1	95PVPBC39 x (NB9040 x SEGO)	79	116	P	YE
N577R	7547	98M7614-2	95PVPBC39 x (NB9040 x SEGO)	78	120	P	YE
N578R	7550	98M7617-1	(CE145-66 x DR290) x (KS4NP3-C1 x TX430)	80	124	P	YE
N579R	7563	98M7639-1	WSV387 x TX430	75	164	T	YE

1. Lines were planted on 28 May 1999 at Mead, Nebraska, USA.
P = purple; T = tan; W = white; YE = yellow endosperm; R = red.

either new late-maturing food quality grain hybrids, or forage hybrids.

Ten g of seed of individual A-B line pairs and R-lines are available upon completion of a UNL material transfer agreement from the Department of Agronomy and Horticulture, University of Nebraska-Lincoln, PO Box 830817, Lincoln, NE 68583-08817, USA (Fax 402-472-3654). Seed will be supplied free to public institutions on request.

Biotechnology

Examining Plant Defense Responses to Greenbug Attack in Sorghum Using DNA Microarray Technology

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Introduction

Plant resistance to insects and pathogens depends on expression of defense genes as well as regulatory genes

and is mediated via constitutive and induced defense mechanisms. Great progress has been made in studies of plant defense responses against pathogens. In contrast, understanding of genetic resistance and related molecular events in plant defense responses to insect pests has lagged behind that of host-pathogen interactions (Kazan et al. 2001). To gain novel insights into the molecular mechanisms of plant resistance to insects, high-throughput parallel gene expression analysis, using cDNA microarray-based methods, has been used to examine gene expression patterns in young seedlings of sorghum *(Sorghum bicolor)* in response to greenbug feeding. This provided the opportunity to discover the genes that are regulated by insect feeding as defense gene expression contributes to induced resistance against insect pests. This article reports preliminary results of gene expression dynamics in sorghum seedlings during greenbug feeding. The large-scale cDNA microarray analyses of expression profiles of defense genes that respond to attack by virulent greenbugs are underway.

Materials and Methods

Sorghum plants were grown in fiats in a greenhouse. One-week old seedlings (at the 2-3 leaf stage) with two fully expanded leaves were infested with virulent biotype 1 greenbug (*Schizaphis graminum*) (Porter el al. 1997) that was obtained from greenhouse-maintained cultures reared on susceptible barley (*Hordcum vulgare*) plants according to Andrews et al. (1993). Three days after infestation, sorghum leaves were collected and quickly frozen in liquid nitrogen until use.

Total RNA was isolated by TRIzol regent (Invitrogen, California, USA) from both infested and non-infested (control) seedling tissues following the manufacturer's instruction. For subtractive hybridization. Poly (A^+) RNA was extracted using an oligo-dT cellulose column (Ambion, Texas, USA). Differentially expressed transcripts were selected using a PCR-Select™ cDNA subtraction kit (Clontech, California) and a subtratctive cDNA library was made with the PCRII vector (a T/A cloning kit, Invitrogen, California) following the manufacturer's protocol. For the preparation of microarrays, a total of 2500 cDNA clones were amplified from plasmid clones derived from the cDNA library. The concentration of the PCR products was determined by gel electrophoresis and optical density (OD) measurement with a UV-Vis spectrophotometer. The PCR products were briefly purified by precipitation with ethanol, dissolved in an appropriate volume of nano-pure water, and adjusted to a final concentration of 200 ng μl^{-1}. Microarrays were produced on amino-silane-coated slides (GAPSII coated slides; Corning Inc., Corning, NewYork, USA), and cDNA clones were spotted in triplicate by robotic spotting (PixSys 550 Microarrayer). Multiple house-keeping genes and randomly selected cDNA clones were also printed on the same array to serve as internal controls. Negative controls on the array included several heterologous genes from the human DNA, vector DNA without inserts and spotting buffer only.

For probe preparation, mRNA from each treatment was labeled for each probe using dendrimer-based methodology (the 3DNA Array 350 expression array detection kit, Genisphere, Pennsylvania, USA). Briefly, one microgram of mRNA was used to make cDNA probes for hybridization to the microarray. Probes were made by reverse transcription of mRNA in the presence of either Cy5 or Cy3 labeled dUTP (Amersham, New Jersey, USA) using Superscript II (Invitrogen, California). Microarrays were hybridized with Cy3 or Cy5 fluorescent-labeled probe pairs in a hybridization chamber (Corning, New York) according to the instruction of the Array detection kit. The microarrays were scanned using Scan Array Express (Packard Bioscience, Connecticut, USA), and spot finding and quantitation were carried out using GenePix software. The data were normalized by total fluorescence levels where the total fluorescence from each channel of each array was balanced to equal the average fluorescence in the five arrays.

Results and Discussion

In this study, high-throughput micoarray technology was used to monitor changes in gene expression in sorghum in response to attack by greenbugs. The transcription products were compared in parallel, ie, two genotypes of sorghum: resistant and susceptible to greenbug biotype I. A set of defense-responsive cDNA clones was generated by suppression subtractive hybridization (SSH) in which greenbug-resistant genotype (P1550670) mRNA was used as 'tester' and greenbug-susceptiblc genotype (Tx7000) mRNA was used as 'driver'. In this way, the cDNA clones were enriched for those genes over-expressed or specific to P1550607 plants when compared to those in Tx7000 plants. Microarrays, made from 2304 SSH inserts from the tester and 12 controls, were hybridized with a mix of the PI550607 cDNA probe labeled with Cy5 fluorochrome (red) and the Tx7000 probe labeled with Cy3 fluorochrome (green). Spots with red and green fluorescence indicated greater relative expression in 'tester' and 'driver', respectively; yellow fluorescence indicated equal expression in both genotypes.

Microarray technology showed comprehensive gene activation in sorghum seedlings that were exposed to virulent greenbug biotype I. These genes were related to

self-defense, signal transduction (for gene regulation), photosynthesis, carbon and nitrogen metabolism, cytoskeleton and other cellular activity. In this analysis, we examined the changes that occurred in the abundance of transcripts corresponding to 2304 cDNA clones (SSH inserts), and only changes in transcript abundance in excess of 3-fold that of controls in all replicate experiments were accepted. In the resistant seedling tissues, the abundance of 38 transcripts was increased more than 3-fold, whereas that of 26 transcripts was significantly reduced. Thus, data analysis revealed a total of 64 cDNA clones with differential expression patterns in response to greenbug infestation.

The cDNA clones that showed differential expression were sequenced. The resultant sequences were then annotated by comparison to GenBank databases using the BLAST search program. Sequence similarity search allowed putative functions to be assigned to 32 transcripts. Among those up-regulated genes, defense genes such as cysteine proteinase inhibitor (PI) and NBS-LRR (the nucleotide binding site - leucine rich repeat family of resistance genes), were observed in the resistant genotype following greenbug feeding. It is believed that these defense genes were induced by the host defense system to combat insect attack. However, a large group (approximately 34%) of the genes show no previously described function or homology. Thus, many of these identified genes need to be characterized by in vivo and in vitro experiments to understand their exact function during the defense process.

The data generated from the preliminary analyses demonstrate that the microarray technology is a very promising method for global and simultaneous analysis of a large number (eg, thousands) of transcripts in a plant, which allow us to identify and clone genes known only through their phenotype. Analysis of expression profiles in sorghum plants in response to greenbug feeding can improve our overall understanding of the molecular basis of the crop defense response to other insect pests as they may share some common resistance mechanisms. Comparative genomic studies of sorghum-greenbug interactions may also provide the opportunity to select targets for development of more durable resistance.

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A High-density Genetic Recombination Map of Sequence-tagged Sites for *Sorghum* for Comparative Structural and Evolutionary Genomics of Tropical Grains and Grasses

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We have reported (Bowers et al. 2003) a genetic recombination map for *Sorghum* of 2512 loci spaced at average 0.4 cM (ca. 300 kb) intervals based on 2050 restriction fragment length polymorphism (RFLP) probes, including 865 heterologous probes that foster comparative genomics of *Saccharum* (sugarcane), *Zea* (maize), *Oryza* (rice), *Pennisetum* (millet, buffelgrass), the Triticeae (wheat, barley, oat, rye) and *Arabidopsis.* Mapped loci identify 61.5% of the recombination events in this progeny set.

This genetically-anchored set of sequence-tagged sites provides transferable DNA markers suitable for a wide range of investigations in structural, functional and evolutionary genomics in several major grain and

biomass crops. Genetically-mapped sequence tagged sites such as these can be used to discover single-nucleotide or small insertion/deletion polymorphisms that can then be genotyped by many technologies. This possibility increases the value of these loci and reduces the costs associated with their wider utilization. A total of 130 loci that contain simple-sequence repeats have further advantage of being relatively allele-rich, a benefit in studies that require differentiation between closely-related genotypes.

This framework of genetically-anchored sequence-tagged sites will also provide a foundation for physical mapping and ultimately assembling a robust finished sequence of the sorghum genome. This map permits us to assign loci to 'bins' of about 0.77 cM; on average, this represents about 300 kb of genomic DNA based on a consensus genome size estimate of 750 Mbp. To orient different loci within 0.77 cM bins, we are hybridizing the genetically-mapped probes to bacterial artificial chromosome (BAC) libraries for both *Sorghum propinquum* and *S. hicolor.* Since the two BAC libraries each provide about 10x coverage of the genome, and are comprised of individual BACs that average about 120 kb in length, this will permit us to resolve the order of closely-linked loci to an average resolution of about 12 kb, assuming that the breakpoints of individual BACs are more or less evenly distributed through the genome. By simply hybridizing the 2050 mapped probes to the 10x-coverage BAC libraries, we expect to identify about 20,000 BACs in each library, comprising about half of the genome. Further, both libraries have been fingerprinted, permitting the resulting 'contigs' to be extended further. By selective BAC end-sequencing and the use of comparative approaches made possible by the alignment of our genetically-mapped sequences to the nearly-completed rice sequence, a robust genetically-anchored physical map is expected to coalesce.

Non-random patterns of DNA marker distribution provide clues as to the locations of interesting and important features of sorghum genome organization. On most chromosomes, at least one significant concentration of loci appears to correspond to the centromeric region. Co-hybridization of centromeric probes with genetically-mapped RFLPs has associated concentrations of centromeric repeats with marker-dense regions of 8 of the 10 linkage groups. Due to the repetitive nature of these probes and the possibility that not all copies are centromeric, these data can only be taken as tentative indications of the possible locations of the sorghum centromeres.

Differences in the abundance of dominant genetic marker loci suggest that a chromosome structural rearrangement has occurred since the divergence of *S. bicolor* and *S. propinquum* from a common ancestor. The ribosomal DNA, and a large flanking area may have moved in one of the two sorghums since their divergence from a common ancestor, a hypothesis that we are further investigating.

By virtue of a very high level of DNA polymorphism, the *S. bicolor x S. propinquum* cross has proven especially facile for 'comparative mapping' of DNA clones that have been previously mapped in other taxa. To foster opportunities to use the relatively small genome of sorghum to help advance genomics in the larger genomes of many other tropical Poaceae, we have mapped 865 heterologous DNA clones from 8 other taxa. Despite the clear value of the comparative approach for fostering progress in study of gene arrangement in complex genomes (eg, *Saccharum)* or under-explored taxa (eg, *Pennisetum, Cynodon, Echinochloa* and *Panicum*), it is equally important to note that a remarkable 45% of comparative data fell in regions other than those we infer to correspond between sorghum and maize. Many of these incongruities are likely to reflect non-chromosomal rearrangement mechanisms that are becoming clear from microsynteny studies and studies of ancient duplication, or possibly rapid divergence or deletion of hypomethylated DNA.

The patterns of distribution of duplicate loci in sorghum are clearly not random, with many small islands of co-linearity evident. However, for about 30% of the genome we can discern no corresponding duplicated region, and another 30% shows correspondence to two or more unlinked regions. Duplication of sorghum chromatin appears to more closely resemble the pattern observed for rice, in which the completed sequence has largely borne out early hints of ancient segmental duplication. Much more data will be needed to unravel the details of the relationship(s) between individual duplicated segments in sorghum, as well as their relationships (if any) to those in close relatives such as sugarcane and maize, or distant relatives such as rice or even *Arabidopsis.*

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Agronomy

Sorghum Diversity for Germination and Coleoptile Elongation Under Cool Conditions

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Introduction

In the Great Plains and other regions of the world where sorghum *(Sorghum bicolor)* is grown, temperatures are sub-optimal during germination, emergence and early seedling growth. Increased cold tolerance would facilitate rapid and uniform germination and emergence, and thereby improve seedling establishment. It would also facilitate earlier planting, faster development and greater yield potential, which is usually correlated with days to maturity. Finally, it would allow expansion of sorghum into cooler regions where it currently is not grown.

For most sorghum genotypes, temperatures below 15°C cause poor germination, slow growth and poor stand establishment. Below a genetically-dependent 'base temperature' (Tb), growth ceases altogether. For photoperiod insensitive genotypes, growth and development are a function of heat units ('degree days') accumulated relative to this Tb. This response is modified by day length in photoperiod-sensitive genotypes. Literature values for sorghum Tb are generally about 10°C, but there is scant data available on the degree of genetic variability for Tb. Furthermore, there is little understanding of the physiological mechanisms underlying seedling cold tolerance.

Our overall objectives have been to: (1) establish the degree of genetic variability for seedling cold tolerance among a range of sorghum cultivars; (2) identify underlying physiological mechanisms for these differences; and (3) develop physiologically-based selection tools to assist sorghum breeders in the development of cold-tolerant cultivars. In this article, we summarize our research findings thus far.

Materials and Methods

Forty-nine sorghum entries, including commercial and experimental hybrids, parental lines and cultivars from China, Ethiopia, Rwanda, South Africa and Egypt, were grown in a growth chamber under several controlled

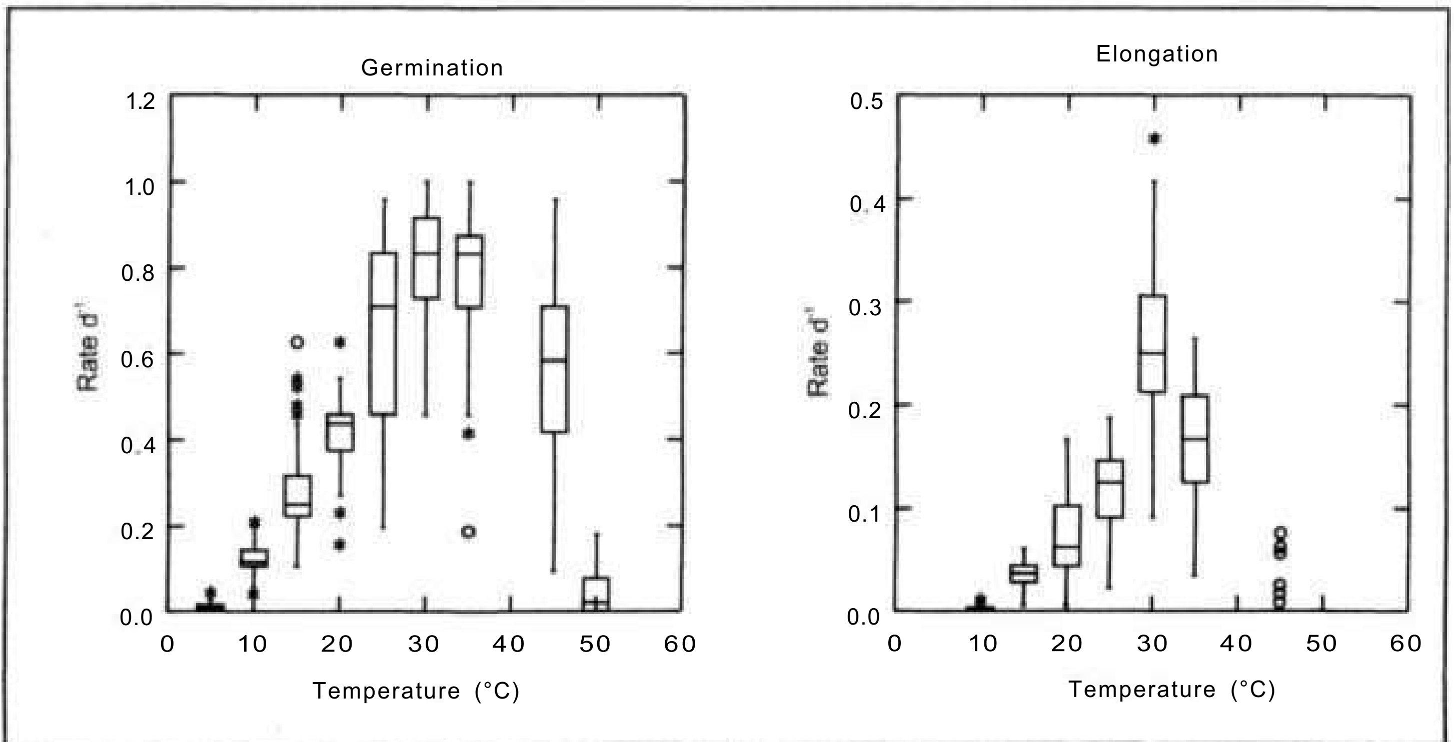

Figure 1. Box-and-whisker plot of temperature response of germination and elongation rates of 49 sorghum cultivars.

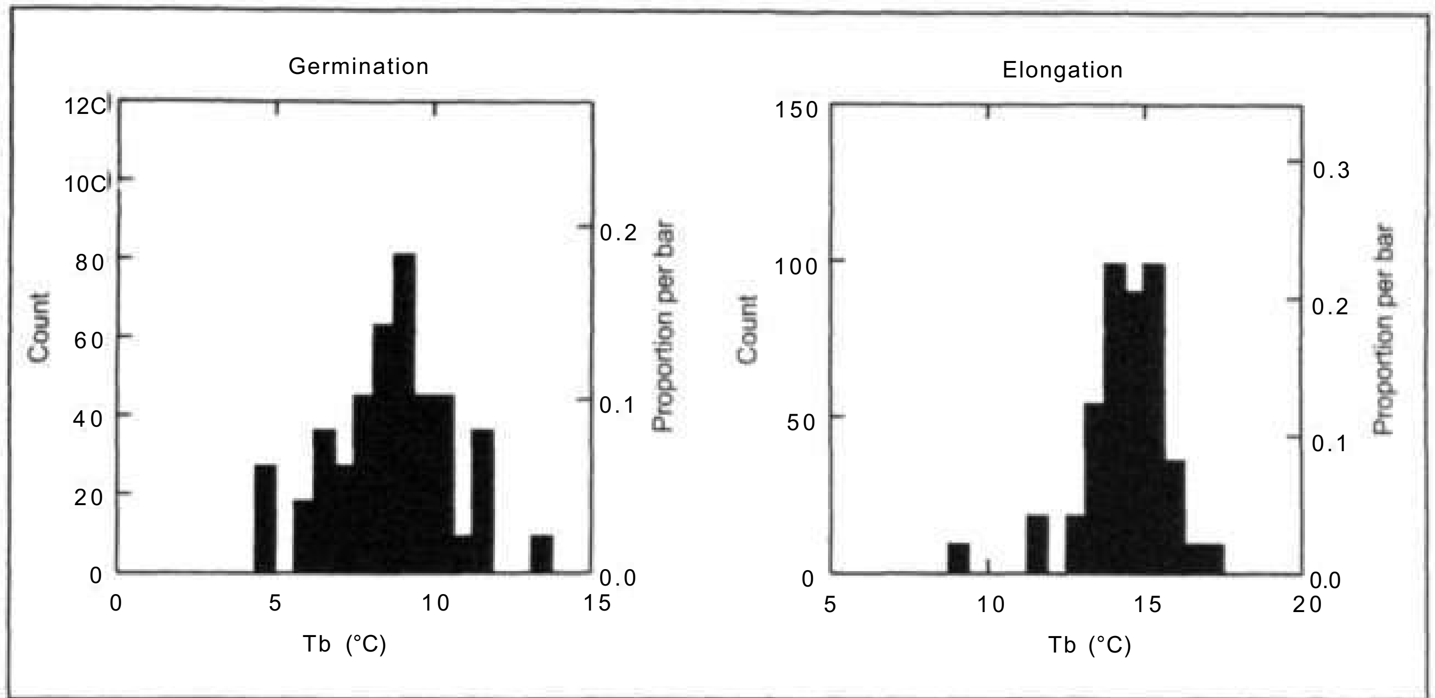

Figure 2. Frequency distribution of temperature base (Tb) for germination and elongation of 49 sorghum cultivars.

temperature regimes ranging from 5 to 50°C. These entries had given remarkably consistent results during three years of field emergence studies conducted at Pendleton, east Oregon, where conditions are reliably cool and moist in the spring. We have suggested that east Oregon can serve as a fairly reliable field screen for seedling emergence under cool conditions.

For each temperature regime, 12 seeds of each entry were planted in moistened paper towels. Daily or every few days, depending upon the temperature regime, towels were opened to determine percentile germination and coleoptile length. Coleoptiles were considered 'elongated' when their length reached 25 mm. This served as a surrogate for ability to emerge in a particular temperature regime. Percentile germination and emergence data were used to calculate germination and elongation rates, which were regressed on temperature to determine Tb. There were two replications (each with twelve seeds) for each entry in all temperature regimes. The temperature range included very warm temperatures so that we could use the same data set to calculate optimum temperature. To, and 'ceiling' temperature (Tc), above which there is no crop growth and development. At the end of the experiment, plants were separated into shoots and roots, and weighed to obtain fresh mass.

Additional measurements under controlled conditions were also recorded: chlorophyll concentration or 'green up' ability, and membrane thermostability.

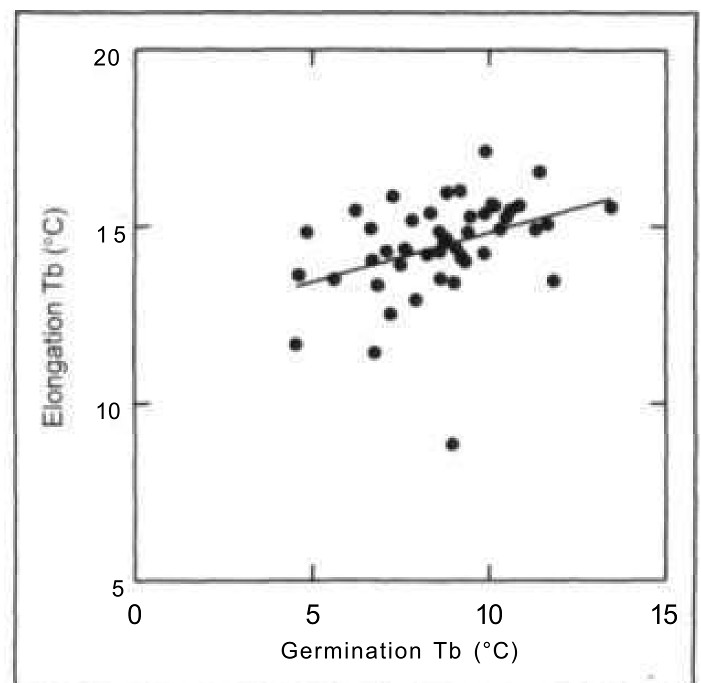

Figure 3, Relation between temperature base (Th) for germination and elongation of 49 sorghum cultivars.

Results and Discussion

The magnitude and distribution of emergence and elongation rates varied with temperature, as shown for the 49 entries by box-and-whisker plots in Figure 1. Genotypic differences existed as well for germination and elongation Tb (Fig. 2). Our data suggest a mean Tb value for germination of 8.7°C, with a range of 4.6 to 13.4°C, and a mean Tb value for elongation of 14.5°C, with a range of 8.8 to 17. 1°C. Although germination Tb was less than elongation Tb, the two were correlated (Fig. 3), challenging suggestions by other researchers that germination, emergence and early seedling growth under cold temperatures are independent. The relation between germination and elongation rates also challenges the suggestion of independence (Fig. 4). Data scatter in Figure 4 appears to increase with rate, but when points are associated with particular temperatures, it appears that the relation between germination and elongation rates is approximately linear for a given temperature. However, slopes and intercepts change with temperature. This may be because of the differential response of shoot and root growth to temperature, as shown by fresh mass response to temperature (Fig. 5).

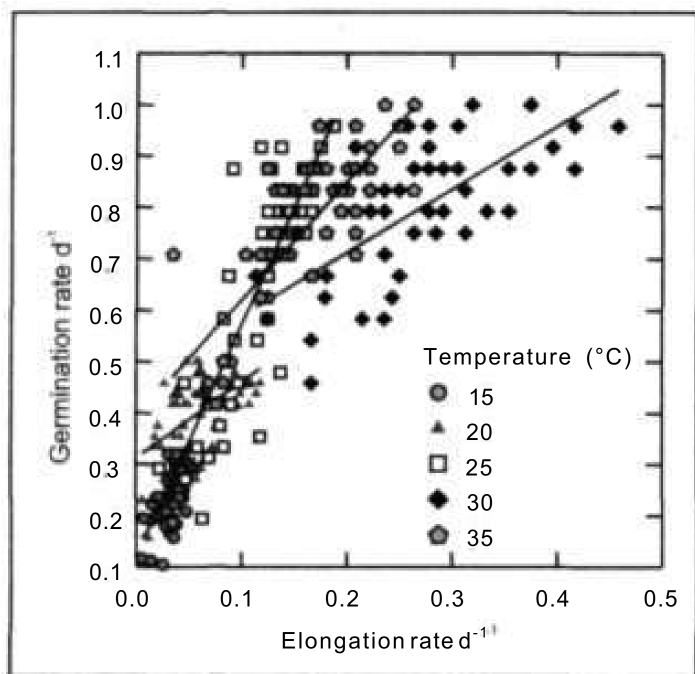

Figure 4. Temperature effect on relation between germination and elongation rates of 49 sorghum cultivars.

There was no relation between Tb of germination and elongation and rates of germination and emergence (data not shown), suggesting that rates of development and growth were independent. Preliminary results also suggest no relation between Tb and 'green up' ability or membrane thermostability.

Thus far our field and growth study data indicate that cultivars from the highlands of Africa, including Ethiopia, South Africa and Rwanda, are the most cool tolerant. The commercial hybrids from Dekalb, including DK 18C, 18EC, DK 66, and DK 41yC, also continue to

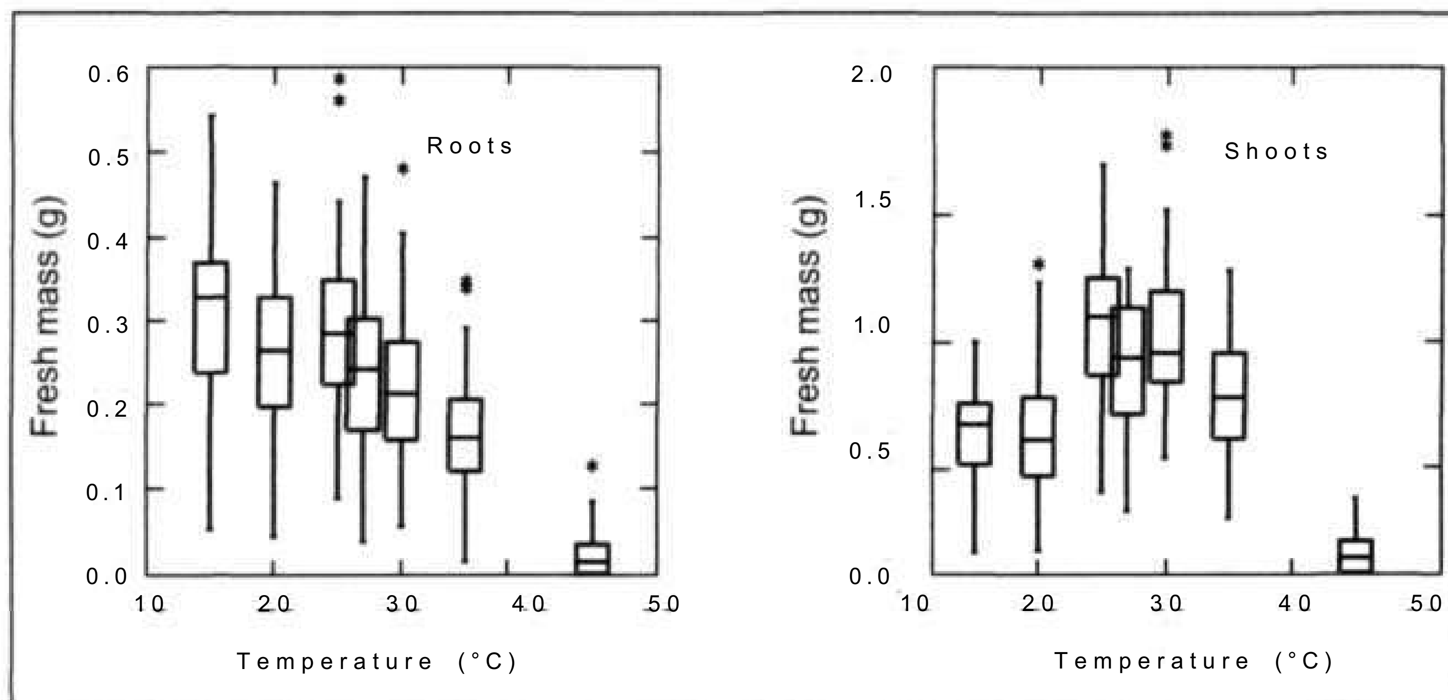

Figure 5. Differential response of root and shoot fresh mass to temperature for 49 sorghum cultivars.

show consistent and superior performance. Currently, we are working with respiration and chlorophyll fluorescence measurements of contrasting cultivars to further elucidate physiological mechanisms of adaptation to cold temperatures in seedlings.

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Seedling Establishment and Seeding Rate Response of Grain Sorghum in Northeastern Oregon, USA

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Grain sorghum *(Sorghum tricolor)* has attracted the attention of producers as a potential alternative crop in northeastern Oregon in USA, which is dominated by winter wheat *(Triticum aestivum)/*sumner fallow cropping systems. In this region, 70% of mean annual rainfall is received during the winter, and spring weather rapidly changes from cool and wet to hot and dry. By the time soil temperatures are optimal for planting sorghum, it is highly unlikely that seedbed moisture will be sufficient for germination and emergence. To be a viable crop in northeastern Oregon, sorghum must be able to emerge under cool conditions, when moisture is available. Since sorghum has not been grown in this environment, there is no information on optimal seeding rate. We conducted field research during two years to screen sorghum genotypes for the ability to emerge under cool conditions and to determine optimal seeding rate. There was a wide range among 48 cultivars for emergence ability, and data from the two years were very consistent (Fig. 1). Cultivars were clustered into four groups: (1) high seedling establishment and low yield; (2) medium seedling establishment and low yield; (3) medium seedling

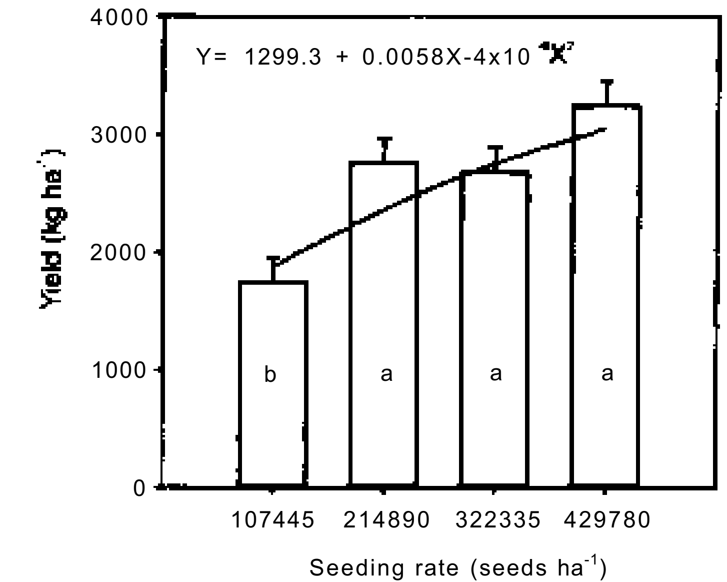
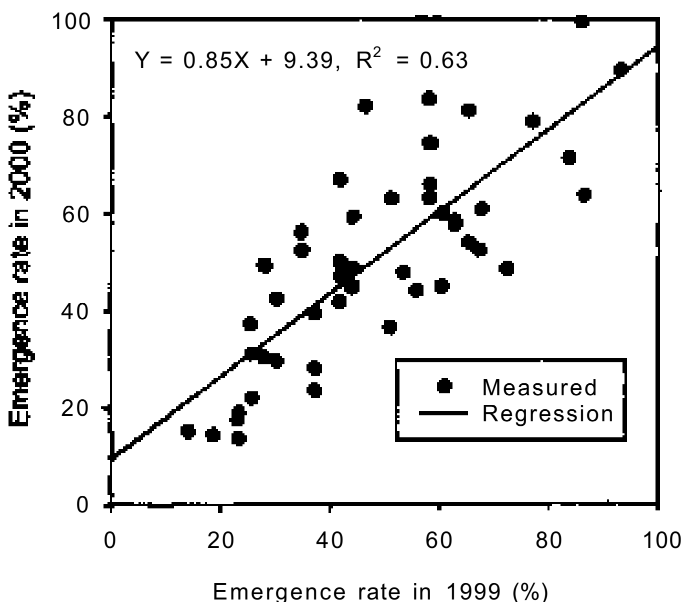


Figure 2. Mean response of four sorghum hybrids to seeding rate during two years in northeastern Oregon, USA.



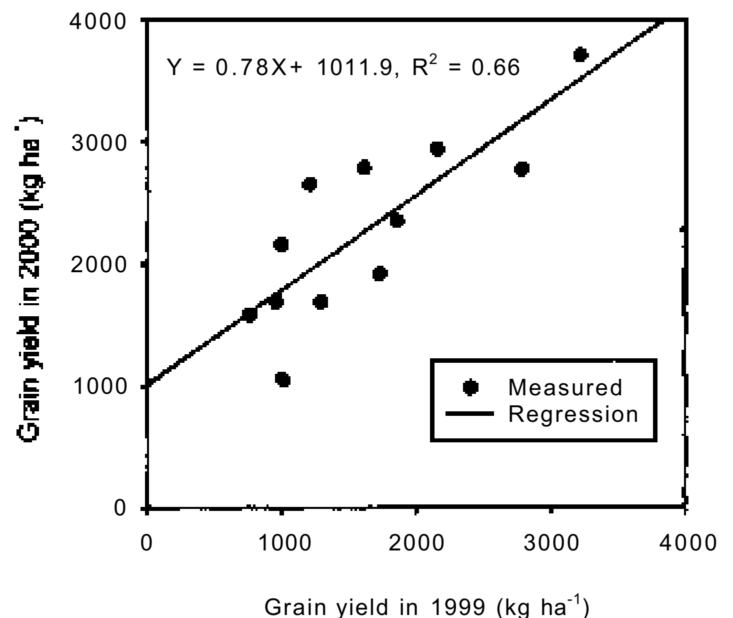


Figure 1. Field emergence and yield of 48 sorghum cultivars grown during two years in northeastern Oregon, USA.

establishment and medium yield; and (4) high seedling establishment and high yield. For the four hybrids evaluated (DKL18C, DKL28EC, Pioneer 8925 and Pioneer 8950), optimum seeding rate was 214,890 to 322,335 seeds ha^{-1}, which gave average yields of 2546 to 2753 kg ha^{-1} under dryland conditions (Fig. 2). This research was supported by a grant from the National Grain Sorghum Producers, USA.

Correlation Analysis Between Soil Chemical Properties, Nutrient Uptake and Yield of Winter Sorghum as Influenced by Cultural Practices

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Introduction

Sorghum (*Sorghum bhicolor*) is a staple food grown in northern Karnataka, India for food, fodder and fuel requirements. The yields of winter sorghum in the northern dry zone (zone 3, semi-arid tropics) of Karnataka during postrainy season are low. The reasons for low yields of winter sorghum in this region includes, low and erratic rainlall coupled with intermediate drought during cropping season, low fertility status of soil, especially nitrogen (N), and lack of adoption of improved cultural practices. The yields of winter sorghum in the region can be improved through in situ moisture conservation during rainy season, which not only conserves the soil moisture but also reduces nutrient loss. The soil physico-chemical properties during the growing season and nutrient uptake by the crop ultimately determines the crop growth, yield components and yield of sorghum during postrainy season. A field experiment was conducted during the postrainy season in 1994/95 and 1995/96 to research the correlation analysis among soil physico-chemical properties, nutrient uptake and grain yield of winter sorghum as influenced by cultural practices.

Materials and Methods

A field experiment was conducted on Vertisols (Typic-Chromosterts) at the Regional Research Station, Bijapur, situated in the semi-arid tropical region of northern Karnataka, 16°49' N latitude, 75°42' E longitude and an altitude of 594 m above mean sea level during postrainy season in 1994/95 and 1995/96. Total rainfall of 585.8 and 629 mm distributed over 36 and 47 rainy days was received during 1994/95 and 1995/96, respectively. During 1994/95 and 1995/96, nearly 72% (424.5 mm) and 61 % (384.2 mm) of rainfall was received during the cropping season.

The soil at the experimental site was black clayey with infiltration rate 10 mm h^{-1}, bulk density 1.28 Mg m^{-3} pH 8.6 and electrical conductivity 0.30 dS m^{-1}. These soils are low in organic carbon (3.6 g kg^{-1}), available N (125 kg ha^{-1}), low to medium in available phosphorus (P) (29 kg ha^{-1}) and high in available potassium (K) (410 kg ha^{-1}). The experiment was conducted on 1% slope in split-split plot design. Moisture conservation treatments consisted of compartmental bunding and ridges and furrows in main plots during 3rd week of July 1994 and 3rd week of June 1995. In the sub-plot, *Leucaena* loppings (2.5 t ha^{-1}) and farmyard manure (FYM) (2.5 t ha^{-1}) were incorporated during 3rd week of August and Ist week of September, respectively. Vermicompost (at 1.0 t ha"1), N fertilizer (0, 25 and 50 kg ha^{-1}) as per the treatments through urea and recommended dose of P (25 kg ha^{-1}) through single super phosphate were applied at the time of sowing. Sorghum cultivar M 35-1 was sown on 4 October 1994 and 15 September 1995 to a depth of 5 cm and 15 cm apart in 60 cm rows and harvested on 15 February 1995 and 25 January 1996, respectively. Grain yield from net plot was harvested; sun-dried and weighed.

Soil moisture in the top 60-cm profile was collected from sowing to harvest at 30-day intervals and was converted on volume basis using bulk density and further consumptive use was worked out. Bulk density was measured by core sampler method (Black 1965) and infiltration rate by double ring infiltrometer (Richards 1954). Soil samples collected at harvest of the crop during 1995/96 at 0-15 and 15-30 cm soil depths in all the replications were analyzed for available N by alkaline permanganate oxidation method (Subbaiah and Asija 1959). available P_2O_5 by Olsen's method (Jackson 1967), available K by extracting with neutral normal ammonium acetate, photometrically (Muhr et al. 1965). The nutrient content in plant parts (leaves, stem and grain) was analyzed for N by micro-Kjeldahl method, P by vandeo molybdate method and K by triacid method (Jackson 1967). The nutrient content in different plant parts was expressed in percentage and was multiplied by dry matter to obtain uptake at harvest. Statistical analysis for all the characters was worked out by the methods suggested by Gomez and Gomez (1984).

Results and Discussion

Grain yield and soil moisture. Plots with compartmental bunding and ridges and furrows out-yielded flat bed plots during 1994/95, 1995/96 and in the pooled analysis (Table 1). In the pooled data, compartmental bunding and ridges and furrows increased the grain yield significantly by 23% (1567 kg ha^{-1}) and 26% (1603 kg ha^{-1}), respectively as compared to flat bed. Higher yield of winter sorghum with moisture conservation practices was due to conservation of soil moisture and reduction in water, soil and nutrient losses (Bhaskaran and Solaimalai 2002). Among the organic sources applied, significantly higher grain yield of 1570 kg ha^{-1} was observed with *Leucaena* application as compared to FYM (1472 kg ha^{-1}) and vermicompost (1405 kg ha^{-1}) and the increase was 7% and 12%, respectively. Higher grain yield with *Leucaena* application over other sources of organic materials was

Table 1. Grain yield of winter sorghum as influenced by moisture conservation practices, organic materials and nitrogen levels at Bijapur, Karnataka, India.

Treatment	Grain yield (kg ha^{-1}) 1994/95	1995/96	Pooled
In situ moisture conservation			
Flat bed	1238	1314	1276
Compartmental bunding	1517	1563	1567
Ridges and furrows	1658	1547	1603
SEm+	62,6	43.9	38.2
CD (0.05)	246	172.2	124.7
Organic materials			
Farmyard manure (2.5 t ha^{-1})	1486	1457	1472
Vermicompost (1.0 t ha^{-1})	1398	1411	1405
Leucaena loppings (2.5 t ha^{-1})	1582	1557	1570
SEm+	50.9	36.3	31.3
CD (0.05)	156.9	112.0	91.3
Nitrogen level (kg ha^{-1})			
0	1274	1263	1268
25	1536	1509	1522
50	1657	1653	1655
SEm+	37.5	52.9	24.9
CD (0.05)	108.2	95.0	69.0

Table 2. Correlation coefficient analysis for available nitrogen, phosphorus and potassium at harvest at two soil depths and grain yield *of* winter sorghum during postrainy season 1995/96 at Bijapur, Karnataka, India[1].

Soil depth (cm)	Available nitrogen (kg ha^{-1}) 0-15[2]	15-30[2]	Available phosphorus (kg ha^{-1}) 0-15	15-30	Available potassium (kg ha^{-1}) 0-15	15-30	Grain yield (kg ha^{-1})
Available nitrogen (kg ha^{-1})							
0-15	1.000	0.884**	0.302	0.465*	0.765**	0.737**	0.862**
15-30		1.000	0.377*	0.543**	0.760**	0.736**	0.905**
Available phosphorus (kg ha^{-1})							
0-15			1.000	0.879**	0.274	0.278	0.531**
15-30				1.000	0.339*	0.287	0.716**
Available potassium (kg ha^{-1})							
0-15					1.000	0.956**	0.777**
15-30						1.000	0.721**
Grain yield (kg ha')							1.000

1. * = Significant at 5% level; ** = Significant at 1 % level.
2. Soil depth (cm).

Table 3. Correlation coefficient analysis among uptake of nutrients (nitrogen, phosphorus and potassium) by leaf, stem, grain and total plant at harvest with grain yield of winter sorghum at Bijapur, Karnataka, India[1].

Parameters	1	2	3	4	5	6	7	8	9	10	11	12	13
1	1.000	0.871**	0.926**	0.940**	0.961**	0.904**	0.902**	0.913**	0.728**	0.932**	0.869**	0.913**	0.923**
2		1.000	0.880**	0.912**	0.883**	0.927**	0.882**	0.895**	0.734**	0.899**	0.793**	0.870**	0.904**
3			1.000	0.997**	0.927**	0.956**	0.969**	0.976**	0.811**	0.958**	0.930**	0.960**	0.991**
4				1.000	0.940**	0.966**	0.971**	0.979**	0.810**	0.966**	0.925**	0.962**	0.993**
5					1.000	0.935**	0.901**	0.916**	0.759**	0.921**	0.881**	0.915**	0.919**
6						1.000	0.930**	0.947**	0.805**	0.958**	0.904**	0.950**	0.960**
7							1.000	0.999**	0.793**	0.939**	0.901**	0.932**	0.962**
8								1.000	0.775**	0.949**	0.910**	0.943**	0.970**
9									1.000	0.814**	0.858**	0.886**	0.833**
10										1.000	0.931**	0.984**	0.967**
11											1.000	0.975**	0.928**
12												1.000	0.967**
13													1.000

1. ** = Significant at 1% level; 1 = N uptake by leaf; 2 = N uptake by stem; 3 = N uptake by grain; 4 = Total N uptake; 5 = P uptake by leaf; 6 = P uptake by stem; 7 = P uptake by grain; 8 = Total P uptake; 9 = K uptake by leaf; 10 = K uptake by stem; 11 = K uptake by grain; 12 = Total K uptake; 13 = Grain yield.

due to conservation of higher amount of moisture with higher nutrient availability. In the pooled data, application of 25 kg N ha^{-1} increased the grain yield by 20% (1522 kg ha^{-1}) and further increase in N dose up to 50 kg ha^{-1} increased the grain yield by 31% (1655 kg ha^{-1}) as compared to control (1268 kg ha^{-1}) (Table 1).

Soil chemical properties. Availability of N, P and K in top (0-15 cm) and subsoil (15-30 cm) at harvest were positively and significantly correlated with grain yield (Table 2). The correlation coefficient values for available N was 0.862 in 0-15 cm soil profile and 0.905 in 15-30 cm soil profile at harvest during 1995/96. Similar values for available P and K were 0.531 and 0.716 at 0-15 cm soil depth and 0.777 and 0.721 at 15-30 cm soil depth, respectively. The above correlation coefficient values clearly indicate that the application of N plays a very important role in increasing sorghum yields followed by K and P in the Vertisols of the semi-arid tropics of Karnataka (zone 3) under dryland situations. Increase in K availability in Inceptisols of Maharashtra, India increased the grain yield of winter sorghum and was positively correlated with sorghum grain yield (Amrutsagar and Sonar 2000). Saha (2000) also observed in the terrain soils of West Bengal that the availability of N and its different forms decreased with increase in soil depth and had a positive and significant correlation among them. Bhaskar Rao et al. (2001) reported that the initial soil test values had a positive and significant correlation with postharvest soil test values for all the three nutrients (N, P and K applied) in Karimnagar, Warangal, Nizamabad and Adilabad districts of Andhra Pradesh. Significant correlation between rice (*Oryza sativa)* yield with initial soil test values and fertilizer doses of N, P and K applied was observed in farmers' fields in these districts.

Nutrient uptake at harvest. Adoption of in situ moisture conservation practices with supply of nutrients through both organic and inorganic sources not only resulted in conservation of moisture and nutrients in the soil profile but also increased their availability in the soil profile at various stages of crop growth further resulting in the higher uptake of nutrients with improved crop growth and yield in winter sorghum. Nitrogen, P and K uptake by leaf, stem and grain and total uptake by plant were significantly and positively correlated with grain yield at harvest (Table 3). Higher availability and uptake of water and nutrients by different plant parts at various stages of crop growth resulted in improved crop growth with higher dry matter production in ear at harvest. This proved important for higher grain yield in winter sorghum. Correlation coefficient between N uptake by leaf (0.923), stem (0.904), grain (0.991) and plant (total) (0.993) and P and K uptake by leaf (0.919 and 0.833), stem (0.960 and 0.967), grain (0.962 and 0.928) and plant

(total) (0.970 and 0.967), respectively was significantly and positively correlated with grain yield. Nutrient uptake among different plant parts and total was positively and significantly correlated. Tamboli and Daftardar (2000) reported that the different P fractions in Vertisols were significantly correlated with grain yield and P uptake of pigeonpea (*Cajanus cajan*). Sharma and Swami (2000) also reported that significant and positive correlation existed between K availability, uptake, and dry matter production in maize (*Zea mays*), soybean *(Glycine max)* and *dhaman* grass in the Aridisols of Rajasthan, India.

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Ideal Sowing Dates and Genotypes for Summer Irrigated Sorghum in Maharashtra, India

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Introduction

Sorghum *{Sorghum bicolor)* is an important staple food source for humans and its stalk is a fodder source for cattle in India. It ranks third in India in area and production after rice *(Oryza sativa)* and wheat (*Triticum aestivum).* It is mostly grown in the *kharif* (rainy) season (June-October) and postrainy *(rabi)* season (October-February) in Maharashtra, India. Recently, in some parts of Maharashtra, the crop is also being grown during summer (January-April). In Nanded district of Maharashtra, *kharif* sorghum is an important component of the cropping system besides banana (*Musa paradisiaca)* and cotton *(Gossypium* sp). Whenever *kharif* sorghum fails or its grain quality is affected by grain molds due to rains in September and October (124 mm and 108 mm), it is then replanted in the summer under irrigated conditions to meet the demand of high quality grain. The area of summer sorghum in Nanded and adjoining districts of Parbhani and Hingoli fluctuates from year to year depending upon the availability of irrigation as well as the prevailing prices of grain and fodder in the market. Experiments conducted at the Water Management Scheme, Parbhani revealed that about 2 t ha^{-1} grain yield can be harvested from summer sorghum.

Photoperiod sensitivity in sorghum influences the selection of genotypes during *rabi* and summer seasons. Until equinox (21 March), <12 hours photoperiod influences the genotype performance in terms of transformation from vegetative to reproductive phase. This has an indirect impact on the final leaf number and yield. High temperatures during the grain-filling stage may increase maintenance respiration and translocation of nutrients to the grain and thus impact yield.

Research was conducted to ascertain the optimum sowing time and suitable genotypes of irrigated sorghum for the summer season in Maharashtra, India.

Materials and Methods

The experiment was conducted for two years (2000/01 and 2001/02) in summer season on medium black soil, at Sorghum Research Station, Marathwada Agricultural

Table 1. Total dry matter and yield as influenced by various treatments in summer sorghum at Parbhani, Maharashtra, India[1].

Treatment	Total dry matter (t ha⁻¹)		Fodder yield (kg ha⁻¹)		Plant height (cm)		Grain yield (kg ha⁻¹)		Grain yield (g plant⁻¹)		1000-seed mass (g)		Pooled			
	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Total dry matter (t ha⁻¹)	Grain yield (kg ha⁻¹)	Fodder yield (kg ha⁻¹)	Harvest index
Sowing date (D)																
D_1 (51 MW, 19 December)	10.28	7.78	6915	5353	176	163	3354	2432	31	45	30	40	9.03	2895	6134	33
D_2 (1 MW, 5 January)	11.39	7.66	7870	5373	182	166	3520	2183	28	41	29	38	9.53	2853	6621	30
D_3 (3 MW, 18 January)	9.92	7.75	7601	5911	181	172	2036	1877	27	37	24	38	8.84	1958	6756	23
SE±	0.26	0.20	415	206			132	76					0.18	63	177	
CD at 5%	0.72	0.55	NS	NS	7.3	5.19	361	210	2.0	3.5	0.7	0.5	NS	191	NS	
Genotype (G)																
G_1 (M 35-1)	11.75	8.16	8217	5873	199	194	3538	2074	30	38	31	39	9.96	2806	7045	28
G_2 (SPV 655)	10.77	9.03	7737	6788	192	186	2720	2307	27	41	30	39	9.91	2514	7262	26
G_3 (CSV 216R)	11.11	9.63	8240	7644	218	206	3162	1987	27	40	28	39	10.40	2575	7943	25
G_4 (SPV 1333)	9.40	6.68	7523	4398	141	129	1942	2288	27	34	22	39	8.05	2116	5959	27
G_5 (CSH 14)	9.99	5.21	7378	3507	143	123	2618	1706	27	41	20	37	7.61	2163	5442	30
G_6 (CSH 15R)	10.16	7.68	5677	5063	186	164	3857	2619	33	39	35	40	8.92	3239	5370	36
Mean	10.54	7.73	7462	5545	179	167	2973	2164	29	41	28	39	9.14	2569	6504	29
SE±	0.37	0.28	352	189			145	77					0.11	49	115	
CD at 5%	1.02	0.77	976	523	8.0	7.34	416	214	NS	4.9	1.1	0.7	0.34	136	319	

1. Year 1 = 2000/01; Year 2 = 2001/02; MW = Meteorological week; NS = Not significant.

University, Parbhani. Sowing dates, ie, D_1 [51 meteorological week (MW), 19 December], D_2 (I MW, 5 January) and D_3 (3 MW, 18 January) were tested as main plot treatments and six genotypes as sub-plot treatments: G_1 (M 35-1), G_2 (SPV .655). G_3 (CSV 216 R), G_4 (SPV 1333), G_5 (CSH 14) and G_6 (CSH 15R). The experiment was conducted under irrigated condition in split plot design with four replications. After harvesting the *kharif* crop, 2-3 harrowings were given before sowing the crop. Sowing was done as per the treatments on flat bed with check basins to facilitate irrigation. A pre-plant irrigation followed by an irrigation immediately after planting was used to facilitate uniform and quick emergence. A total of eight irrigations was given for each crop. The depth of water applied per irrigation was 60 mm.

Plant height (cm), grain yield (g $plant^{-1}$) and 1000-seed mass (g) were recorded. The data was subjected to statistical analysis. The data on total dry matter, grain and fodder yields, ancillary observations and pooled analysis are given in Table 1.

Results and Discussion

Total dry matter. Pooled analysis indicated that total dry matter was the highest in the crop sown in D_2 (9.53 t ha^{-1}) and significantly superior to D_3 (Table 1). This showed that for harvesting higher total dry matter the ideal sowing windows are from 3rd week of December (51 MW) to J'" week of January (I MW). The moderate temperature (mean maximum 30 to 32°C and mean minimum 10 to 12°C) during crop phase I and II resulted in better vegetative growth and translocation of nutrients to the grain. The harvest index recorded in D_1 crop (33%) and D_2 crop (30%) was high compared to late sowing in D_3 crop (23%), whereas the genotype CSH 15R recorded highest harvest index of 36%'.

Sowing dates. In the first year, summer sorghum sown on D_2 had highest grain yield of 3520 kg ha^{-1} and was significantly superior to later sowing on D_3 (Table 1). During the second year, sowing on D_1 gave significantly higher yield (2432 kg ha^{-1}) than the later sowing dates. Similarly, sowing on D_2 also gave significantly higher grain yield than D_3. In pooled analysis, it was observed that the crops sown on D_1 and D_2 recorded similar grain yields which were significantly superior to later sowing in D_3. This may be due to ideal maximum temperatures around 30-34°C during vegetative and flowering periods resulting in better translocation to reproductive structures, seed set and seed development. In the crop sown on D_3, the flowering period coincided with higher mean maximum temperatures of around 40-41 °C, which adversely affected the seed set and translocation of nutrients resulting in poor grain yields. The yield attributing characters such as grain yield per plant and 1000-seed mass were also significantly higher in the crop sown on D_1. This indicated that summer sorghum sown from 51 MW to 1 MW is congenial in terms of productivity.

Genotypes. In both the years of experimentation as well as in pooled analysis CSH 15R out-yielded all the genotypes in terms of grain yield. The harvest index and the test weight of CSH 15R were high when compared to other genotypes. In the first year, the grain yield per plant of CSH 15R was also greater than that of other genotypes. Also, M 35-1 and CSV 216R produced good grain yield. The highest monetary return of Rs 13976 ha^{-1} was also recorded by the genotype CSH 15R.

Interaction. The interaction of sowing date x genotype for grain and fodder yield was significant (Table 2). The pooled data indicated that in all the sowing dates CSH 15R produced highest grain yield, while CSV 216R had the highest fodder yield.

Table 2. Grain and fodder yield (kg ha^{-1}) as influenced by sowing date (D) x genotype (G) interaction treatments (pooled) in summer sorghum during 2000-02 at Parbhani, Maharashtra, India.

Sowing date[1]	G_1(M 35-1)	G_2(SPV 655)	G_3(CSV 216R)	G_4(SPV 1333)	G_5(CSH 14)	G_6(CSH 15R)
D_1 (51 MW, 19 December)	3025 (6206)[2]	2828 (6640)	3283 (6703)	2252 (6380)	2626 (5598)	3355 (5295)
D_2(1 MW, 5 January)	3125 (7386)	2795 (7274)	3059 (7760)	2376 (5840)	2240 (5668)	3521 (5546)
D_3 (3 MW, 18 January)	2270 (7542)	1918 (7863)	1380 (9383)	1718 (5407)	1620 (5210)	2840 (5269)
SE±	147 (346)					
CD at 5%	409 (959)					

1. MW = Meteorological week.
2. Values in parentheses arc fodder yields.

Conclusions

From the above results, it is concluded that sowing of summer sorghum between 51 MW and 1 MW (19 December to 5 January) is more productive as compared to later sowing in 3 MW (18 January). The genotype CSH 15R can be recommended to those farmers who are interested in higher grain yield, whereas CSV 216R can be recommended to farmers for **high** fodder yield.

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Effect of Different Sowing Dates on Photosynthate Accumulation and its Partitioning in Postrainy Season Sorghum

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Introduction

In India, postrainy season sorghum *(Sorghum bicolor)* is mainly grown in the states of Maharashtra, Andhra Pradesh and Karnataka under rainfed condition. The soil moisture conserved during the rainy season is used for the growth of postrainy season sorghum. Under such conditions, sowing time influences sorghum grain yield. Mulik et al. (1996) reported that the normal sowing of sorghum (40th meteorological week) gave highest grain yield. Early sowing increases the incidence of pests such as shoot fly, stem borer, etc whereas the late-sown crop is severely affected by soil moisture stress at the time of flowering and grain development. Therefore, this experiment was initiated to study the effect of different sowing dates on photosynthate accumulation, its partitioning and grain yield in postrainy season sorghum.

Materials and Methods

The field experiment was conducted on medium black soil at the Sorghum Research Station, Marathwada Agricultural University, Parbhani, Maharashtra during postrainy season sorghum of 2001/02. The treatments consisted of four genotypes M 35-1, CSH 15R, CSV 14R and RSLG 262 sown on three sowing dates at one-month intervals, ie, normal (29 September), mid late (29 October) and late (29 November). The experiment was sown in factorial randomized block design replicated thrice having gross plot size 2.7 m x 5.0 m and net plot size 1.8 m x 4.4 m. The plant spacing adopted was 45 cm x 15 cm. One irrigation was given at the time of flowering to plots of the first sowing date and two irrigations were given at the time of sowing and flowering to plots of second and third sowing dates. The recommended doses of fertilizers were applied. Five plants from each plot were selected randomly and observations were recorded on days to 50% flowering, days to physiological maturity, leaf area index, plant height, dry matter accumulation at physiological maturity and its partitioning, grain yield (g m^{-2}), harvest index and test weight (1000-grain mass).

Results and Discussion

Sowing date significantly influenced different morphological and physiological characters studied and grain yield. Also, significant differences among the genotypes were observed for all traits except leaf area index, dry matter accumulation in leaf and partitioning of dry matter in leaf at physiological maturity (Table 1). Days to physiological maturity were significantly affected due to sowing date. Plants in the second sowing date matured 11 days late, while those in the third date matured nine days late when compared with the first sowing date. Leaf area index at physiological maturity was significantly higher in third sowing date (1.02) than in other sowing dates. Maximum plant height was recorded in second sowing date (190 cm) which was similar to that in first sowing date (186 cm). The crop in the second sowing date accumulated significantly higher panicle dry matter at physiological maturity (538 g m^{-2}) whereas in the third sowing date, the crop accumulated higher dry matter in stem (615 g rn^{-2}) and total dry matter (1094 g m^{-2}). Hiremath and Parvatikar (1985) revealed that the high grain yield was related to high total biomass production. Panicle partitioning was similar in first sowing date (53.9%) and second sowing date (52.1%) but was significantly superior over the third sowing date (32.4%). Grain yield (422 g m^{-2}), harvest index (40.7 %) and test weight (39.4 g) were significantly higher in the second sowing date compared to other plots. This may be due to optimum moisture available in the soil at the time of (lowering and grain-filling stage, ie, 31 mm rainfall was received during the second week of January 2002. The grain yield of mid late and normal sowing date crops was significantly more compared to the late-sown crop. Dahatonde and Moghe (1991) reported similar results with grain yields being affected due to delayed sowing in the postrainy season.

Table 1. Sowing date and genotypic differences in morphological and physiological characters contributing to grain yield in postrainy season sorghum, 2001/02 at Parbhani, Maharashtra, India.

Treatment[2]	Days to PM	Leaf area index at PM	Plant height at PM (cm)	Dry matter accumulation at PM[1] ($g\ m^{-2}$)				Partitioning (%) of dry matter at PM	Grain yield ($g\ m^{-2}$)	Harvest index (%)	Test weight (g)
				Stem	Leaf	Panicle	Total				
Sowing date											
D1	118	0.88	186	334	107	511	952	53.9	334	34.3	36.7
D2	129	0.58	190	401	97	538	1036	52.1	422	40.7	39.4
D3	127	1.02	180	615	125	354	1094	32.4	240	21.9	26.6
SE±	0.18	0.05	2.51	14.6	4.2	11.0	23.3	0.74	10.9	0.88	0.41
CD at 5%	0.52	0.15	7.37	42.7	12.2	32.3	68.2	2.18	31.9	2.57	1.19
Genotype											
M 35-1	126	0.85	197	470	107	475	1052	45.2	363	33.8	35.3
CSH 15R	124	0.73	180	413	102	425	940	46.1	286	30.3	31.7
CSV 14R	125	0.89	181	491	117	489	1097	44.6	344	31.2	34.6
RSLG 262	124	0.84	183	425	112	482	1019	48.6	336	33.8	35.8
SE±	0.21	0.06	2.9	16.9	4.8	12.7	26.9	0.85	12.6	1.01	0.47
CD at 5%	0.6	NS[3]	8.5	49.3	NS	37.3	78.7	2.51	36.9	2.97	1.37
Genotype × Sowing date											
SE±	0.36	0.11	5.03	29.0	8.4	22.1	46.6	1.48	21.8	1.76	0.81
CD at 5%	1.04	NS	NS	NS	24.5	NS	NS	NS	63.9	NS	2.37
CV (%)	0.49	20.0	4.71	11.27	13.3	8.13	7.85	5.58	11.4	9.42	4.1

1. PM = Physiological maturity.
2. D1 = 29 September 2001; D2 = 29 October 2001; D3 = 29 November 2001.
3. NS = Not significant.

Table 2. **Grain yield and test weight of sorghum genotypes sown on different dates at Parbhani, Maharashtra, India.**

Treatment[1]	M 35-1	CSH 15R	CSV 14R	RSLG 262	Mean
Grain yield (g m^{-2})					
D1	385	301	359	292	334
D2	439	360	462	425	422
D3	263	196	210	292	240
Mean	363	286	344	336	332
Test weight (g)					
D1	40.9	32.5	37.9	35.6	36.7
D2	40.4	36.2	40.7	40.4	39.4
D3	24.7	24.9	25.2	31.4	26.6
Mean	35.3	31.2	34.6	35.8	34.2

1. D1 = 29 September 2001; D2 = 29 October 2001; D3 = 29 November 2001.

Genotypic differences indicated that CSH 15R and RSLG 262 matured significantly earlier than M 35-1 and CSV 14R. Plant height (197 cm) was significantly higher in M 35-1 than in other genotypes. CSV 14R had higher stem, panicle and total dry matter accumulation and was similar to M 35-1, RSLG 262 for total dry matter accumulation. For stem partitioning, M 35-1, CSH 15R and CSV 14R were significantly superior to RSLG 262. However, panicle partitioning (48.6%) was significantly higher in RSLG 262 than in M 35-1 and CSV 14R. M 35-1, CSV 14R and RSLG 262 were similar for grain yield, harvest index and test weight and significantly superior to CSH 15R.

Interaction effects were not significant for most of the characters except for grain yield, test weight, days to 50% flowering, days to physiological maturity and leaf dry matter accumulation (Tablel). CSV 14R in the second sowing date gave significantly higher grain yield (462 g m^{-2}) than other genotypes (Table 2). The test weight was significantly higher (40.9 g) in M 35-1 in the first sowing date and was similar when compared to CSV 14R (40.7 g), M 35-1 (40.4 g) and RSLG 262 (40.4 g) in the second sowing date. As the sowing time in the postrainy season is not predictable, the stability of performance is important. The data supports the conclusion that M 35-1 is the most stable genotype for grain yield and test weight when sown at normal time or late.

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Evaluation of Sorghum Genotypes for Drought Tolerance

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Introduction

The area under postrainy season sorghum *(Sorghum bicolor)* in Maharashtra, India has been stable for the last three decades as the crop is equally valued for its grain and fodder. The postrainy season sorghum in Maharashtra occupies 3.2 million ha of area with production of 2.1 million t and productivity 658 kg ha^{-1} (NRCS 2001). The last three decades witnessed a 30% rise in postrainy season productivity from 0.48 to 0.621 ha^{-1} at the national level (Nerkar 1998). The crop is mainly grown on moisture stored in situ during rainy season (June to September). The low productivity of sorghum in medium to deep black soils of Karnataka, southern Maharashtra and Andhra Pradesh is due to the poor adaptation of improved cultivars in these drought-prone areas (Patil 2002). Considering these situations, this experiment was conducted to evaluate and identify the sorghum genotypes for drought tolerance in postrainy season.

Table 1. Genotypic differences in morphological and physiological characters contributing to grain yield in postrainy season sorghum, 2000/01 at Parbhani, Maharashtra, India[1].

Genotype	Days to PM	Dry matter accumulation PM ($g\ m^{-2}$)			Partitioning (%) at PM of panicle	Grain yield ($t\ ha^{-1}$)	Fodder yield ($t\ ha^{-1}$)	1000-grain mass (g)	Harvest index (%)	RWC (%) at flowering	CSI at flowering	Leaf stay green (%) at PM
		Stem	Panicle	Total								
RSLG 262	126	118	223	397	56.0	1.19	1.9	40.2	48.4	76.5	0.415	42.8
RSLG 227	128	138	313	519	60.1	1.17	2.8	40.2	52.7	75.3	0.280	38.0
RSLG 383	125	167	383	629	61.7	1.12	3.3	41.5	53.2	80.2	0.357	42.8
RSLG 241	127	132	284	483	58.8	1.01	2.4	41.5	48.1	75.3	0.077	39.1
RSP 1	124	125	263	453	58.2	0.91	2.3	36.3	49.7	75.6	0.435	37.4
RSP 3	125	162	348	589	60.2	0.93	2.9	45.3	46.6	76.7	0.396	41.5
PBS 2	127	130	326	520	62.8	1.44	2.5	47.6	54.9	74.8	0.338	44.7
CR 4	126	151	319	541	59.0	1.49	3.3	41.8	50.1	77.9	0.299	39.4
CR 6	129	134	315	505	62.2	1.20	2.5	39.1	53.1	77.8	0.367	31.1
CR 9	125	135	337	543	62.0	1.35	3.0	38.4	53.1	70.9	0.522	34.8
RS 29	146	277	328	696	47.2	1.07	4.0	19.9	34.3	76.9	0.257	41.4
M 35-1	128	229	288	481	59.7	1.49	2.4	43.5	48.8	81.2	0.280	38.0
Sel 3	124	149	283	503	56.1	1.04	2.8	38.3	47.9	74.8	0.154	40.2
CSV 14R	125	190	405	683	59.4	1.58	3.8	45.9	51.4	81.1	0.319	40.5
SE±	0.50	10.8	22.9	35.5	1.7	0.04	0.18	0.37	1.92	0.52	0.018	4.44
CD at 5%	1.46	35.9	66.6	103.1	5.0	0.12	0.54	1.07	5.59	1.51	0.052	NS
CV (%)	0.69	14.0	12.6	11.4	5.1	5.82	11.2	1.6	6.74	1.17	9.6	19.52

1. PM = Physiological maturity; RWC = Relative water content; CSI = Chlorophyll stability index; NS = Not significant.

Materials and Methods

A field experiment with 14 genotypes was conducted in randomized block design with three replications on medium black soils during the postrainy season 2000/01 at the Sorghum Research Station, Marathwada Agricultural University, Parbhani, Maharashtra. The crop was sown on 10 October 2000 and harvested on 27 February 2001. The crop was grown on residual soil moisture and was not irrigated. The spacing adopted was 45 cm between rows and 15 cm between plants. The gross plot size was 2.7 m x 5.0 m and net plot size was 1.8 m x 4.4 m. Recommended fertilizer doses were given. Five plants were selected from each plot for recording observations on different physiological characters.

Results and Discussion

The genotype RSP 1 and Sel 3 matured earlier than rest of the genotypes (Table 1). The plant height differences were not significant; however, M 35-1 recorded maximum plant height. Leaf area index (4.21) at flowering and total biomass production (696 g m^{-2}) at physiological maturity was significantly high in RS 29. Panicle partitioning was maxiumum in PBS 2 (62.8%) followed by CR 6 (62.2 %) and CR 9 (62.0 %).

Among the 14 genotypes evaluated, CSV 14R recorded significantly higher grain yield (1.58 t ha^{-1}) followed by M 35-1 and CR 4 (1.49 t ha^{-1}). The genotype RS 29 possessed significantly higher fodder yield (4 t ha^{-1}) than rest of the genotypes except CSV 14R (3.8 t ha^{-1}). Relative water content (%) at panicle initiation was significantly high in Sel 3 while at 50% flowering, it was high in M 35-1 followed by CSV 14R and RSLG 383. The genotype RSLG 241 had lowest chlorophyll stability index.

The difference in leaf stay greenness was not significant; however, maximum non-senescence score (%) at physiological maturity was recorded in PBS 2. The increase in grain yield in PBS 2, CR 4, CR 6 and CR 9 was due to increase in total biomass (520 g m^{-2}, 541 g m^{-2}, 505 g $m^{-2}$and 543 g m^{-2}, respectively), panicle partitioning (62.8%, 59.0%, 62.2% and 62.0%, respectively), harvest index (54.9%, 50.1 %, 53.1 % and 53.1 %, respectively) and test weight (47.6 g, 41.8 g, 39.1 g and 38.4 g, respectively).

The same genotypes performed better for drought tolerance parameters like relative water content at flowering (74.8%, 77.9%, 77.8% and 70.9%, respectively), chlorophyll stability index at 50% flowering (0.338, 0.299, 0.367 and 0.522, respectively) and leaf stay greenness at physiological maturity (44.7%-, 39.4%., 31.1% and 34.8%, respectively) in comparison with checks M 35-1, Sel 3 and CSV 14R. On the basis of the above yield and drought tolerance parameters studied, the genotypes PBS 2, CR 4, CR 6 and CR 9 were found to be high yielding with tolerance to drought.

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Screening Sorghum Germplasm for Tolerance to Soil Salinity

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Introduction

Sorghum (*Sorghum bicolor*) is known to be relatively more tolerant to salinity than other crops, such as maize (*Zea mays*) or legumes and thus has the potential to replace maize in saline soils (Igartua et al. 1994). The existence of large interspecific (Yang et al. 1990) and intra-specific (Maas 1985, Azhar and McNeilly 1988, De La Rosa-Ibarra and Maiti 1995) variation for salinity tolerance offers a scope for integrating these tolerant crop genotypes with appropriate management practices to better exploit the saline soils.

Most crops are sensitive to salt stress at all stages of plant development, including seed germination, vegetative stage and reproductive stage. In sorghum, seed germination and seedling establishment seem to be more sensitive to soil salinity than subsequent development stages. However, screening methods aimed at crop productivity as a goal, need to concentrate on the quantity and quality of the yield of either fodder (shoot biomass) and/or grain. Variation in the whole-plant reaction to salinity has been considered as the best means to identify salinity tolerant genotypes (Shannon 1984). Salt-tolerant plants at vegetative stage are also less sensitive to stress at later stages of growth. Therefore, the objective of this study

was to screen a diverse set of improved hybrid parents and germplasm lines of sorghum tor their ability to produce higher biomass under saline soil conditions during pre-anthesis stage.

Materials and Methods

One hundred entries comprising popular varieties, hybrids and improved lines of sorghum were screened in a greenhouse at 20-28°C in a randomized complete block design (RCBD) with three replications at ICRISAT, Patancheru, India. There were two salinity treatments: (1) Control: irrigated with deionized water; and (2) Saline: irrigated with 250 mM NaCl solution (EC 23.4 dS cm^{-1}) once at the time of sowing and later irrigated with deionized water. Sixteen seeds of each entry were sown in one 12.5-cm diameter plastic pot on 29 March 2003 and irrigated with deionized water or saline solution to field capacity previously estimated for the soil (Krishnamurthy et al. 2003). To avoid waterlogging during subsequent irrigations, the water needed was determined by regular weighing of representative pots. A maximum of four plants pot^{-1} were retained after thinning at 10 days after sowing (DAS) in the control. One plant per pot was sampled at 18, 25, 32 and 39 DAS. Sampling was done as described by Krishnamurthy et al. (2003). The total plant biomass for each sample was subjected to ANOVA as a two factor RCBD and the genotypic means were obtained. All the four individual sample genotypic means of total biomass produced under saline condition and the four calculated ratios of total biomass under saline condition as that of the control were used for clustering the entries into different classes using Numerical Taxonomy and Multivariate Analysis System (NTSYSPC), version 2.1 from Exeter Software, New York, USA. Similarity/dissimilarity matrix was obtained based on Euclidean distances and thus the entries were grouped on the basis of UPGMA (unweighted pair-group method of arithmetic average).

Results and Discussion

Germination and seedling emergence were delayed under salinity stress. Seedlings emerged in 8 to 10 DAS under salinity compared to 4 DAS in the control. The total plant biomass of entries under salinity showed significant variation at all stages of sampling. However the salinity x genotype interaction was significant in the first three samples only (Table 1). The cluster analysis of the entries on the basis of total biomass production under salinity in all stages and the relative production inclusive of all growth stage samples has indicated at least 4 major

Table 1. Analysis of variance and its significance for salinity treatments, sorghum genotypes and their interactions for total dry matter $plant^{-1}$ of samples at different days of sowing (DAS).

Source of variation	Mean sum of squares and significance level[1]			
	14 DAS	25 DAS	32 DAS	39 DAS
Salinity levels (S)	12.500***	73.790***	189.250***	15275***
Sorghum genotypes (G)	0.014***	0.120***	0.280**	1.080**
S x G	0.011*	0.100***	0.290**	063 INS
Residual	0.009	0.06	0.190	0.706

1. * = Significant at P = <0.05; ** = Significant at P = <0.01; *** = Significant at P = <0.001; NS = Not significant.

Table 2. Cluster group means of total biomass (g $plant^{-1}$), the ratio of total biomass under 250 mM saline condition to that of control at 18, 25,32 and 39 days after sowing (DAS) and the comparative reaction of the tested sorghum entries'.

Sorghum entries	18 DAS		25 DAS		32 DAS		39 DAS		Reaction
	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	
13	0.067	0.222	0.193	0.248	0.241	0.169	0.626	0.315	Sensitive
55	0.074	0.205	0.271	0.294	0.448	0.303	1.251	0.575	Tolerant
13	0.105	0.261	0.276	0.259	0.340	0.197	1.908	0.666	Tolerant (needs confirmation)
19	0.113	0.306	0.380	0.382	0.700	0.479	2.056	0.856	Highly tolerant

1. Pair-wise analysis of means by multivariate analysis showed that the clusters listed were different at 0.001 probability level.

Table 3. Sorghum entries grouped on the basis of pre-anthesis total biomass production under 250 mM saline water irrigated condition and the ratio of biomass under salinity to that of control.

Group	Entries
Sensitive	ICSV 96020, SP 20614B, ICSR 91012, ICSB 677, ICSB 678, ICSB 406, ICSB 89002, SP 20666B. SPDM 94014 (ICSB 517), ICSB 415, ICSR 93033, ICSB 88010, SPDM 94024 (ICSB 218)
Highly tolerant	CSV 15, ICSB 766, ICSV 95030, NTJ 2, ICSV 145, S 35, ICSB 676, ICSV 112, ICSB 300, ICSR 196, SP 40669, SPA2 94029 (ICSB 725), SP 40672, SPV 1022, SPDM 94006 (ICSB 203), ICSR 91005, ICSR 89010, SP 40646, ICSR 93034

groups at a similarity coefficient of 60%, excluding one entry. The consideration of the relative biomass production is expected to account for the variation of the entries in growth vigor. The genotypes that performed consistently across all the sampling stages can be grouped into sensitive, tolerant and highly tolerant entries based on the group means of the total biomass and its ratio relative to control plants, for all the sampling dates (Table 2). Almost all entries that have only partially emerged under salinity in all three replications were grouped under the sensitive category (Table 3). As in pearl millet *(Pennisetum glaucum)* (Krixhnamurthy et al. 2003), some of the elite germplasm lines of sorghum that are particularly known for their specific desirable characters also exhibited better tolerance to salinity. These putative salinity tolerant entries have other desirable characteristics: (1) stable across environments (CSV 15 and ICSV 112); (2) stay-green after maturity (ICSB 676, SP 40646 and SP 40672); (3) resistance to grain mold (ICSV 95030); (4) resistance to leaf blight (ICSB 300); (5) resistance to downy mildew (SPDM 94006); (6) resistance to *Striga* (ICSV 145); and (7) high grain and fodder yield and quality (CSV 15 and ICSR 93034).

A selected set of sorghum lines based on their contrasting performance are being tested again for confirmation. Also, determination of various ionic compositions of the plant tissues is being carried out to delineate the mechanisms of salt tolerance. The same material is being tested at the International Center for Biosaline Agriculture (ICBA), Dubai, UAE as part of a collaborative project on salinity tolerance.

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Pathology

Prevalence of *Claviceps sorghi* on Sorghum in Karnataka, India

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Introduction

Sorghum *(Sorghum bicolor)* is a staple food crop of northern Karnataka, India. It contributes to about 38% of total sorghum production in Karnataka. *Claviceps sorghi,* an ergot pathogen of sorghum is indigenous to the Indian subcontinent and causes considerable loss in sorghum production. After the discovery of *C. africana* in India (Bogo and Mantle 1999), it was advocated that *C. sorghi* has been replaced by *C. africana,* a highly aggressive ergot pathogen of the African continent (Frederickson et al. 1991, Bandyopadhyay et al. 1998). However, we have been observing the prevalence of *C. sorghi* in northeastern Karnataka area every year as reported here.

Materials and Methods

Several field trips were undertaken to five districts of northern Karnataka during flowering to physiological maturity stages of sorghum crops during the *kharif* (rainy) season of 2001. Prevalence of ergot was determined by random row counting method (Rajasab 1980). Total number of sorghum plants present in randomly selected rows and also those showing ergot symptoms were counted to calculate percentage of ergot incidence. Mean disease incidence in different fields within a district is represented as disease incidence (%) of that district. Disease prevalence and sclerotial development were correlated with sorghum varieties grown and the prevailing environmental factors such as temperature, relative humidity and rainfall.

Infected panicles of sorghum crops grown in different locations were labeled in fields and observations were made from flowering stage up to physiological maturity. Size, shape and mass of sclerotia collected from different locations were estimated. Frequency of sclerotial formation on different varieties of sorghum was also recorded. Sclerotial anatomy was studied by observing thin, hand section of sclerotia. Both field and laboratory observations were made to record production of secondary conidia in affected panicles.

Results and Discussion

An average disease incidence of 12.2% was observed in the five districts. Maximum incidence was observed in Bidar (24.9%) followed by Gulbarga (16.8%), Raichur (10.8%), Bellary (6.8%) and Koppal (1.6%). Disease incidence was more in October than in other months. Low temperature (15 to 22°C) and higher relative humidity (70 to 78%) prevailed during September to October and favored disease development. These observations are similar to those of Ramaswamy (1968) on ergot of pearl millet caused by *C. fusiformis.* Sangitrao (1982) has reported greater incidence of sorghum ergot during December and January in Maharashtra, India. Early morning showers for 5 to 6 days during anthesis seem to favor maximum disease development.

Prevalence of ergot disease was more (73.0%) on sorghum variety M 35-1 followed by CSH 9 (12.3%), Bidar Local (10.2%), Soppin Jola (8.2%), Hallin Jola (3.8%) and Raichur Local (1.3%). Sclerotia were long, curved, protruding structures, white to dusty white and hard or soft with tapering ends. Due to weathering (rain and wind action) in some locations, the tips of sclerotia became papery. The anatomy of sclerotia showed highly mature base with immature tip. The morphology of sclerotia varied with sorghum varieties. In longitudinal section, sclerotia showed compact light brown to reddish

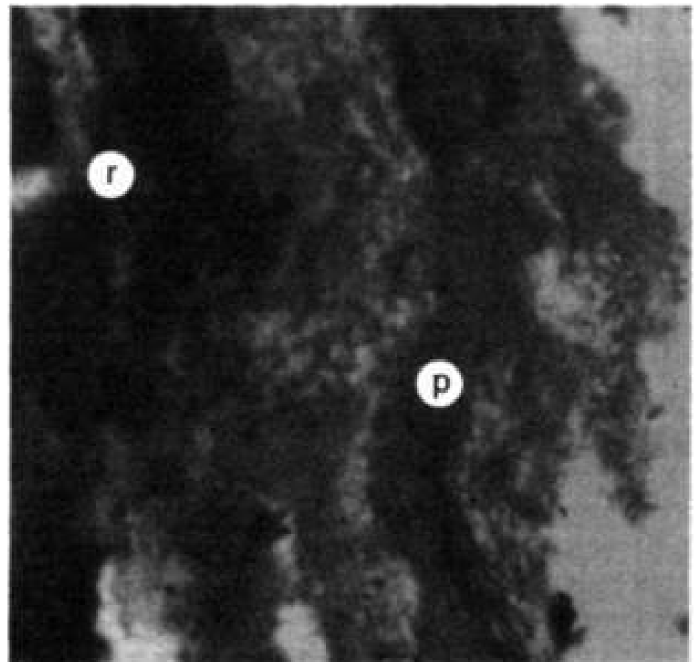

Figure 1. Longitudinal section of sclerotium of sorghum ergot pathogen: inner hard dark brownish rind (r) in the center and plectenchymatous mycelia (p) with macro and microconidia.

Table 1. Morphology of sclerotia of sorghum ergot pathogen collected from different districts of northern Karnataka, India.

Location	Sorghum variety	Size of sclerotia (Length × Breadth) Mean of 25 sclerotia (mm)	Range (mm)	Shape	Mass[1] (g)	Color	Texture
Sannur (Gulbarga district)	CSH 9	15.24 × 2.6	13–19 × 2–4	Long, cylindrical, curved	1.74	White	Hard
Bidar (Bidar district)	M 35-1	7.2 × 1.7	6–9 × 1–3	Short, cylindrical, straight	1.05	Dusty white	Soft
Bhagyanagar (Bidar district)	Bidar Local	8.24 × 2.2	8–10 × 2–3	Short, cylindrical, straight	1.25	Dusty white	Soft
Bhagyanagar (Bidar district)	Hallin Jola	8.62 × 2.4	8–10 × 2–3	Short, cone shaped, straight	1.25	Gray or light brown	Hard
Humnabad (Bidar district)	M 35-1	7.1 × 2.1	6–9 × 1–3	Short, cone shaped straight	0.95	Dusty white	Soft
Dongergaon (Humnabad, Bidar district)	Soppin Jola	4.2 × 2.1	3–6 × 2–3	Small, circular, embedded within glumes	0.80	Light brown	Hard

1. Mean of 100 sclerotia.

brown rind in the center surrounded by plectenchymatous mycelium with macro and microconidial mass (Fig. 1). These observations are similar to those of Frederickson et al. (1999). Based on our field observation on morphology of sclerotia, we recognize four types: (1) long, cylindrical, curved and hard; (2) short, cylindrical, straight and soft; (3) short, cone shaped, straight and hard or soft; and (4) small, circular and hard (embedded within glumes) (Table 1 and Fig. 2). Morphology of the first three types of sclerotia described here are typical of those produced by *C. sorghi* (Frederickson et al. 1991, Bandyopadhyay et al. 1998, Tsukiboshi et al. 1999, Pazoutova et al. 2000, Pazoutova and Bogo 2001). But, the fourth type is morphologically similar to the sclerotia produced by *C. africana* (Frederickson et al. 1999). Morphology of sclerotia reported here (types 1 to 3) are characteristic of *C. sorghi* and distinctly different from those of other species of *Claviceps* infecting sorghum. This observation confirms the

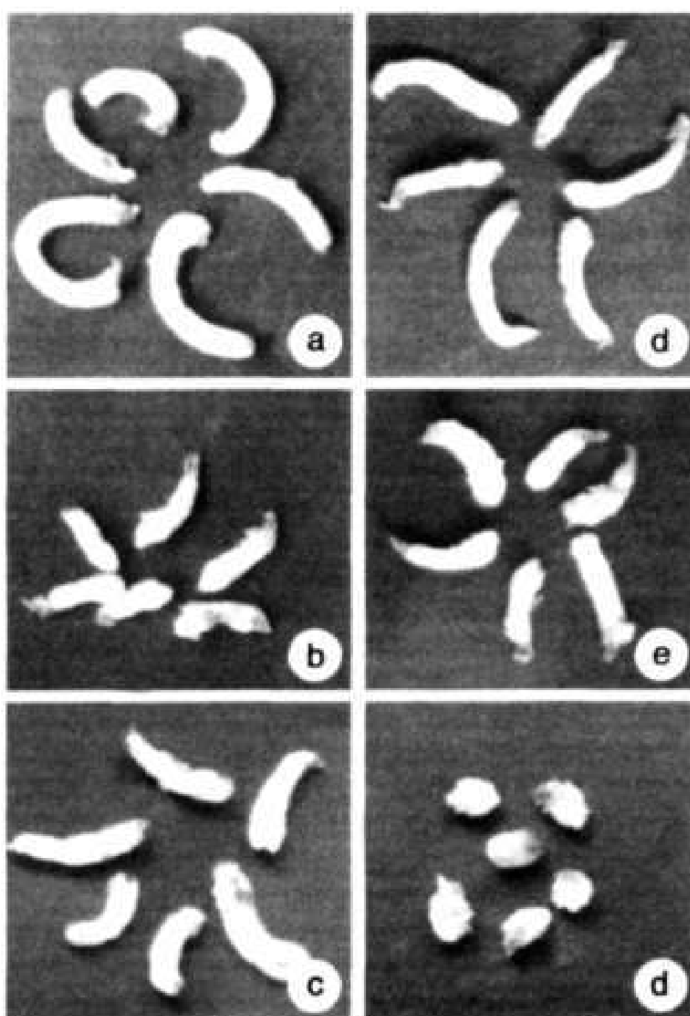

Figure 2. Variation in morphology of sclerotia collected from ergot infected sorghum in different locations of northern Karnataka, India: (a) Sannur (Gutharga district); (h) Bidar (Bidar district); (c) Bhagyanagar (Bidar district); (d) Bhagyanagar (Bidar district); (e) Humnabad (Bidar district); and(f) Dongergaon (Bidar district).

prevalence of C. *sorghi* as a predominant species in this region. The type 4 sclerotia observed here suggest the coexistence of *C. sorghi* and *C. africana* in India.

Based on a comparative study of *C. sorghi* and C. *africana,* Frederickson et al. (1991) and Bandyopadhyay et al. (1998) indicated that the ability of *C. africana* in producing secondary conidia may be considered as a differentiating character of this species. Subsequently, occurrence of *C. africana* in India was reported by Bogo and Mantle (1999). Further, Pazoutova et al. (2000) reported that *C. africana* has a greater epidemiological advantage, ie, dispersal efficiency, than *C. sorghi* as it produces secondary conidia in vivo. However, in this study, profuse production of secondary conidia was also observed in *C. sorghi.* Therefore, the production of secondary conidia may not be considered as a differentiating character of the two species. Pazoutova and Bogo (2001) have concluded that *C. sorghi* is present in Central India as a minor pathogen. However, in this study, only one of the 74 isolates resembled *C. africana* and the remaining 73 were morphologically similar to *C. sorghi* indicating that it is a major pathogen in South India. Thus C. *sorghi* has retained its original niche without replacement by *C. africana* It is necessary to conduct further studies on *C. sorghi* and to better understand its diversity and distribution.

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Prevalence of Sorghum Ergot in Southeast Asia

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Introduction

Ergot is a serious endemic disease in most of the sorghum *(Sorghum bicolor)* producing countries of the world, with most recent outbreaks being in central and South America (Reis et al. 1996). It is caused by the fungus *Claviceps* spp. Three species are predominant: *C. africana* is prevalent in southern and eastern Africa, South America, Southeast Asia, Australia, and India; *C. sorghi* in India and Southeast Asia; and *C. sorghicola* in Japan.

Ergot can cause widespread damage of male-fertile cultivars in farmers' fields when environmental conditions favorable to the pathogen occur at flowering (Molefe 1975, Kukedia et al. 1982, Navi et al. 2002). In addition, ergot has great potential to damage sorghum nurseries and cause significant damage to hybrid seed production. Losses from ergot have been estimated at 10-80% in India and South Africa and 10-100% in Brazil (Bandyopadhyay et al. 1996). In this article, we report

prevalence and distribution of ergot pathogens in different geographic regions of Vietnam, Thailand and Myanmar.

Materials and Methods

Locations surveyed. The objective of the survey in Southeast Asia was to understand the diversity in sorghum ergot pathogen and prevalence of different species as was done in India by Bandyopadhyay et al. (2002). The disease was identified using the identification keys of Frederiksen and Odvody (2000). Incidence and severity from each sorghum field was recorded from an area of approximately 12 m^2 at three spots selected at random. Disease incidence (%) was recorded based on number of plants infected out of the total plants counted, and the severity was recorded on 0-100% based on floral infection (%) in individual panicles (0% = healthy and 100% = entire panicle infected).

Extensive on-farm disease surveys were conducted between August and November 2002 in Vietnam, Thailand and Myanmar. We surveyed 21 farms in two provinces (Sonla and Nghean) in Vietnam; 178 farms in 7 provinces (Nakhon sawan, Lopburi, Saraburi, Kanchanaburi, Nakhonratchasima, Sa Keo and Suphanburi) in Thailand; and 87 farms in 10 townships (Taktone, Nyaungoo, Onetwine, Nwahtogy, Nyangoo, Tuangtha, Monywa, Chuangoo, Yezagyo and Kyaukpadaung) in Myanmar.

Ergot prevalence and sampling. A total of 24 ergot samples were collected during the survey (Table 1); of these, two were from Vietnam, 18 from Thailand, and four from Myanmar. The samples were placed separately in brown paper bags, air-dried and stored at laboratory conditions (25±1°C) for further studies at the United States Department of Agriculture (USDA) laboratory of Dr Paul Tooley at Fort Detrick, Maryland, USA for their cultural characteristics and their genetic diversity.

Pathogenicity test of samples collected in Thailand. Conidial suspensions of the ergot samples collected in Thailand were spray-inoculated separately using conidial spore suspension at the concentration adjusted to 1 x 10^6 conidia ml^{-1} (Tonapi et al. 2002) on to sorghum cultivar 296A at stigma emergence stage. The study was conducted under controlled environment at the Division of Plant Pathology and Microbiology, Department of Agriculture, Bangkok, Thailand. The inoculated panicles were covered with brown paper bags and incubated for 3-5 days at 25±1°C. Further, the plants were incubated under greenhouse conditions (25±1°C) for disease development. From the infected panicles, 5-6 infected spikelets were collected in sterilized paper bags and dispatched to the Foreign Diseases and Weed Science Research Institute, USDA, Fort Detrick,

Cropping Pattern

Sorghum is a minor crop in Vietnam and is grown in very small areas in remote hilly regions mainly for fodder.

Table 1. Prevalence of sorghum ergot in Southeast Asia.

Province/District/ Division/Township	Village	No. of fields surveyed	No. of fields with ergot	Disease incidence (%)	Disease severity (%)	No. of samples collected
Vietnam		21	2			
Mochau	Hangchang			Traces	2-7	2
Thailand		178	18			
Lopburi, Moung	Nikhom			8-10	2-60	2
Lopburi, Moung	Khoktoom			Traces	2-10	3
Lopburi, Pathanikhom	Delang			2-5	5-15	1
Lopburi, Moung	Khoukeinlai			Traces	2-15	2
Nakhon sawan, Moung	Nongpring			Traces	10-40	
Saraburi, Wang moung	Manavan			10-30	50-90	
Saraburi, Wang moung	Namsuk			5-20	30-70	
Saraburi, Paphuthabat	Saraburi			2-15	20-100	
Kanchanaburi, Dhamakantiya	Dhamakantiya			Traces	10-100	
Sa Keo, Wangnamyen	Sa Keo			20-60	80-100	
Saraburi, Wang moung	Wang moung			5-20	60-100	
Suphanburi, Uthong	Suphanburi			15-80	45-100	
Myanmar		87	4			
Onetwine, Mandalay	Shawbin			2-40	10-80	2
Onetwine, Mandalay	Beckone			Traces	5-40	1
Onetwine, Mandalay	Oktwin			2-15	20-80	1

The sorghum genotypes were tall, with sweet stalk, red grains, and take >150 days to mature. In Thailand, hybrid sorghums are predominant over varieties and forage types. In Myanmar, sorghum is grown for food as well as for fodder. Sorghum varieties in Myanmar were similar to those of Thailand and Vietnam. During the survey the crop was in various growth stages from vegetative to physiological maturity or harvestable maturity stages.

Prevalence of Ergot in Farmers' Fields

The most obvious external symptom of ergot observed on panicles (on nodal tillers or on the main plant) was the honeydew exudation from the infected flowers. Honeydew was either uniformly yellow-brown to pink or superficially dull white. However, no sclerotial stage symptoms were observed.

In Vietnam, ergot incidence was in traces with a severity from 2 to 7%. In Thailand, disease incidence ranged from traces to 80% and severity from 2 to 100% while in Myanmar, disease incidence ranged from traces to 40% and severity from 5 to 80% (Table 1). The samples from Myanmar and Vietnam appear to be *C. sorghi.* Putative *C. africana* types were observed only in the Thailand samples collected from Saraburi, Manavan and Namsuk villages (Saraburi province) and Suphanburi (Suphanburi province). *Claviceps sorghi* was also observed in some samples from Thailand. Reproductive potential of ergot pathogen(s) is an important determining factor, which decides the relative predominance of one species, over the other. Results from molecular analysis are awaited to distinguish species or variability within the species.

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Simple Techniques for Production of Secondary Conidia and Ergot Inoculation in Sorghum

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Introduction

Ergot (sugary disease), caused by several species of *Claviceps* including *C. africana,* is a serious panicle disease in most of the sorghum *(Sorghum hicolor)* producing countries of the world (Bandyopadhyay et al. 1998). Airborne secondary conidia are the primary source of inoculum of *C. africana* (Bandyopadhyay et al. 1998) and are responsible for the rapid spread of the pathogen (Frederickson et al. 1989,1991,1993). Secondary conidia are produced on sterigmata from germinated macroconidia from the honeydew. To date, all infection studies have been conducted with mixed suspensions of macroconidia and secondary conidia, sprayed onto stigmas. However, in nature this does not occur, as the

secondary conidia are not deposited in a suspension on the stigmas, except when carried there by raindrops (Tonapi et al. 2002). In this article, we describe techniques to produce and harvest secondary conidia. and to inoculate stigmas; these techniques mimic natural infection.

Materials and Methods

Isolate and sorghum line. The research was conducted at the School of Agriculture and Horticulture, University of Queensland, Gatton, Australia during 2000/01. The C. *africana* isolate 10765 was maintained and inoculated onto the sorghum male sterile line AQL 33. Secondary conidia were produced by streaking fresh honeydew collected from infected panicles of AQL 33 on 2% water agar and by pouring diluted honeydew suspension on moist soil medium in 9-cm petri dishes and incubated at 20°C in the dark for 36 h.

Harvesting techniques. The water agar plates were inverted with the lids partially opened and air moving at 0.2 m sec^{-1} to 3 m sec^{-1} was directed over the secondary conidia. The lid was then closed and the bottom of each petri dish was tapped gently to dislodge the secondary conidia, which were collected inside the lid. In the case of secondary conidia on moist soil, air moving at 0.2 m sec^{-1} to 3 m sec^{-1} was directed over the surface to dislodge the secondary conidia, which were collected on 2% water agar plates held vertically 2 cm downwind of the soil. The efficiency of the harvest was calculated by excising five bits of 1 cm^2 sporulating segments of the agar before the secondary conidia were dislodged, shaking them in 10 ml deionized water, and determining the conidial concentration using a hemacytometer. The mean number of conidia per cm^2 was then calculated. The mean efficiency of harvest (no. harvested x 100/secondary conidia produced per plate) was then determined.

Inoculation methods. Three methods of inoculation (spray, brushing and air movement) with secondary conidia were compared. Twelve panicles of an ergot susceptible sorghum line AQL 33 at 50% flowering were inoculated, and plants were incubated in the greenhouse at 22±3°C for seven days. Each panicle was rated for percentage of infected spikelets.

Spray inoculation: Secondary conidia freshly harvested from water agar plates were suspended in deionized water and the concentration was adjusted to 1 x 10^4 conidia ml"^{1}. The suspension was sprayed onto the panicles until runoff using a hand sprayer.

Brushing technique: Secondary conidia were collected from the lids of the inverted agar plates with a 1.5 cm wide flat brush. They were then brushed onto the stigmas, which were dry, or which had been moistened by a fine spray of deionized water before inoculation.

Air movement technique: Four blocks of inoculum containing the secondary conidia grown on moist soil medium were placed in the wind tunnel and individual plants with panicles at 50% flowering (whose stigmas had been moistened by a fine spray of deionized water before inoculation) were placed at the same height as the soil, 45 cm downwind of the soil. An inbuilt fan blew air at velocities ranging from 0.2 to 10 m sec^{-1} over the sporulating surfaces towards the flowering panicles. The panicles were then covered with paper bags and incubated in a greenhouse at 22±3°C for seven days.

Results and Discussion

Of the three inoculation methods, brushing secondary conidia onto dry or moist stigmas was more efficient than spraying them onto stigmas in an aqueous suspension, or using air movement technique (Table 1). Brushing conidia on stigmas produced 70-80% infection compared with 32% with spray and 3% with air movement methods. This difference in infection may be due to the number of secondary conidia that lodged on individual stigmas, rather than the relative efficacy of the method. The results due to air dislodging of secondary conidia through wind tunnel and natural deposition onto the stigmas mimicking the natural infection process resulted in 3.4% infection at wind velocity of 10 m sec^{-1}. No infection was observed at wind velocities <10 $msec^{-1}$. The use of air moving across the surface of moist soil on which there is secondary sporulation to dislodge secondary conidia and deposit them on flowering panicles holds potential for infection studies and for the screening of sorghum lines and hybrids for resistance to *C. africana.* Further studies are required to optimize the efficiency of harvest and deposition of conidia on stigmas by manipulating factors such as air speed, relative humidity, temperature and soil moisture.

Table 1. Inoculation techniques and infection rates using secondary conidia of the sorghum ergot fungus *Claviceps africana.*

Inoculation technique	No. of florets		Infection (%)
	Inoculated	Infected	
Spray inoculation	100	32	32
Brushing onto dry stigmas	110	77	70
Brushing onto wet stigmas	110	88	80
Air movement	85	4	3
Mean	101.3	50.3	46.3
SEm±	5.9	19.7	17.7

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Variability and Viability of Sorghum Ergot Sclerotia

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Introduction

Sorghum ergot pathogen (*Claviceps sorghi* and *C. africana*) infects ovaries that develop into spore bearing masses (sphacelia) in sorghum (*Sorghum bicolor)* panicles. The hard textured sclerotia of *C. africana* rarely protrude more than a few millimeters beyond the glumes while those of *C. sorghi* and *C. sorghicola* may protrude 15-20 mm beyond the glumes. For several ergot pathogens, sclerotia are the resting structures through which they survive in the interval between harvest and the next crop. The sclerotium germinates to produce asci, which produces ascospores that can infect the new crop. How long can these sclerotia remain viable and cause infection? Sangitrao et al. (1997) have reported viability of sclerotia for a maximum of three years. In this article, results on variability and viability of 10-year-old sorghum ergot sclerotia are reported.

Materials and Methods

Ergot sclerotia collected from sorghum crop during 1992 from Akola (20°70' N and 77° 10' E) in Maharashtra, India were stored under laboratory conditions (25±1"C) at ICRISAT, Partancheru, India. The morphological variability of sclerotia was studied by measuring their size and shape. The viability was tested by pathogenicity tests. To test the pathogenicity, 25 sclerotia of varying morphology were macerated in 30 ml sterilized distilled water using pestle and mortar. The suspension was filtered through sterilized muslin cloth. The filtrate had only mycelial bits and no conidia were seen. The filtrate was made up to 50 ml and was transferred to 100 ml atomizer. The inoculum was sprayed on 10 panicles of sorghum cultivar 296A at 50% stigma emergence stage, using 5 ml panicle^{-1}. The inoculated panicles were covered with polythene bags to maintain high relative humidity ($\geq$95%) at 25°C and were placed in the greenhouse (25±2°C) for five days. Before the appearance of honeydew in the panicles, spikelets containing sphacelia

were collected in sterilized minigrip bags. The sphacelia were scooped out and surface sterilized in 0.1 % sodium hypochlorite, followed by thorough washing in sterile distilled water. The sphacelia were cut into small bits and were plated on potato-dextrose agar (PDA) and incubated at 25°C for 30 days with 12 h light/dark cycle. Later the culture was characterized for radial growth, colony color, puckering nature, sporulation and sectoring. The sclerotial samples and culture were deposited at the Mycological Herbarium, Indian Agricultural Research Institute, New Delhi, India and the herbarium number was obtained.

Results and Discussion

The pathogenicity test carried with 10-year-old sclerotia (Herbarium number: 44440) recorded 65% infection indicating that sclerotia can remain viable for several years and can still cause infection. Sclerotial viability has been reported to be for 3 years based on its germinability in soil under greenhouse conditions (Sangitrao et al. 1997). However, we report here the viability of 10-year-old sclerotia based on pathogenicity test.

The sclerotial morphology indicated wide variation in their size (3-10 mm in length) and basal width (1.5-3 mm). The distal width varied from 1 to 2 mm. The sclerotial shape was both straight and curved (Fig. 1). The sclerotia were categorized into six groups: (1) short and straight with slight curvature; (2) long and curved; (3) long and curved with constricted distal end; (4) short and curved; (5) small and oval; and (6) branched.

The colonies were white, cottony, compact and granular. Radial growth of the colony varied from 27 to 30 mm with distinct sporulation towards the periphery and devoid of puckering and sectoring. Based on Munsell's scale, the colony pigmentation matched at 10YR/7/3 (Anonymous 1973).

Figure 1. Variability in morphology of ten-year-old sclerotia from Akola, Maharashtra, India (size: 0.3-1.0 cm in length, a = basal end, and b = distal end).

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Mechanical Harvesting Reduces Sphacelia/Sclerotia Levels of *Claviceps africana*

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Introduction

In Australia, ergot caused by *Claviceps africana* is endemic on *Sorghum* species used for grain and forage production, and on *Sorghum* weed species (Ryley et al. 2003). The disease has a significant impact on the Australian sorghum *(Sorghum bicolor)* industry by necessitating the use of triazole fungicides in breeder's nurseries and hybrid seed production, forcing the adoption of new management practices for sorghum grain growers, and creating uncertainty about the toxicity of sphacelia/sclerotia (Ryley et al. 2002). Australian research has demonstrated that high levels of dihydroergosine, the major alkaloid component of sphacelia/sclerotia, is detrimental to livestock by causing agalactica in cows and sows (Blaney et al. 2000b), and hyperthermia and reduced weight gain in beef cattle (Blaney et al. 2000a). In Australia, the maximum allowable limit for sphacelia/sclerotia in sorghum grain intended for stockfeed is 0.3% (w/w), although there is considerable variation in the alkaloid content between sphacelia/sclerotia of similar ages (Blaney et al. 2003).

Management options for sorghum grain growers include early planting to reduce the risk of flowering during cool weather in late March-April, sowing when soil moisture and nutrient levels are optimum to assist in

even crop flowering, and adjusting row width to minimize tiller production (Ryley and Blaney 2002). Options at harvest include killing tillers and late flowering plants with herbicides to reduce honeydew contamination at harvest, segregating badly ergot-infected parts of the paddock, and increasing the fan speed in harvesters to maximize the number of sphacelia/ sclerotia which are ejected from the harvester. This last process is effective because sphacelia/sclerotia weigh 0.007-0.015 g, which is in the order of 2-4 times lighter than a typical sorghum grain.

Three categories of sphacelia/sclerotia are often observed after mechanical harvesting of ergot-infected sorghum crops: (1) mature sclcrotes which are light tan to reddish brown, 2.5-5.0 mm long x 1.5-2.5 mm wide, with a rough surface and a mean mass of approximately 0.007 g; (2) sphacelia whose pointed tips protrude past the attached floral elements, and with a mean mass of approximately 0.015 g; and (3) sphacelia covered by the black, convoluted sporodochia of *Cerebella* spp, and with a mean mass similar to the last category. In addition, healthy grain and the three types of fungal bodies described above can be clumped together with honeydew. Only the three sphacelial/sclerotial bodies are considered for the purposes of the 0.3% w/w stockfeed limit.

A study was undertaken in southern Queensland (Qld) and northern New South Wales (NSW) between 1999 and 2001 to quantify the reduction in sphacelia/sclerotia during mechanical harvesting of eight commercial sorghum crops, with the aim of extending more accurate information for the management of sorghum ergot to Australian sorghum growers and harvesting contractors.

Materials and Methods

Sample collection. Eight crops from six properties were used in the study: Crop 1, grower A, at Warwick (Qld) in 1999; Crops 2 and 3, grower B, at Warwick in 2000 and 2001 respectively; Crops 4 and 5, grower C, at Nobby (Qld) in 2000; Crop 6, grower D, at Willowtree (NSW) in 2001; Crop 7, grower E, at Kingaroy (Qld) in 2001; and Crop 8, grower F, at Dalby (Qld) in 2001. The crops were several popular, commercial Australian hybrids. At physiological maturity 5-10 quadrats each approximately 20 m x 20 m were randomly selected within each crop, and from each area 50 sorghum panicles were collected and placed in numbered bags. The areas were marked, and as the harvester passed over them samples of sorghum grain were collected at the auger outlet above the seed collection bin. A total of 1-2 kg of sorghum grain was collected from each area. The harvesters covered the range of machines which are used by growers and contractors to harvest sorghum grain in Australia, and their settings were those used by the growers in their normal harvesting operations.

Preparation of samples and counting of sclerotes. The samples taken prior to harvesting were threshed using a stationary thresher, and the seed and sphacelia/sclerotia were collected. These samples, together with the seed samples taken from the headers at harvest, were dried to approximately 12% moisture in drying ovens at 45°C. Three sub-samples of approximately 200 g were taken from each sample, the seed and sphacelial/sclerotial bodies were separated with the aid of a microscope, and both weighed. The numbers of sclerotes were also counted.

Results and Discussion

The results of the trials are summarized in Table 1. There was considerable variation in the mean number (21-477) and mass *(%* w/w) of sphacelia/sclerotia between crops before harvest (0.12-3.00%), and in the range of values within crops (for example, in Crop 1, 206-1642 and 0.75-12.4% respectively). This variation was also reflected in the "after harvest" data, with mean numbers ranging from 10 to 127 and % w/w from 0.05% to 0.29% between crops, and 36-205 and 0.19-1.05% respectively in Crop 1. In six of the eight crops (Crops 1, 3, 4, 5, 7, 8) the mean numbers and % w/w of sphacelia/sclerotia after harvest were significantly less ($P < 0.05$) than the corresponding values before harvest. The after-harvest % w/w mean values for seven of the eight crops (Crops 2-8) were less than the Australia stockfeed limit of <0.3%, but in three of these (Crops 3, 4 and 7) the upper value of the range was >0.3%. This finding suggests that at least portions of the harvested grain from these crops would have admixtures of sphacelia/sclerotia at high levels to have deleterious effects on livestock.

The reduction in mass (% w/w) of sphacelia/sclerotia as a result of the mechanical harvesting process ranged from 44% for Crop 4 to 76% for Crop 1, and the reduction in numbers ranged from 0% for Crop 2 to 80% for Crop 5. Ribas (1999) reported that the majority of sclerotia are discarded at the harvesting stage, and he provided some limited data to substantiate that claim. His data showed that the 'sclerotia' number was reduced from 0.24% to 0.10% in one sub-field and from 2.34% to 1.65% in another field during harvesting. These are in the order of magnitude of reductions found in the current study.

The differences in reduction (%) between crops may be due to a number of factors. Firstly, there would undoubtedly be differences in the relative number (and

Table 1. Number and mass of sphacelia/sclerotia of *Claviceps africana* before and after mechanical harvesting of 8 commercial sorghum crops.

Crop/Grower	Number per 200g sample		Mass (% w/w per 200g sample)	
	Before	After	Before	After
1/A	206-1642(477)[1]	36-205 (127*)[2]	0.75-12.4 (3.00)	0.19-1.05 (0.71*)[2]
2/B	8-44 (21)	13-33 (21)	0.04-0.24 (0.12)	0.05-0.12 (0.08)
3/B	72-114 (80)	4-57 (25*)	0.28-0.64 (0.43)	0.02-0.54 (0.22*)
4/C	98-225 (139)	13-71 (45*)	0.31-0.74 (0.45)	0.06-0.38 (0.25*)
5/C	42-136 (94)	14-26 (18*)	0.13-0.38 (0.28)	0.07-0.11 (0.08*)
6/D	12-41 (22)	6-36 (15)	0.05-0.20 (0.12)	0.02-0.15 (0.05)
7/E	29-179 (121)	14-54 (43*)	0.24-1.41 (1.02)	0.08-0.48 (0.29*)
8/F	10-33 (26)	5-14 (10*)	0.10-0.32 (0.22)	0.06-0.14 (0.09*)

1. Mean values are given in parentheses.
2. Mean after-harvest values followed by an asterisk are significantly lower ($P < 0.05$) than the corresponding mean before-harvest values using Student's t-test.

mass) of the three sphacelial/sclerotial categories between crops, particularly between sclerotia and the other two catagories. Individual sclerotia are lighter than the sphacelial bodies, so differences before harvest may be further exacerbated during harvesting. Secondly, the relative efficiency of harvesters in reducing sphacelia/ sclerotia may vary depending on the characteristics of the individual harvesters.

Our findings suggest that mechanical harvesting can significantly reduce the admixture levels of sphacelia/ sclerotia in sorghum grain. In all but one of the crops which we studied, the levels of these potentially toxic fungal bodies were reduced to a level less than the Australian sorghum stockfeed limit of 0.3% w/w. Adjustments in fan speed and other settings on individual harvesters to optimize the numbers of sphacelia/sclerotia which are ejected has the potential to further improve harvesting efficiency.

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Use of Polythene Bags to Reduce Grain Mold Infection in Rainy Season Sorghum

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Introduction

Grain mold is one of the serious problems of the rainy (*kharij*) season sorghum (*Sorghum bicolor*) in India.

Severe quantitative as well as qualitative losses are recorded when the crop is exposed to rains at grain formation and development stages. Although 49 fungal species have been reported to be associated with grain mold complex, the species of *Alternaria, Aspergillus, Curvularia, Drechslera, Fusarium, Penicillium* and *Phoma* have been identified as predominant (Navi et al. 1999). The intensity of mold varies according to rainfall pattern during the grain setting to the grain maturity stages (Koteswara Rao 1986). In general, when the disease occurs, the panicles are damaged. Thus comparative studies of healthy and molded grains are difficult as healthy samples of the same variety are not easily available for experimental purpose. Under such a situation either comparison has to be made with the healthy grains obtained from mold-free locality during the same season or from the crop grown during the off-season. Therefore, to obtain healthy grain samples the technique of covering the panicles with polythene bags during the rainy season was tried.

Materials and Methods

A field experiment was conducted during the rainy season 2002 at the Marathwada Agricultural University, Parbhani, Maharashtra, India under sprinkler irrigation. The experiment consisted of 8 sorghum cultivars tested under two treatments: panicles with bags and panicles without bags. Each treatment was replicated thrice. Each cultivar was grown in 4.5-m row plot with about 25 plants in each row. Five panicles per replication were covered with polythene bags (size 15 cm x 30 cm) from milk stage till harvesting of the crop to protect from wetness as and when required. Five panicles per replication were tagged without bags as controls. The panicles were covered for about 40 days during rains or sprinkler irrigation, or at the time of possibile rain and were immediately removed.

Grain mold observations such as percentage germination and fungi associated with the seed were recorded by harvesting the crop at maturity. The grain mold severity was recorded on a scale of 1 to 5 threshed grain mold rating (TGMR), where 1 = mold free; 2 = 1 to 10% grains molded; 3 = 11 to 25% grains molded; 4 = 26 to 50% grains molded; and 5 = >50% threshed grains molded. Data were subjected to randomized block design (RBD) analysis to determine treatment differences.

Results and Discussion

In general, polythene bag cover protected grains from grain mold. Although TGMR in both treatments were statistically significant, treatment with bags was significantly lower than the control (without bags). The grains without bags were moldy and had maximum TGMR (3.55), while grains with bags had minimum TGMR (2.36) (Table 1). The TGMR was minimum in PVK 801 (2.83) and CSH 17 (2.83) and maximum in CSH 18 (3.20) (Table 2). Seed germination was low in molded grains without bags (32.27%) as compared to grains with bags (52.92%) (Table 1). Amongst the genotypes, highest germination was observed in the cultivar PVK 801 (48.35%) and lowest in CSH 14 (31.83%) (Table 2). Similarly, Tripathi (1974) recorded 56% germination in molded grains as compared to 78% in healthy grains. Further, incidence of grain mold fungi *Fusarium moniliforme* (27.43%) and *Curvularia lunata* (33.54%) was high in grains in panicles without bags while incidence was low (14.22% and 25.35% respectively) in panicles with bags (Table 1). Garud et al. (2000) recorded that *Fusarium* infection had negative correlation with germination. Infection by *Curvularia* did not have any effect on seed germination, while germination was drastically affected by infection with *Fusarium* spp. The maximum incidence of *F. moniliforme* was recorded in cultivar CSV 13 (30.86%) and minimum in CSH 9 (17.62%), whereas *C. lunata* infection was highest in cultivar CSH 17 (36.02%) and lowest in PVK 801 (20.01%) (Table 2).

Deshpande (1991) reported that high rainfall during flowering to seed maturity of sorghum favors infection of *C. lunata.* Therefore, in our experiment polythene bags helped in avoiding direct contact of moisture to the

Table 1. Incidence and intensity of grain mold in sorghum panicles.

Treatment	TGMR[1]	Germination[2] (%)	Incidence (%)	
			Fusarium moniliforme[2]	*Curvularia lunata*[2]
Panicles with bags	2.36	52.92	14.22	25.35
Panicles without bags	3.55	32.27	27.43	33.54
CD at *5%*	0.334	4.95	3.70	NS[3]

1. TGMR = Threshed grain moid rating; observations recorded on 1 to 5 scale, where 1 = mold free and 5 = >50% threshed grains molded.
2. Figures are in arcsine transformed values.
3. NS = Not significant.

Table 2. Incidence and intensity of grain mold in sorghum cultivars under two treatments of panicles (with and without bags)[1].

Cultivar	TGMR[2]	Germination'	Incidence (%)	
			Fusarium moniliforme[3]	*Curvularia lunata*[3]
CSH 9	3.08	44.54	17.62	28.75
CSH 14	2.87	31.83	17.75	29.12
CSH 16	2.87	40.49	17.67	34.76
CSH 17	2.83	45.49	23.66	36.02
CSH 18	3.20	47.44	19.73	26.91
CSV 13	3.00	35.91	30.86	28.38
CSV 15	2.95	46.86	21.68	31.59
PVK 801	2.83	48.35	17.65	20.01
CD at 5%	NS[4]	9.91	7.40	NS

1. Values are averages of two treatments.
2. TGMR = Threshed grain mold rating; observations recorded on 1 to 5 scale, where 1 = mold free and 5 = >50% threshed grains molded.
3. Figures are in arcsine transformed values.
4. NS = Not significant.

sorghum grains and thus data indicated that grain mold infection was reduced. Covering panicles with polythene bags during rains can reduce grain mold infection. The use of polythene bags to minimize the grain mold infection is reported for the first time.

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Sorghum Grain Mold: Variability in Fungal Complex

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Introduction

The grain mold complex in sorghum *(Sorghum bicolor)* involves a number of pathogenic and saprophytic fungi that vary in their frequencies and severities under different environmental conditions (Bandyopadhyay et al. 2000). To provide genetic management for grain mold in sorghum, a clear understanding of the major pathogenic fungi and their variability under different environments is critical. Among the major pathogenic fungi, *Fusarium moniliforme (F. verticilloides)* is known to produce fumonisins, a mycotoxin of concern for the use of molded sorghum grains as food and feed (Marasas 1996, Bhat et al. 1997). With the above objective we initiated a collaborative Sorghum Grain Mold Variability Nursery (SGMVN) between ICRISAT and the All India

Coordinated Sorghum Improvement Project (AICSIP) of the Indian Council of Agricultural Research (ICAR). The nursery was coordinated by ICRISAT and conducted at four locations in India during the rainy season 2002. The results of the trials are presented.

Materials and Methods

The SGMVN-2002 consisted of 10 sorghum lines that had shown moderate to high levels of tolerance to grain mold in previous field screenings at ICRISAT, Patancheru, India and possessed desirable agronomic traits, and two check lines (a resistant and a susceptible). The nursery was established at four locations, Akola and Parbhani in Maharashtra, and Palem and Patancheru in Andhra Pradesh. Each entry was grown in two rows, each 4 m long and in two replications. The recommended agronomic and cultural practices for raising a good sorghum crop were followed at each location.

Sprinkler irrigation was provided on dry days for 30 min in the evening during flowering to crop maturity to create high relative humidity (RH) (>95%) necessary for fungal infection and mold development. No artificial inoculation with any mold fungi was done. Damage by insect pests, particularly by shoot fly, stem borer, and head bug was minimized by timely application of pesticides.

Data Recording

Grain mold severity score. Five plants with uniform flowering were tagged in each row of the 2-row plot (10 plants plot^{-1}). At each location, the overall grain mold severity scores were taken on each panicle at physiological maturity (PM) and post-PM (PPM) (10 days after PM) stages on a progressive 1 to 5 scale (1 = no mold, 2 = 1-10%, 3 = 11-25%, 4 = 26-50%, and 5 = >50% grains molded on a panicle). In addition, at Patancheru grain mold infection was also recorded at the hard-dough stage. Since there were no visible grain mold symptoms at the hard-dough stage, grain samples taken from the tagged panicles in each replication, were surface sterilized and plated on moist blotter paper in glass petri dishes at 25 grains per petri dish and 50 grains per replication. These were incubated at 28°C for 3 days and grain colonization by specific fungi were recorded using the above scale.

Threshed grain mold severity score. Threshed grain (10 g) from each panicle, spread in a petri dish was scored for visual rating on a 1 to 5 scale using a magnifying lens under proper lighting. The threshed grain samples of each entry obtained from all the four locations were subjected to the above mentioned blotter test (50 grains per replication) at Patancheru to determine the frequency of major mold fungi on the threshed grains.

Weather variables. Temperature, RH and rainfall from the flowering stage of an early-maturing line to PPM stage of a late-maturing line were recorded at all locations to determine the influence of weather variables on predominance of mold fungi.

Isolation of fungi. Fifty grains of each line obtained from the test locations were surface sterilized and plated on moist blotter paper. These were examined 3 days after incubation at 28°C with 12 h photoperiod. Molded grains were examined under stereobinocular, particularly for the presence of *Fusarium* species. The typical *Fusarium* colonies were aseptically transferred from the grains to potato-dextrose agar (PDA) plates and incubated at 28°C for 5 days for colony growth and further purification.

Results and Discussion

Variation in grain mold severity. The disease pressure as indicated by grain mold severity on the susceptible check SPV 104 at PM was highest (3.8) at Akola, followed by Palem (3.4) and Patancheru (3.0) (Table 1). However, at PPM the highest pressure was at Patancheru (5.0) followed by Parbhani (4.5) and the lowest at Akola and Palem (4.0). The overall field grain mold severity of the 12 sorghum lines at PPM ranged from 2.9 at Palem to 4.0 at Parbhani, and those of threshed grains from 2.8 at Akola to 4.3 at Patancheru. Significant (P <0.001) variations of grain mold severity occurred at different stages for sorghum lines, locations and their interactions, and no sorghum line was found resistant (<2.5 score) at all locations across all stages. However, at PM five lines (Sepon/78-1, ICSV 95001, SPV 351, ICSV 91008 and IS 8545) showed mold severity of <2.5 across 3 locations (Table 1). These lines are likely to have resistance to pathogenic fungi that might have infected the grains during the flowering to milk stages of grain development. This needs further investigation.

Variation in mold fungi. Major fungi recorded on grains in the field at PPM were species of *Fusarium, Ahernaria, Curvularia, Cladosporium, Drechsleru* and *Phoma.* There were significant (P <0.05) variations in severity of these fungi across locations and among sorghum lines at a particular location. *Fusarium moniliforme, Alternaria alternata* and *Curvularia lunata* were more prominent than others. The frequency of the fungi varied across locations: *F. moniliforme* from 32 to 64%, *A. alternata* from 19 to 38%, *C. lunata* from 18 to 23% and *P. sorghina* from 5 to 14% (Table 2). Other fungi appeared in relatively

Table 1. Grain mold severity of the Sorghum Grain Mold Variability Nursery-2002 entries at physiological maturity (PM), post-physiological maturity (PPM), and on threshed grain at four locations in India[1].

	PM				PPM				Threshed grain				Mean across stages			
Entry	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT
IS 18758C-618-2	3.0	-	3.2	2.8	4.0	4.5	3.6	4.7	3.3	4.4	3.7	5.0	3.4	4.4	3.5	4.2
IS 18522	3.1	-	2.6	2.6	4.0	4.3	3.3	4.6	3.6	4.0	3.3	4.8	3.6	4.2	3.1	4.0
ICSV 96101	3.1	-	2.0	2.0	4.0	4.1	2.5	3.6	3.0	3.4	2.5	4.4	3.4	3.8	2.3	3.3
CS 3541	2.8	-	2.4	2.1	3.5	4.0	3.0	4.2	3.1	3.4	3.2	4.2	3.2	3.7	2.9	3.5
Sepon/78-1	2.2	-	2.1	1.4	3.3	3.7	2.1	2.6	2.4	3.4	2.7	4.1	2.6	3.6	2.3	2.7
ICSV 95001	2.0	-	1.8	1.8	3.0	3.9	2.1	3.4	2.0	3.4	2.3	4.4	2.3	3.7	2.1	3.2
IS 30469C-140	3.0	-	3.0	2.4	4.3	4.2	3.6	4.1	3.6	3.3	3.7	5.0	3.6	3.8	3.4	3.8
SPV 351 (ICSV 1)	2.3	-	2.3	2.0	3.2	4.0	3.1	3.7	2.3	3.5	3.2	3.9	2.6	3.8	2.9	3.2
ICSV 91008	2.3	-	2.1	1.4	3.0	3.8	2.8	3.5	2.0	3.3	3.0	4.3	2.4	3.6	2.6	3.1
CSH 9	3.1	-	2.6	2.3	4.0	4.1	3.5	3.9	2.6	3.3	3.6	4.4	3.2	3.7	3.2	3.5
SPV 104[2]	3.8	-	3.4	3.0	4.0	4.5	4.0	5.0	3.8	3.8	4.2	5.0	3.9	4.2	3.9	4.3
IS 8545[3]	2.2	-	1.1	1.1	3.0	3.4	1.2	1.7	2.3	3.2	1.2	2.6	2.5	3.3	1.2	1.8
Mean	2.7	-	2.4	2.1	3.6	4.0	2.9	3.7	2.8	3.5	3.0	4.3	3.1	3.8	2.8	3.4
LSD (*P* <0.05)	0.27	-	0.20	0.30	0.17	0.42	0.20	0.34	0.24	0.13	0.19	0.36	1.21	0.67	1.61	1.52

1. Each value is mean of 2 replications with 10 panicles per replication, based on 1-5 scale where 1 = no mold, 2 = 1-10% mold, 3 = 11-25% mold, 4 = 26-50% mold and 5 = >50% grains molded on a panicle.
AKL = Akola, PAR = Parbhani, PAL = Palem. PAT = Patancheru; - = Data not available.
2. Susceptible check.
3. Resistant check.

Table 2. Frequency of different mold fungi on threshed sorghum grains from the Sorghum Grain Mold Variability Nursery-2002 entries during rainy season 2002 at four locations in India[1].

	Seeds (%) colonized by mold fungi															
	Fusarium moniliforme				*Alternaria alternata*				*Curvularia lunula*				*Phoma sorghina*			
Entry	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT	AKL	PAR	PAL	PAT
IS 18758C-618-2	47	91	29	40	10	19	30	23	17	12	22	31	10	22	10	10
IS 18522	43	85	44	60	12	12	28	18	21	10	19	12	15	3	4	5
ICSV 96101	56	55	54	26	15	40	10	41	15	31	15	17	15	9	0	8
CS 3541	34	93	49	38	12	9	13	29	34	9	17	14	25	16	4	6
Sepon/78-1	23	37	38	36	21	49	12	35	23	31	8	18	11	10	15	6
ICSV 95001	8	94	32	26	49	22	38	37	25	11	23	23	5	12	4	14
IS 30469C-140	56	70	32	36	11	34	36	46	19	19	33	15	22	19	8	8
SPV 351 (ICSV 1)	36	38	31	35	31	57	35	30	32	30	29	17	13	4	2	11
ICSV 91008	30	43	38	18	15	56	14	62	25	17	11	15	21	22	3	5
CSH 9	27	58	28	26	28	35	47	49	35	27	38	20	11	34	4	7
SPV 104[2]	40	70	34	30	11	39	43	39	24	13	27	21	21	7	6	4
IS 8545[3]	7	35	21	17	9	31	49	49	4	2	10	9	3	10	2	6
Mean	34	64	36	32	19	34	30	38	23	18	21	18	14	14	5	8
LSD (P <0.05)	17.1	12.1	14.9	15.4	9.9	10.3	12.3	17.1	15.5	8.8	9.1	11.8	6.9	7.9	6.9	7.0

1. Bach value is mean of 2 replications; 50 sorghum grains per replication were tested using blotter technique at 28°C for 3 days.
AKL = Akola, PAR = Parbhani, PAI. = Palem, PAT = Patancheru.
2. Susceptible check.
3. Resistant check.

Table 3. Infection severity of fungi on the Sorghum Grain Mold Variability Nursery-2002 entries at hard-dough (HD) stage, physiological maturity (PM), and post-physiological maturity (PPM) under field conditions at Patancheru, India[1].

Entry	*Fusarium moniliforme*			*Curvularia lunula*			*Phoma sorghina*		
	HD	PM	PPM	HD	PM	PPM	HD	PM	PPM
IS 18758C-618-2	2.2	1.7	2.9	1.7	2.0	3.4	2.1	2.3	2.4
IS 18522	1.9	2.3	3.0	1.2	1.9	2.7	1.0	2.6	2.4
ICSV 96101	1.5	1.5	2.4	1.1	1.4	2.4	1.1	2.5	2.6
CS 3541	1.9	1.9	3.1	1.2	1.4	2.7	1.0	2.5	2.4
Sepon/78-1	1.0	1.6	2.2	1.0	1.2	2.3	1.0	1.5	2.0
ICSV 95001	2.2	1.9	2.6	1.3	1.9	2.6	1.0	1.9	2.1
IS 30469C-140	1.4	1.6	2.6	1.4	2.0	3.1	1.2	2.4	2.5
SPV 351 (ICSV 1)	1.2	1.3	2.8	1.1	1.2	2.7	1.3	2.2	2.4
ICSV 91008	1.4	1.3	2.2	1.3	1.3	2.8	1.0	1.7	2.4
CSH 9	1.6	1.8	2.8	1.4	1.7	2.4	1.0	2.5	2.8
SPV 104 (susceptible check)	2.1	2.1	3.2	1.3	2.3	3.9	1.1	2.4	2.4
IS 8545 (resistant check)	1.1	1.0	1.4	1.1	1.0	1.1	1.0	1.0	1.4
Mean	1.6	1.6	2.6	1.2	1.6	2.7	1.1	2.1	2.3
LSD ($P < 0.05$)	0.31	0.29	0.33	0.26	0.27	0.34	0.17	0.27	0.29

1. Each value is mean of 2 replications with 10 panicles per replication, and is based on 1-5 scale where 1 = no mold, 2 = 1-10% mold, 3 = 11-25% mold, 4 = 26-50% mold and 5 = >50% grains molded on a panicle.

low frequencies and may not be of much consequence to grain molding. Among locations, based on frequency mean, *F. moniliforme* was most predominant at Parbhani (64%) and least at Patancheru (32%); *A. alternata* most at Patancheru (38%) and least at Akola (19%); *C. lunata* most at Akola (23%) and least at Parbhani and Patancheru (18%); and *P. sorghina* most at Akola and Parbhani (14%) and least at Palem (5%) (Table 2).

Frequency of mold fungi at different grain development stages. At the hard-dough stage, *F. moniliforme* was most dominant (mean score 1.6), followed by C. *lunata* (mean score 1.2), and *P. sorghina* (mean score 1.1) while other fungi were either absent or in traces on certain sorghum lines at Patancheru (Table 3). Grain mold severity scores at PM and PPM were almost high for all fungi. These results reveal the pathogenic nature of *F. moniliforme, C. lunata* and *P. sorghina* that might have infected the developing grains during the flowering to milk stages, while other fungi may be weakly pathogenic or saprophytic. We suggest that screening and evaluation for grain mold resistance should focus primarily on the major pathogenic fungi.

Weather variables and grain mold severity. The period of flowering to PPM varied from 34 days at Patancheru to 59 days at Palem, and considerable variations in temperature and RH were recorded across locations (Table 4). The mean temperature varied from 12°C (minimum at Palem) to 39°C (maximum at Akola); RH from 21% (minimum at Akola) to 100% (maximum at Parbhani); the number of rainy days from 5 (at Parbhani) to 12 (at Akola); and rainfall from 22 mm (at Parbhani) to 166 mm (at Akola). The threshed grain mold severity score on the susceptible check SPV 104 was maximum (5.0) at Patancheru and minimum (3.8) at Akola and Parbhani; it was 4.2 at Palem. In general, higher RH seems to have positive correlation with mold severity. A detailed analysis of individual weather variables in relation to infection by individual mold fungi at each location is required to better understand the weather-mold relationships.

Isolation of fungi. We made about 500 isolations of *Fusarium* spp from the molded sorghum grain samples from different locations. These cultures would be studied for speciation and their potential for fumonisins production under the ICRISAT-USAID collaborative project at Iowa State University, Ames, Iowa, USA.

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Table 4. Weather variables at four locations in India in the Sorghum Grain Mold Variability Nursery-2002 during rainy season 2002.

Location	No. of days[2]	Temperature[1] (°C)		Relative humidity[1] (%)		No. of rainy days	Total rainfall (mm)
		Minimum	Maximum	Minimum	Maximum		
Akola	48	18-24	25-39	21-98	53-98	12	166
Parbhani	42	17-33	29-37	29-76	68-100	5	**22**
Palem	59	12-22	26-36	26-85	66-95	6	92
Patancheru	34	14-27	26-38	25-85	79-99	6	69

1. Range.
2. From flowering to PPM; sprinkler irrigation was provided at all locations except Palem during this period.

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Sorghum Grain Mold: Resistance Stability in Advanced B-lines

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Introduction

Grain mold resistance breeding in sorghum *(Sorghum bicolor)* at ICRISAT and in Indian national programs has focused on developing varieties, restorer lines, and hybrid seed parents utilizing resistance from germplasm lines of diverse geographical origin. During the past few years, ICRISAT has developed a large number of high-yielding, grain mold resistant B-lines using pedigree breeding with single- and three-way crosses and selecting the progenies under high disease pressure in field screenings (Reddy et al. 2000). Resistance stability of some selected elite B-lines was tested through a collaborative Sorghum Grain Mold Resistance Stability Nursery (SGMRSN) established in 2002. The results of trials conducted at diverse locations in India are presented.

Materials and Methods

The nursery and its management. The SGMRSN is a collaborative nursery between ICRISAT and the All India Coordinated Sorghum Improvement Project (AICSIP) of National Research Centre for Sorghum (NRCS) under the Indian Council of Agricultural Research (ICAR), coordinated by ICRISAT. The nursery was established at Akola, Parbhani, Palem and Patancheru in India. It included 43 F_6 to F_8 male-sterility maintainer progenies from 17 crosses involving 20 B-lines, 8 inbred lines and one B-line population that had shown desirable agronomic traits and grain quality, moderate grain yield potential and moderate to high level of grain mold resistance at Patancheru, and two resistant and two susceptible check lines.

Each entry was grown in 2 rows, 4 m long in 2 replications. The recommended agronomic and cultural practices were followed at each location. Sprinkler irrigation was provided on dry days for 30 min per day in the evening during the flowering to post-physiological maturity (PPM) stages to maintain high relative humidity (RH) (>95%). No artificial inoculation was done with any mold fungi. Damage by insect pests, particularly by shoot fly, stem borer and head bug was minimized by timely application of pesticides.

Data Recording

Plant traits. Data were recorded for quantitative traits such as days to 50% flowering (DTF) and plant height at each location, and for other traits such as glume coverage, panicle compactness and grain color only at Patancheru as the latter traits are least influenced by weather factors.

Field grain mold severity. Five plants with uniform flowering in each row of the 2-row plot (10 plants $plot^{-1}$) were tagged and the overall grain mold severity scores were taken on a progressive 1 to 5 scale (1 = no mold, 2 = 1-10%, 3 = 11-25%, 4 = 26-50% and 5 = >50% grains molded on a panicle) at PPM, 10 days after physiological maturity (PM).

Threshed grain mold severity. Threshed grain (20 g) from the bulk of 10 panicles per plot, spread in a petri dish was scored for mold severity on the above 1 to 5 scale, using a magnifying lens under proper lighting.

Grain hardness. From each plot 50 grains were subjected to grain hardness tester (Kiya Seisakusho Ltd., Tokyo, Japan) after the grain samples were dried to 7% grain moisture level.

Results and Discussion

Variation in plant traits. Significant (P <0.05) variations occurred for DTF and plant height between sorghum lines within and across locations; and also for glumes coverage, panicle compactness and grain color between sorghum lines. The mean and range of each trait for the 43 test lines and for resistant and susceptible check lines are given in Table 1. The mean DTF for 43 test lines varied from 68 (at Palem) to 77 (at Akola), and the mean plant height from 175 cm (at Parbhani) to 198 cm (at Patancheru) compared with 122-182 cm for susceptible checks and 233-281 cm for the resistant checks across locations.

The mean glumes coverage for test lines was 42% compared with 31% for susceptible check and 50% for

Table 1. Plant traits and grain mold severity of 47 entries in the Sorghum (train Mold Resistance Stability Nursery during rainy season 2002 at four locations in India.

Parameter	Lines[1]	Akola		Parbhani		Palem		Patancheru	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Days to 50% flowering	Test lines	77	65-88	74	60-77	68	63- 73	73	60-85
	S lines	72	60-84	70	61-78	61	56-66	61	49-73
	R lines	85	81-88	77	76-77	67	61-72	75	72-78
	LSD (P<0.05)	3.1	-	1.0		2.1		3.4	-
Plant height (cm)	Test lines	190	126-261	175	117-238	177	148-245	198	133-245
	S lines	122	119-125	128	127-129	182	178-185	130	120-140
	R lines	273	190-355	281	207-338	233	208- 258	253	190-315
	LSD (P<0.05)	25.4		9.8	-	14.1	-	23.3	-
Grain hardness[2] (kg seed ')	Test lines	6.6	4.9-8.0	5.4	2.2-8.2	6.8	4.1-11.4	2.9	0.9-6.4
	S lines	5.8	4.9-6.6	4.5	4.1-4.9	6.3	4.6-8.0	2.0	1.6 2.0
	R lines	7.8	7.8	10.0	9.0-10.9	9.7	8.5-10.8	7.2	6.2-8.1
	LSD (P<0.05)	1.04	-	0.74	-	3.1	-	2.2	
Glumes coverage[2] (%)	Test lines							42	25-75
	S lines							31	25-38
	R lines							50	25-75
	LSD (P <0.05)							25.7	
Grain mold severity at PPM	Test lines	2.6	1.8-3.3	3.9	2.8-4.8	1.8	1.2-2.7	2.6	1.2-3.8
	S lines	4.4	4.0-4.7	4.4	4.1-4.8	3.7	3.6-3.8	4.8	4.6-4.9
	R lines	1.5	1.3-1.7	3.4	3.3-3.6	1.7	1.0-2.4	2.1	1.0-3.2
	LSD (P <0.05)	0.54	-	0.45	-	0.20	-	0.34	
Grain mold severity on threshed grain	Test lines	2.5	2.0-3.5	4.4	3.4-5.0	1.8	1.1-2.9	2.8	1.3-3.7
	S lines	4.0	4.0	5.0	5.0	3.9	3.8-3.9	5.0	5.0
	R line	1.5	1.0-2.0	3.3	3.0-3.5	1.8	1.1-2.4	1.7	1.0-2.3
	LSD (P <0.05)	0.70		0.20	-	0.16	-	0.37	-

1. Test lines 43. S (susceptible) lines 2. R (resistant) lines 2.
2. Observations of samples from the four locations were recorded at Patancheru.

Table 2. Agronomic traits and grain mold severity of selected sorghum B-lines across four locations in India during rainy season 2002[1].

Entry	Pedigree	Days to 50% flowering	Plant height (cm)	Grain color	Glumes coverage (%)	Panicle compactness[3]	100-grain mass (g)	Grain hardness (kg $seed^{-1}$)	Mold severity[2] (1–5 scale)	
									At PPM	Threshed grain
SGMR 14	(ICSB 392 × SP 1792-1)-3-1-1-1-1-1	76	192	Red	50	SC	2.17	5.8	2.2	2.4
SGMR 19	((IS 13817 × ICSB 270) × ICSB 392:Red)-2-1-1-1-1	75	162	Red	50	C	2.58	6.1	2.1	2.4
SGMR 20	((IS 13817 × ICSB 270) × ICSB 392:Red)-2-1-1-2-1	76	148	Brown	38	C	1.75	6.5	2.2	2.4
SGMR 21	((IS 13817 × ICSB 270) × ICSB 392:Red)-2-1-1-4-1	76	175	Brown	50	SC	2.20	5.2	2.3	2.5
SGMR 23	(IS 8614 × ICSB 293)-2-1-1-1-4-1	76	191	Brown	75	SC	1.59	3.8	2.4	2.4
ICSB 383	(ICSB 17 × IS 10646)-5-1-2	74	221	Brown	38	SC	1.86	4.4	1.8	2.1
ICSB 392	(ICSB 37 × IS 10475B)-2-2-1-3-1	73	183	Red	50	SC	2.51	5.9	2.3	2.5
ICSB 403	(ICSB 42 × IS 23585)-1-7-1-2-2	70	176	Brown	38	SC	2.28	4.4	2.3	2.4
Bulk Y[4]		57	138	White	38	L	3.02	4.9	4.4	4.4
IS 14384[5]		76	317	Red	75	L	1.88	8.4	1.7	1.5
Mean		73	186	–	42	–	2.33	5.5	2.6	2.9
LSD (P <0.05)		1.5	11.0	–	25.7	–	0.38	1.69	0.97	0.97

1. Mean of four locations except grain color, glumes coverage and 100-grain mass that were recorded only at Patancheru. Grain hardness of the samples from the four locations was also recorded at Patancheru.
2. 1 = No mold, 2 = 1–10% mold, 3 = 11–25% mold, 4 = 26–50% mold, and 5 = >50% grains molded on panicle; PPM = post-physiological maturity.
3. SC = semi-compact; C = compact; L = loose.
4. Susceptible check.
5. Resistant check.

the resistant check. Thirty-eight of the 43 lines had semi-compact panicle, 3 had compact, and 2 had loose panicles, compared with loose to semi-compact panicles of the resistant and susceptible check lines. Grain color varied from white (17 lines), red (17 lines) and brown (9 lines). The susceptible check lines had white grain while one resistant check line had white grain and the other red grain. These plant traits have been shown to be associated with grain mold resistance in several studies (Esele et al. 1993, Audilakshmi et al. 1999, Rooney and Klein 2000).

Variation in grain hardness. Significant variations were recorded for grain hardness between entries within and across locations (Table 1). The mean grain hardness of the 43 test lines varied from 2.9 kg $seed^{-1}$ (at Patancheru) to 6.8 kg $seed^{-1}$ (at Palem) while it was 7.2-10.0 kg $seed^{-1}$ in the resistant check lines and 2.0-6.3 kg $seed^{-1}$ in susceptible checks across locations. Grain hardness is considered to be one of the most desirable traits often positively correlated with mold resistance (Audilakshmi et al. 1999). Most white- and bold-grain sorghums have soft endosperm and thus they are more susceptible to mold fungi than the red-grain or brown-grain sorghums that have smaller grain size (Reddy et al. 2000).

Grain mold severity scores. Grain mold severity of the 43 test lines differed significantly between and within locations. The mean grain mold severity at PPM varied from 1.8 (at Palem) to 3.9 (at Parbhani), and that of threshed grains from 1.8 (at Palem) to 4.4 (at Parbhani), compared with 1.5 to 3.4 in resistant checks and 3.7 to 4.8 in the susceptible checks across locations (Table 1). Generally, mold severity scores of sorghum lines at PPM and of threshed grains were similar at a location. Pooled ANOVA for threshed grain mold severity indicated highly significant (P <0.001) effects of location, entry, and location x entry interaction; of these, location effect was more pronounced than the other two.

Resistance stability. Of the 43 test lines, 8 (SGMRs 14, 19,20,21, 23, ICSBs 383, 392 and 403) recorded 1 to 2.5 mold severity across locations compared with 4.4 on the susceptible check Bulk Y and 1.6 on the resistant check IS 14384 (Table 2). These eight lines are derivatives from six crosses involving 12 B-lines and inbreds. The different traits in these lines varied: DTF from 70 to 76 days; plant height from 148 to 221 cm; grain color from red to brown; glumes coverage from 38 to 75%; panicle compactness from compact to semi-compact; 100-grain mass from 1.59 to 2.58 g; and grain hardness from 3.8 to 6.5 kg $seed^{-1}$. These B-lines that have stable resistance and desirable agronomic traits could be converted into A-lines for utilization in hybrid programs.

Relationships between agronomic traits and mold severity. Significant negative correlations were found between DTF and threshed grain mold severity, and between plant height and threshed grain mold severity. In late-maturing tall lines, grain mold severity tends to decrease probably because of relatively dry period prevailing towards the end of the crop season resulting in less humid microclimate than that of shorter plants which are usually shaded by taller plants. Rooney and Klein (2000) reported strong negative correlation between plant height and grain mold incidence, and found association between quantitative trait loci (QTLs) for plant height and grain mold incidence on linkage groups D and E. In this study, however, a negative and weak correlation was found between grain hardness and threshed grain mold severity, which was unexpected. This could be partly due to the equipment and method used to determine grain hardness.

Grain mold severity scores at PM (not reported here) were usually different from those at PPM and that of threshed grain, but those at PPM and of threshed grain were similar. We, therefore, suggest that mold scoring should be done twice; first, at PM in the field and second, of threshed grain in the laboratory. However, it is important to determine the right PM stage (black-layer formation) for each sorghum line in the field nursery to record the data at the right time. We suggest that when more than 50% grains in the middle portion of a panicle of most plants in a line show black-layer formation, this should be considered as PM. The nursery will be conducted again during 2003 crop season to confirm the results.

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Reduction of Sorghum Seedling Vigor by Inoculation with *Fusarium thapsinum* and *Curvularia lunata* at Anthesis

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The two most common fungi associated with molded seed of sorghum *(Sorghum bicolor)* are *Fusarium thapsinum* (FT) *(F. moniliforme* mating group F) and *Curvularia lunata* (CL) (Bandyopadhyay et al. 2002, Prom et al. 2003). These fungi have proven quite aggressive in the developing kernel. These fungi typically cause discoloration, molding on the grain surface, endosperm degradation, reduced grain-filling ('small-seed syndrome' in the case of *Fusarium* spp) and reduced germination (Bandyopadhyay et al. 2002, Prom et al. 2003). Reduced seedling vigor, as measured by seedling height, however, has not been reported in association with grain molded seed.

Earlier reports have indicated that important levels of infection occur at or near anthesis. Nene (1975) inoculated sorghum panicles with *Fusarium* and *Curvularia* spp at varying times after panicle emergence and found the greatest mold occurring when panicles were inoculated 3-7 days after emergence from the boot. Rao and Williams (1977) conducted a similar study and found that the greatest reduction in kernel viability occurred when panicles were inoculated at anthesis compared with later inoculations.

Four sorghum cultivars were tested in a recent study to determine the effect of early inoculations on vigor of surviving kernels. Sureno is a white-tan, zerazera variety that is resistant to grain mold. RTx2911 is highly grain mold resistant, derived from a SC719-11E*SC650 cross and is a bright-red *kafir-caudatum* plant type. SC170 is a white-grained, white-pigmented *caudatum* line which is moderately susceptible to grain mold and moderately resistant to grain weathering (personal observation). RTx430 is a highly susceptible variety derived from SC170 and RTx2536.

Inoculations of sorghum panicles were made precisely at anthesis with FT or CL at 1×10^6 conidia ml^{-1} suspended in a 0.5% gelatin solution and measured using a hemacytometer. Mock-inoculations (control) were

Table 1. Seedling height (mm) of four sorghum lines inoculated with *Fusarium thapsinum* (FT), *Curvularia lunata* (CL), or mock-inoculated with water (control) at anthesis.

Genotype	Treatment	14 DDP[1]	% Control[2]	17 DDP[1]	% Control'
Sureno	Control	232.5	-	377.6	-
	FT	230.1	98.9 ab	352.7	93.4 a
	CL	221.8	95.4 b	344.2	91.1 a
SC 170	Control	244.8	-	361.2	-
	FT	155.6	63.6 d	288.5	79.9 b
	CL	85.3	34.8 f	160.6	44.5 c
RT x 2911	Control	182.2	-	275.6	-
	FT	185.7	101.9 a	255.1	92.6 a
	CL	158.8	87.2 c	220.5	80.0 b
RTx430	Control	212.7	-	298.5	-
	FT	100.5	47.2 e	146.2	49.0 c
	CL	63.4	29.8 g	150.8	50.5 c

1. A total of 30 seedlings were harvested and measured in each genotype x treatment category at 14 and 17 days post-planting (DPP) with the exception of RTx2911 where only 20 seedlings were harvested.
Seedlings were measured (in mm) from the crown to the tip of the first leaf as an estimation of seedling vigor.
2. Overall % Control values for 14 DPP are not significantly different if followed by the same letter (*P* <0.05, Bonferroni's test).
3. Overall % Control values for 17 DPP are not significantly different if followed by the same letter (*P* <0.05. Bonferroni's test).

conducted using sterile distilled water. To favor fungal infection and colonization, panicles were covered with pollinating bags after inoculation. Panicles were harvested 60 days after inoculation and the grain was collected, placed in standard manila seed envelopes and stored at 20-23°C for 90 days. At that time kernels were planted at a depth of 2.5 cm in a standard 1:1 peat:perlite soil and allowed to germinate and grow for up to 17 days under glasshouse conditions. In all of three independently conducted experiments (1999, 2000 and 2001) seedlings were harvested in each genotype x treatment category at 14 and 17 days post-planting (DPP). Seedlings were measured from the crown to the tip of the first leaf to estimate vigor.

Seedlings germinated from kernels obtained from control and treated panicles (Table 1). Significant differences between percentages of control for the two treatments and the four genotypes were observed (Table 1). Overall values for CL treatments were significantly lower for each genotype except for Sureno (resistant). This suggests that CL may be a much more aggressive fungus in the developing kernel than FT, a result that has been observed previously (Bandyopadhyay et al. 2002, Prom et al. 2003). The highly resistant cultivars, Sureno and RT x 2911, showed significantly larger seedling heights than SC170 or RTx430 when FT and CL treatments were compared. These trends are duplicated in the measurements taken at both 14 and 17 DPP.

Issues such as endosperm quality, germination rate and seedling vigor are important when sorghum is being produced for seed. This data set suggests that infections of grain at anthesis with high levels of inoculum and relative humidity maintained throughout grain development can lead to seedlings with greatly reduced vigor. Castor (1981) suggested that "seedlings which develop from fungal colonized grain, may be less vigorous than under normal conditions." This is certainly evidenced here through values of estimated vigor for seedlings growing from kernels that 'survived' spikelet inoculations at anthesis.

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Field Evaluation of Sorghum Germplasm Accessions Against Foliar Diseases

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Introduction

Several foliar diseases attack sorghum *(Sorghum bicolor)* and cause premature drying of leaves, resulting in reduced grain and fodder yields. Some foliar pathogens such as *Colletotrichum graminicola* infect grains also, reducing their germinability and vigor, and can be disseminated to new areas (Cardwell et al. 1989). Though several control methods are available, employment of host-plant resistance is the most economic and dependable strategy. An effective resistance breeding program requires diverse sources of multiple disease resistance. This article presents the reaction of sorghum germplasm accessions to five foliar diseases of sorghum.

Materials and Methods

Seeds of 592 sorghum germplasm accessions, received from the National Research Centre for Sorghum (NRCS), Rajendranagar, Hyderabad, Andhra Pradesh, India, were grown in the vicinity of a multiple foliar disease sick plot at the university farm, Udaipur, Rajasthan, India during the rainy season 2002. Infector rows of a susceptible line 'Kekri local' were planted simultaneously around the germplasm accesssions. For comparison, three resistant checks SPV 462, CSV 15 and C 43, and a susceptible check SU 52 were planted randomly after every 20 rows. The germplasm accessions were planted in single rows of 5 m, with 45 cm between rows and 15 cm between plants in each row. Standard agronomic practices for fertilizers (80 N:40 P:40 K kg ha^{-1}), pesticides (furrow application of carbofuran granules 10 g at 3 g row^{-1} and whorl application of endosulfan granules in 25-day-old plants)

and weedicide (pre-germination spray of Atrazine at 0.05%) were followed, but no fungicide was used.

Cultures of the foliar pathogens *Colletotrichum graminicola* (anthracnose), *Exserohilum turcicum* (common leaf blight), *Gloeocercospora sorghi* (zonate leaf spot), *Cercospora sorghi* (gray leaf spot) and *Bipolaris sorghicola* (target leaf spot) were multiplied on autoclaved sorghum grains in conical flasks at 28±l°C for 7 days till good sporulation occurred. Plants of Kekri local (25 days old) were inoculated by placing 1 or 2 cultured grains in the whorl of individual plants; a single pathogen was inoculated each day, in the sequence as mentioned above.

Foliar disease reaction of the entries was evaluated when majority of genotypes reached soft-dough stage. Ten plants in each entry were tagged randomly and their top five leaves were scored on a progressive 1-5 scale (Sharma 1980), where 1 = no infection, 2 = traces to 10% leaf area covered, 3 = 11-25%, 4 = 26-50% and 5 = >50% leaf area covered by each disease. Genotypes with scores of 1-2 were considered resistant, 2.1-3 as moderately resistant, 3.1-4 as susceptible and 4.1-5 as highly susceptible.

Results and Discussion

Of the 592 accessions evaluated, 189 accessions showed a score of 1-2 for all the five foliar diseases and were considered to be multiple disease resistant. In addition, 71 accessions showed resistant reaction to three diseases (anthracnose, gray leaf spot and target leaf spot) but were moderately resistant to zonate leaf spot and common leaf blight. Forty-one accessions were resistant to two diseases (anthracnose and gray leaf spot) and moderately resistant to zonate leaf spot, common leaf blight and target leaf spot. The remaining entries showed either moderate resistance or were susceptible to highly susceptible to one or more than one disease (Table 1).

Table 1. Reaction of sorghum germplasm accessions to foliar diseases at Udaipur, Kajasthan, India during rainy season 2002.

Reaction to foliar diseases	No. of accessions
Resistant to 5 diseases (zonate leaf spot. anthracnose, common leaf blight. gray leaf spot and target leaf spot)	189
Resistant to 3 diseases (anthracnose, gray leaf spot and target leaf spot) and moderately resistant to 2 diseases (zonate leaf spot and common leaf blight)	71
Resistant to 2 diseases (anthracnose and gray leaf spot) and moderately resistant to 3 diseases (zonate leaf spot, common leaf blight and target leaf spot)	41
Moderately resistant or susceptible or highly susceptible to one or more diseases	291

A total of 221 accessions showed moderate resistance to zonate leaf spot, while 210 accessions showed susceptible reaction and six accessions (IS 699, IS 13817, IS 25069, IS 25400, IS 25591 and IS 25601) showed high susceptibility to zonate leaf spot. For common leaf blight, 125 accessions showed moderate resistance, while 43 accessions showed susceptible and 2 (IS 13657 and IS 25067) showed highly susceptible reactions. Three accessions, IS 13466, IS 13901 and IS 14305 were susceptible to gray leaf spot, while only 7 (IS 453, IS 2814, IS 3140, IS 4002, EJ 30, EJ 33 and EJ 34) showed susceptible reaction to foliar anthracnose. Fifteen accessions showing resistant reaction to all the foliar diseases, showed susceptible reaction to grain anthracnose. These were: IS 9958, IS 13240, IS 13407, IS 13853,IS 13947, IS 14282, IS 14002,IS 19143,IS 19331, IS 20730, IS 22235, IS 24507, IS 26784 and IS 29323), and 6 (IS 24443, IS 24445, IS 29329, IS 29482, IS 29576 and IS 40139) showed moderate resistance to grain anthracnose. Of the three resistant checks, C 43 and CSV 15 were resistant to all the five diseases, while SPV 462 showed moderate resistance to leaf blight, but was resistant to all the other leaf spots. SU 52 showed susceptible reaction to gray leaf spot and common leaf blight and also had 10% incidence of sorghum downy mildew *(Peronosclerospora sorghi),* which was observed for the first time in Rajasthan. None of the other accessions showed downy mildew infection.

The germplasm accessions showing resistance to foliar diseases showed susceptibility to grain anthracnose. This confirms the earlier observation that in some genotypes, different genes govern foliar and grain infection to anthracnose (Mathur et al. 2000). Little information is available on target leaf spot of sorghum (Dalmacio 2000), but in this evaluation accessions showing susceptible and moderately resistant reactions to target leaf spot were identified. The multiple resistant accessions that have been identified will be useful in the breeding program. Also, those accessions identified as susceptible and moderately resistant may prove useful for studying population biology and virulence diversity, and need to be explored for use as differential hosts.

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Evaluation of Elite Sorghum Accessions for Multiple Disease Resistance

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Introduction

Several plant diseases reduce grain and fodder yields of sorghum *(Sorghum bicolor)* and its stover quality (Bandyopadhyay et al. 2001). Participatory rural appraisal studies in India by Rama Devi et al. (2000) indicated that sale of crop residues to peri-urban milk producers accounted for approximately 50% of the income from sorghum cropping in rural areas of the Deccan Plateau of Andhra Pradesh, Karnataka and Maharashtra, and diseased residues command much lower price in the fodder market. Adverse effects of foliar and panicle diseases on quality and quantity of sorghum grain, fodder and residues have recently been reported (Bandyopadhyay et al. 2000, 2001). Most sorghum diseases can be effectively managed through host-plant resistance. The objective of this study was to identify resistance to multiple diseases in the selected agronomic elite landrace accessions and breeding lines of sorghum. In this article we report both agronomic features and multiple disease resistance of some of the accessions for their possible use in resistance breeding program.

Materials and Methods

Germplasm accessions. During the rainy season 2001, a total of 1671 sorghum accessions, originating from different countries were evaluated for multiple diseases reaction at ICRISAT under natural disease pressure. Of the 1671 accessions, 945 were elite landraces and 726 were breeding lines. Each accession was grown in an un-replicated plot of 2 rows, each of 4 m length, in Vertisol at ICRISAT, Patancheru, India. The space between the rows was 75 cm and between plants in each row was 10 cm. The crop was raised following the standard agronomic practices.

Evaluation for agronomic traits and biotic stresses. Each accession was evaluated for days to 50% flowering, plant height (cm), grain color and overall plant score. Plant scores were recorded on a 1-5 scale, where 1 = excellent, 2 = very good, 3 = good, 4 = poor and 5 = very poor. Diseases were identified using identification keys of Frederiksen and Odvody (2000). Incidence (%) of various diseases was recorded based on number of plants infected of the total plants observed in each plot of 2 rows from flowering (all foliar diseases) to maturity. Disease severity was recorded on 0-100% scale for all diseases except maize stripe virus (MStV). The severity of MStV was recorded considering plant stunting and panicle exertion symptoms at maturity on a 1-5 scale (Navi et al. 2003).

Results and Discussion

Weather during June to September 2001 was congenial for disease development. During June to September there were 54 rainy days with 525 mm rainfall, mean temperature of 21-23°C minimum and 29-33°C maximum, relative humidity 82-93% in the morning and 52-71% in the evening, and wind velocity 5-15 km h^{-1}.

Several diseases were observed on the sorghum plants: anthracnose *(Colletotrichum graminicola),* bacterial leaf streak *(Xanthomonas campestris* pv *holcicola),* ergot *(Claviceps sorghi)* and (C. *africana),* maize mosaic virus (MMV) (a rhabdovirus transmitted by the delphacid plant hopper *(Peregrinus maidis),* maize stripe virus (MStV) (a tenuivirus transmitted by *P. maidis),* leaf blight *(Exserohilum turcicum),* rough leaf spot *(Ascochyta sorghina),* rust *(Puccinia purpurea),* downy mildew *(Peronosclerospora sorghi),* gray leaf spot *(Cercospora sorghi),* oval leaf spot *(Ramulispora*

Table 1. Origin of 945 agronomic elite sorghum landraces evaluated for disease resistance under field conditions during rainy season 2001, ICRISAT, Patancheru, India.

Origin	Number of accessions		Origin	Number of accessions	
	Evaluated	Disease free		Evaluated	Disease free
Argentina	4	0	Nepal	1	0
Australia	9	0	Niger	6	0
Botswana	22	1	Nigeria	17	11
Burkina Faso	6	0	Pakistan	5	0
Cameroon	10	2	Philippines	4	0
Chad	4	0	Russia and CIS	71	5
China	14	0	Senegal	2	0
Cuba	1	0	Somalia	9	0
Dominican Republic	1	0	South Africa	136	0
Egypt	2	0	Sri Lanka	1	0
El-Salvador	1	0	Sudan	157	45
Ethiopia	10	3	Swaziland	27	3
Ghana	13	0	Syria	1	0
India	184	4	Tanzania	2	0
Indonesia	1	0	Thailand	2	0
Jamaica	2	0	Togo	1	0
Kenya	7	0	Turkey	5	0
Lesotho	56	1	Uganda	5	0
Malawi	5	2	Unknown	1	0
Mali	11	0	USA	16	0
Mauritania	1	0	Yemen	10	0
Mexico	1	0	Zambia	1	0
Namibia	8	0	Zimbabwe	92	5

Table 2. Agronomic traits of 82 disease-free sorghum landrace accessions evaluated during rainy season 2001, ICRISAT, Patancheru, India[1].

Accession (IS no.)	Origin	Days to 50% flowering	Plant height (cm)	Plant score[2]	Grain color
919	Sudan	78	210	3	Chalky white
1084	India	62	220	3	Straw
2262	Sudan	51	280	3	Chalky white
2263	Sudan	70	320	3	White
2311	Sudan	56	255	3	Chalky white
2319	Sudan	70	230	1	Chalky while
3076	Sudan	75	245	3	Chalky white
3511	Sudan	56	135	3	Chalky white
6910	Sudan	56	300	5	Light brown
6916	Sudan	75	230	5	Light brown
6953	Sudan	57	295	5	Brown
7036	Sudan	61	120	3	Light brown
8328	India	61	245	1	Straw
9283	Sudan	69	200	1	Chalky white
9677	Sudan	61	280	5	Straw
9816	Sudan	62	275	3	Gray
9957	Sudan	75	235	3	Brown
9982	Sudan	61	260	1	White
12467	Sudan	57	150	1	Straw
14429	Lesotho	61	185	3	Light red

continuted

Table 2. *continued.*

Accession (IS no.)	Origin	Days to 50% flowering	Plant height (cm)	Plant score[2]	Grain color
15019	Cameroon	64	265	3	Gray
15838	Cameroon	71	385	5	Straw
19036	Sudan	56	200	3	White
19059	Sudan	66	245	1	White
19060	Sudan	60	285	3	Straw
19066	Sudan	64	340	5	White
19077	Sudan	56	220	1	White
19123	Sudan	57	280	5	White
19143	Sudan	64	230	3	Gray
19154	Sudan	58	170	1	Straw
19176	Sudan	73	255	5	Straw
19183	Sudan	75	220	3	White
19204	Sudan	52	235	3	Straw
19305	Sudan	59	150	3	White
19574	Sudan	56	120	1	White
20945	India	75	260	3	Straw
21639	Malawi	68	365	3	Straw
21662	Malawi	79	380	3	Straw
21951	Ethiopia	131	245	5	Straw
22313	Botswana	80	380	3	White
22380	Sudan	77	250	3	Light brown
22495	Sudan	69	235	3	Straw
22517	Sudan	72	360	5	White
22518	Sudan	56	150	1	White
22539	Sudan	72	280	3	Purple
22542	Sudan	70	270	3	Gray
22557	Sudan	64	320	3	Light brown
22563	Sudan	54	125	1	White
22906	Sudan	59	200	3	Reddish brown
23385	Sudan	56	120	1	Straw
24694	Ethiopia	54	150	1	Straw
24695	Ethiopia	75	265	1	Straw
24889	Nigeria	70	255	1	Straw
24978	Sudan	70	215	3	Purple
25009	Sudan	75	355	5	Light brown
25010	Sudan	79	335	5	Reddish brown
25011	Sudan	79	360	5	Reddish brown
25030	Sudan	75	310	5	Gray
26860	Nigeria	61	235	3	Straw
26861	Nigeria	64	185	1	Straw
26862	Nigeria	64	160	1	Straw
26863	Nigeria	70	170	1	Straw
26864	Nigeria	64	220	1	White
26866	Nigeria	70	260	1	Straw
26869	Nigeria	66	245	1	Straw
26871	Nigeria	68	245	1	Straw
26872	Nigeria	68	220	1	Straw
26914	Nigeria	66	230	1	Straw
27046	Zimbabwe	70	250	1	Straw
27063	Zimbabwe	64	340	3	White
27068	Zimbabwe	77	380	5	Brown
29306	Swaziland	64	300	3	Light red
29307	Swaziland	66	300	3	Light red

commuted

Table 2. *continued.*

Accession (IS no.)	Origin	Days to 50% flowering	Plant height (cm)	Plant score[2]	Grain color
29308	Swaziland	68	325	3	Reddish brown
29673	Zimbabwe	77	400	3	White
30073	Zimbabwe	70	250	1	Straw
32318	India	59	230	1	Straw
35884	Russia and CIS	72	335	3	Straw
40120	Russia and CIS	51	145	1	Straw
40131	Russia and CIS	57	155	1	Straw
40146	Russia and CIS	51	140	1	Straw
40148	Russia and CIS	52	135	1	Straw

1. Accessions were free from anthracnose, bacterial leaf streak, ergot, maize mosaic virus, maize stripe virus, leaf blight, rough leaf spot, rust, downy mildew, gray leaf spot, oval leaf spot, smuts, tar spot and zonate leaf spot.
2. Recorded on 1-5 scale based on panicle exertion, grain color and days to flowering, where 1 = excellent, 2 = very good, 3 = good, 4 = poor and 5 = very poor.

Table 3. Incidence and severity ranges of sorghum diseases in 726 breeding lines during rainy season 2001, ICRISAT, Patancheru, India.

Disease	Incidence[1] (%)	Severity[2] (%)
Anthracnose	13-88	5-100
Bacterial leaf streak	3-10	5-20
Ergot	2-3	2-9
Leaf blight	10-40	4-6
Maize mosaic virus	2-3	Trace-5
Maize stripe virus (MStV)	2-6	4-5
Rust	10-100	2-75
Rough leaf spot	10-20	2-13
Downy mildew	Trace	Trace
Gray leaf spot	Trace	Trace
Oval leaf spot	Trace	Trace
Tar spot	Trace	Trace
Zonate leaf spot	Trace	Trace

1. Recorded from flowering to maturity for all foliar diseases except MStV; incidence of MStV recorded at maturity
2. Recorded on 0-100% scale, except MStV on 1-5 scale.

sorghicola), tar spot (*Phyllachora sorghi*), zonate leaf spot (*Gloeocercospora sorghi*), covered kernel smut (*Sporisorium sorghi*), head smut (*Sporisorium reilianum*), long smut (*Sporisorium ehrenhergii*) and grain mold.

Of the 945 landrace accessions from 46 countries, 82 accessions from India, Lesotho, Botswana, Zimbabwe, Russia and CIS, Swaziland, Cameroon, Sudan, Ethiopia, Malawi and Nigeria were free from all diseases observed (Table 1). A total of 651 accessions from the above 11 countries exhibited field tolerance to multiple diseases, while 294 accessions from 35 countries showed various levels of susceptibility to diseases. Of the 82 accessions that were free from diseases, 31 had excellent plant traits (score 1) with chalky white to straw grain color, 51-75 days to 50% flowering and 120-260 cm plant height (Table 2). The incidence and severity on 726 breeding lines were quite variable and none had multiple disease resistance (Table 3). However, at crop maturity, downy mildew, gray leaf spot, oval leaf spot, tar spot and zonate leaf spot were observed in traces. Of all the diseases observed, MStV is emerging as an important disease of sorghum.

The results provide some useful information on potential risks of bacterial streak and MStV. Sorghum accessions with multiple disease tolerance were identified for their possible use in resistance breeding program.

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The Pattern of Spore Liberation in Major Mold Pathogens of Sorghum

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Introduction

Grain mold of sorghum *(Sorghum bicolor),* caused by a complex of fungi (Navi et al. 1999), poses severe threat to sorghum production and utilization. The principal grain mold fungi in India are *Fusarium moniliforme, Curvularia lunula, Phoma sorghina, Alternaria ahernata, Exserohilum turcicum, Gonatobotrytis* spp and *Aspergillus* spp (Anahosur 1992). The disease occurs when the crop maturity coincides with warm and humid weather. The spread of the disease in the field is so rapid that it becomes increasingly difficult to manage the disease after receiving a rain-shower during physiological or normal maturity. Such a rapid spread of the disease is possible only when the inciting pathogens have the capability of brisk spore production and dissemination mechanisms. However, little information pertaining to pattern (fluctuation in the amount of spore released across hours in a day) and duration of spore liberation in mold pathogens is available. Thus a study was undertaken on the biology of the pathogens to investigate the actual period of spore liberation for different pathogens.

Materials and Methods

To understand the pattern and active period of spore liberation of four mold pathogens, a 7-day Burkard volumetric spore trap was set up in a sorghum field at 0.3 m above crop canopy during *kharif* (rainy) season 2002, where CSH 11 was raised. The weather during the sampling period was moderately favorable for grain mold development. A maximum temperature range of 28.7-31.4°C and minimum temperature range of 20.1-22.2°C, with 95-100% relative humidity prevailed during the period. Total rainfall of 78.4 mm was distributed in 2 rainy days during this period. The air was sampled for spores at the rate of 0.6 m^3 h^{-1} through an orifice 2 mm x 14 mm and directed at the vaseline coated Melinex tape moving at a rate of 2 mm h^{-1}. Spore count was made on hourly basis for four major pathogens *(F. moniliforme, C. lunata, A. alternaia* and *E. turcicum),* by counting the total number of spores available in 2 mm width in Melinex tape, which represented the spores collected in one hour. Spore count was made on hourly basis for 7 days consecutively during maturity stage. The data were presented from 0 h to 24 h with an interval of 2 h, to reveal the active period of spore dispersal by the pathogens in a 24-h day cycle. Again within the active period of spore liberation (which corresponds to the availability of higher spore count in a day), the peak period of spore liberation for major grain mold pathogens was identified.

Results and Discussion

Spores of all the four major mold pathogens were encountered throughout the sampling period of seven days at all hours in a day. Though spores were encountered consistently, higher spore count was observed during **a** particular period in a day. The spore count of *F. moniliforme* increased significantly from Indian Standard Time (IST) 1800 to 0200-0400 of the following day (Table 1). This was linked with the active period of spore liberation. The spore count during the early hours of morning until mid-day was comparatively low (Table 1). During mid-day (at 1000-1600) the spore count was low indicating low levels of spore liberation. The same trend was observed with *C. lunata* and A *ahernata* (Table 1). Observation on hourly spore count of *E. turcicum* did not show any defined pattern, as throughout the sampling period the spore count was consistent. So an active period of spore count was not observed with *E. turcicum.* In the other three pathogens, a peak period of spore liberation was observed. The peak period of spore liberation for *F. moniliforme* was at 2000-2400 while it was at 2200-2400 for *C. lunata* and at 1800-2000 for A. *ahernata.* Thus during this time, the pathogens are rapidly dispersing spores which increases the inoculum load in the air. The importance of ideal environment conditions (temperature of 20-25°C and relative humidity of 90-100%) during the late evening and night hours for mold development was theorized by Bandyopadhyay et al. (2002), when they conducted mist and shelter experiments to investigate the epidemiology of grain molds.

Table 1. Spore count of major mold pathogens during crop maturity stage on sorghum in Hyderabad, India, rainy season 2002.

	No. of spores (m^{-3} of air sampled)[1]				
Time[2] (h)	*Fusarium moniliforme*	*Curvularia lunula*	*Alternata alternata*	*Exserohilum turcicum*	Total
0800-1000	33 e	25 c	27 ef	19 bd	104
1000-1200	24 g	16 d	22 f	19 cd	81
1200-1400	25 fg	16 d	27 ef	23 ab	91
1400-1600	24 g	17 d	31 de	16 d	88
1600-1800	32 ef	25 c	40 c	22 ab	119
1800-2000	44 c	32 b	58 a	24 a	158
2000-2200	58 a	36 b	51 b	20 ab	165
2200-2400	52 ab	47 a	47 b	19 bcd	165
0000-0200	47 bc	34 b	40 c	22 abc	143
0200-0400	43 cd	23 c	36 c	21 abc	123
0400-0600	42 cd	20 cd	36 cd	19 bcd	117
0600-0800	37 de	24 c	30 de	21 abc	112
Total	461	315	441	245	
SEm±	2.4	1.8	2.0	1.5	
LSD {P <0.05)	6.7	5.1	5.5	4.1	

1. Average spore count values obtained on seven days were converted to whole numbers nearer to the actual value. Means followed by the same letter within a row are not significantly different.
2. Indian Standard Time (IST).

The duration of active and peak period of spore liberation may determine the inoculum load in the air. Supporting the statement, in our experiment, the inoculum load (number of spores m^{-3} of air) of *F. moniliforme,* C. *lunata* and *A. alternata* were more when compared to *E. turcicum.* Thus the dusk and night hours in a day may be crucial for development and spread of the disease, as spore liberation and infection might take place during this period.

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Enhancing Germination and Seedling Vigor of Mold Infected Sorghum Seeds Using Bioagents

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Introduction

Grain mold of sorghum *(Sorghum bicolor),* a major disease with complex etiology, causes severe yield loss when the grain maturity coincides with warm humid weather. A severe mold infestation reduces the market value of the grain rendering sorghum cultivation economically unviable. Many of the pathogens associated with grain molds such as *Fusarium, Aiternaria, Bipolaris, Curvularia, Drechslera* and *Exserohilum* were reported to produce toxins (Sivanesan 1991), though toxicity problems in human beings are rarely reported. In addition, grain mold fungi reduce seed mass, grain density, germination and seedling vigor of the germinating seeds, thus making the grain unsuitable for use by the farmers. Though the regular fungicides used for seed treatment are found to inhibit growth of the seedborne pathogens, their role in improvement of seed quality is poorly understood (Raju et al. 1999). In this

study, efforts were made to evaluate the enhancement of germination and seedling vigor of mold infected seeds using biological agents, and to evaluate the effectiveness on growth of the pathogens in germinating seed.

Materials and Methods

Severely mold infected seeds from the sorghum cultivar CSV 11 were used for the study, which was grown during the 2002 rainy season in the National Research Centre for Sorghum (NRCS), Hyderabad, Andhra Pradesh, India. Fungal biocontrol agents such as *Trichoderma viride, T. harzianum, T. hamatum* and *T. koeningii* and the bacterial bioagent, *Pseudomonas fluorescens* obtained from Tamil Nadu Agricultural Univiersity (TNAU), Coimbatore, Tamil Nadu, India were maintained in potato-dextrose agar (PDA) and *Pseudomonas* agar, respectively. To enable proper seed treatment the talc-based formulations of the biocontrol agents were prepared. To obtain formulation of *P. fluorescens,* the bacterial bioagent was inoculated in Kings B broth, incubated at 26± 1°C in a BOD incubator for 48 h and centrifuged at 10000 g for five minutes. The supernatants were discarded and the pellets were suspended in sterile water, to which talcum powder was added (25 g talc for 100 ml of *P. fluorescens* suspension). The mixture was dried in shade and stored for use. It had a bacterial concentration of approximately 1×10^8 colony forming units (cfu)g^{-1}.

The fungal bioagents *Trichoderma* spp used in this study were inoculated in PDA petri plates and incubated at 25± 1 °C for 7 days. From the 7-day-old culture, conidia were harvested and were suspended in 100 ml of sterile water, to which 25 g of talcum power was added. This gave a concentration of 11×10^6 cfu g^{-1} for *T. viride,* 8×10^6 cfu g^{-1} for *T. harzianum,* 7.4×10^6 for *T. hamatum* and 9×10^5 cfu g^{-1} for *T. koeningii.* To test the effect of bioagents in enhancing the germination of molded seeds, they were treated (as liquefied paste) with the formulations of the bioagents at 4 g kg^{-1} of seed. To compare the effect of bioagents with popular fungicides used for seed treatment, captan and thiram were included in the treatments at 2 g kg^{-1}. The treated seeds were incubated for 3 days in moist blotter paper, and placed in petri plates. To estimate the seedling vigor the treated seeds were incubated for 7 days using the roll towel method, which permits normal growth of root and shoot of the germinating seedlings. The seedling vigor was calculated by the formula:

Seedling vigor = [shoot length (cm) + root length (cm)] x germination (%)

Three replications were maintained for each treatment and in each replication 25 seeds were plated for observation. Controls were maintained by incubating non-treated molded seeds and healthy seeds (obtained from seed storage unit) for comparison.

Results and Discussion

The bioagents enhanced the germination and vigor of the seedlings obtained from moldy seeds (Table 1). Of all the treatments, *P. fluorescens* effected maximum germination (88%) and seedling vigor (2636), followed by *T. viride* (87% and 2478, respectively). Less grain mold incidence (12%) was observed in treatment with *P. fluorescens,* followed by *T. viride* (13%) and thiram (21%) compared to 53% mold incidence in molded seeds alone. The seedlings

Table 1. Effect of biocontrol agents on mold incidence, seed germination and seedling vigor in sorghum.

Treatment	Mold incidence[1] (%)	Germination[1] (%)	Seedling vigor[1]		
			Shoot length (cm)	Root length (cm)	Vigor index
P. fluorescens	12 ab	88 ab	19 a	11 a	2636 b
T. viride	13 b	87 b	18 ab	11 ab	2478 c
Thiram	21 bc	79 bc	17 bc	10 be	2055 d
T. harzianum	25 cd	75 cd	15 cd	10 abc	1885 e
Captan	27 cd	73 cd	17 bc	9 cd	1856 e
T. hamatum	34 de	65 de	14 d	10 be	1537 f
T. koeningii	41 e	59 e	11 e	8 d	1116 g
Controls					
Molded	53 f	47 f	5 f	3 e	587 h
Healthy	3 a	97 a	20 a	11 a	2997 a
SEm±	3.3	3.3	0.6	0.5	51.4
CD (0.05)	9.9	9.9	1.8	1.5	152.6

1. Mean of 3 replications with 25 seeds per replication. Means followed by the same letter within a column arc not significantly different at $P = 0.05$.

obtained from the seeds treated with *P. fluorescens* and *T. viride* showed good shoot and root length as compared to that of seedlings obtained from healthy seeds (Table 1). The effect of thiram on enhancing germination of molded seeds was on par with the treatment with *T. viride,* but it did not enhance the vigor of the seedlings when compared to *P. fluorescens* and *T. viride.* This suggests that chemicals used to suppress the growth of pathogens may not act in favor of growth and establishment of the crop. The role of rhizobacteria and fungal bioagents in favoring crop growth in addition to suppression of parasitic as well as saprophytic pathogens has been reported by other researchers (Alka Gupta 2000, Kurze 2001). However, the results of using the fungal bioagents *T. hamatum* and *T. koeningii* were less favorable when compared to those of *P. fluorescens, T. viride* and *T. harzianum.* The reduced efficiency of *T. hamatum* and *T. koeningii* may be attributed to the non-adaptation of these pathogens to the exposed environment in the area of the current study. However, the role of these bioagents cannot be underestimated because genetic improvement of biological control agents is a well established field of commercial application. Thus the biocontrol agents proved to show an edge over the routine chemical seed treatment to ward off seedborne diseases. Though the efficacy of *P. fluorescens* and *T. harzianum* against grain mold pathogen *F. moniliforme* was reported by Raju et al. (1999), this is the first report comparing four well known species of *Trichoderma* with common chemicals used for seed treatment.

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Effects of Pounding and Garlic Extract on Sorghum Grain Mold and Grain Quality

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Introduction

Of the many fungi associated with sorghum (*Sorghum bicolor)* grain mold complex, species of *Alternaria, Curvularia, Drechslera, Fusarium* and *Phoma* are particularly widespread (Navi et al. 1999). Grain infection by mold fungi can also reduce storage quality and seed germination. Apart from affecting grain quality, species of *Fusarium* produce mycotoxins leading to several chronic ailments in humans and animals (Bhat et al. 2000). To improve the quality of molded grain, Stenhouse et al. (1998) suggested dehulling to minimize mold damage observed on the pericarp.

In our limited survey during the 1996 rainy season in Bidar district, Karnataka, India people who consumed molded grain without prior treatment complained of itching, fever, dysentery, loss of appetite and feeling of enhanced body heat particularly in the eyes. Inexpensive and safe method of reducing moldiness would greatly help the use of sorghum grains both for food and feed. Therefore, use of biopesticide, such as garlic extract, was tried along with grain pounding to reduce grain mold infection, as was used in controlling sorghum ergot (Singh and Navi 2000).

Materials and Methods

Collection of sorghum samples. During a survey in 1996, six molded grain samples were collected from farmers' stores in two villages of Karnataka. These samples were from the 1995 rainy season harvest from three sorghum cultivars CSH 1, CSH 9 and Local yellow sorghum.

Identification of fungi. From each sample, 200 grains were surface sterilized in 1% sodium hypochlorite (NaOCl), and washed in sterilized distilled water three times. The grains were plated on blotter paper in sterilized petri dish humid chambers (25 grains per petri dish) and incubated for 5 days at 28±1°C with 12 h light

cycle. Grains were examined under stereoscopic microscope for fungal colonization and under compound microscope for identification. Another set of 200 grains plated without sterilization was observed as detailed above.

Preparation of garlic extract. Peeled garlic cloves (500 g) were crushed in 500 ml sterilized distilled water using pestle and mortar. The crushed suspension was filtred through muslin cloth and the filtrate was considered as 100% stock solution of crude garlic extract. The solution was diluted with water to 50%, 25%, 12.5%, 6.25% and 3.12% concentrations for the study.

Grain pounding and incubation periods. A representative sample of 250 g heavily molded grain of CSH 9 was soaked in lukewarm water for 25 min; the excess water was drained out and the sample was dried under sunlight at ~36°C for 4 h. From this, 125 g grain was pounded using pestle and wooden mortar and remaining 125 g was not pounded. Both the pounded and 'un-pounded' grains were aseptically transferred to sterilized humid chambers (25 grains per petri dish) and incubated at 28±1°C with 12 h light cycle for 24,48 and 72 h. The number of grains colonized in both the lots and their severity on a 1-9 scale (where 1 = no mold and 9 = >75% molded grain) were recorded after each incubation period. The experiment was repeated three times, each time with two replications, with two petri dishes in each replication, and 25 grains per petri dish.

Treatment with garlic extract. A representative sample of 25 g each of sun-dried pounded and un-pounded grain was treated separately using 50%, 25%, 12.5%, 6.25% and 3.12% concentrations of crude garlic extract by slurry method. Controls were maintained with sterilized distilled water treatment. The treated grains were air-dried under shade and 100 grains from each treatment were aseptically transferred to sterilized humid chambers (25 grains per petri dish) and incubated at 28± 1 °C with 12 h light cycle for 72 h. The grains were evaluated for mold incidence (%) and severity.

Results and Discussion

Effect of pounding on grain mold at different incubation periods. There was a considerable reduction in incidence (%) and severity of grain mold in pounded grains compared with un-pounded grains (Table 1). However, with increased incubation period up to 72 h, both incidence and severity increased in pounded grains.

Effect of garlic extract on grain mold of pounded and un-pounded grains. Treatment with garlic extract was effective in reducing grain mold incidence and severity, both in pounded and un-pounded grains. Higher concentrations of garlic extract was more effective than lower concentrations (Table 2). However, concentrations from 12.5% to 50% were more effective on pounded grain than on un-pounded grain. On pounded grain the incidence varied from 0 to 4% and severity from 1 to 4 compared with 28-44% incidence and 6-8 severity on un-pounded grain.

The cost of treating 10 kg molded grain with 6.25% garlic extract was Rs 40 (cost of 10 kg molded grain Rs 30 + pounding cost Rs 6.50 + garlic cost Rs 3.50 for 1 L of 6.25% extract) while the cost of 10 kg healthy grain was Rs 90 (Rs 10 kg^{-1}). Thus the garlic extract treatment is economical for farmers. In addition, garlic extract treatment improved grain and *rati* or *chapatti* (flat bread) color and is eco-friendly and safe for consumption by humans and poultry birds. Pounding alone reduced 60-80% ergosterol content in molded grain of CSH 1 and CSH 9. Thus, there is a scope for treating pounded grain for use in poultry feed. To store molded grain for a month or two, treating with 12.5% garlic extract is effective, and for longer storage 25% garlic extract would be desirable

Table 1. Effect of pounding on sorghum grain mold incidence and severity at different incubation periods in sterilized humid chambers[1].

	Incidence (%)		Severity[2]	
Incubation period (h)	Pounded grain	Un-pounded grain	Pounded grain	Un-pounded grain
24	28	100	2	7
48	56	100	3	9
72	68	100	6	9
LSD (*P* <0.05)	21.14	0.00	1.15	0.45

1. Mean of 3 repetitions each with 2 replications, two petri dishes per replication and 25 grains per petri dish.
2. 1-9 scale, where 1 = no mold and 9 = >75% mold.

Table 2. Effects of different concentrations of crude garlic extract on mold incidence and severity of pounded and un-pounded molded sorghum grains in sterilized humid chambers[1].

Crude garlic extract concentration (%)	Incidence (%)		Severity[2]	
	Pounded grain	Un-pounded grain	Pounded grain	Un-pounded grain
50	0	28	1	6
25	4	44	3	8
12.5	4	44	4	8
6.25	16	56	5	8
3.12	48	80	6	8
Control	84	100	7	9
LSD (P <0.05)	11.62	9.63	0.33	0.41

1. Mean of 3 repetitions each with 2 replications, two petri dishes per replication and 25 grains per petri dish.
2. 1-9 scale, where 1 = no mold and 9 = >75% mold.

(Singh 1996). The pounding and garlic extract treatment could be applied together at large-scale for better utilization of molded grain for human consumption and for poultry feed.

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Application of *Pseudomonas fluorescens* for Enhanced Seed Germination and Seedling Emergence in Sorghum

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Introduction

Seedborne fungi in sorghum *(Sorghum bicolor)* reduces seed germination and emergence (Mathur and Sehgal 1964). Beneficial rhizospheric microorganisms especially bacteria termed as plant growth promoting rhizobacteria (PGPR) affecting plant growth had been studied in various crop plants (Burr and Caesar 1983). Fluorescent pseudomonads have emerged as the most potential group for promoting plant growth and biological control of plant diseases. *Pseudomonas fluorescens* is reported as antagonistic to various plant pathogens and is also recommended for seed dressing (Vidyasekaran and Muthamilan 1995). Attempts were therefore made to assess efficacy of native *P. fluorescens* strains for seed dressing and its effect on seedborne fungal incidence, seed germination, and seedling emergence in sorghum.

Material and Methods

Untreated sorghum seeds of CSH 9, CSH 5 and SPV 86 were used in this study. The seeds were stored in paper bags at room temperature and used as and when required.

Table 1. Effect of *Pseudomonas fluorescens* treatment on seed germination and seedling emergence in sorghum.

	Seed germination (%)			Seedling emergence (%)		
Treatment	CSH 9	CSH 5	SPV 86	CSH 9	CSH 5	SPV 86
Control	70.6	71.3	69.3	67.6	69.9	65.2
P. fluorescens	95.2	94.7	94.3	92.7	91.9	92.7
Fungicide (carbendazim)	93.4	93.2	92.9	91.8	90.4	90.3
SE±	1.39	1.46	1.25	1.11	1.27	1.36
CD (P = 0.05)	4.20	4.38	3.78	3.33	3.85	4.12

For isolation of the bacteria from the rhizospheric soil, 10 g of soil from each sample was suspended in 90 ml of sterile distilled water and shaken for 15 min on a rotatory shaker. Serial dilutions were made up to 10^{-7} and plated on Kings B medium. The colonies producing fluorescent pigment were selected and characterized up to subspecies level of *Pseudomonas* (Palleroni 1984). Thus confirmed strains of *P. fluorescens* were used in the study. The culture was multiplied on Kings B broth and incubated at 27±2°C. After 48 h the broth was cenlrifuged at 10000 g for 10 min and the pellet was resuspended in sterile distilled water. The broth contained approximately 15 x 10^{8} cells ml^{-1}. This suspension was used for seed treatment.

From each cultivar 200 seeds were mixed with 2 ml of *P. fluorescens* suspension and air-dried. The seeds were screened for seed mycoflora by standard blotter test method and percentage incidence of seedborne fungi was recorded (ISTA 1996). Similarly, 200 seeds from each cultivar treated with *P. fluorescens* were placed in paper rolls in four replications. The rolls were kept at 25±2°C in a seed germinator. Observations were recorded at 5 and 15 days after treatment. Ten treated seeds from each cultivar were sown in pots containing field soil. Untreated seeds served as control and seeds treated with fungicide (carbendazim at 4 g kg^{-1}) were used for comparison. The pots were watered as and when required and the emergence was recorded 15 days after sowing. Each treatment was done in three replications and the experiment was repeated twice.

Results and Discussion

A total of 27 bacterial strains were recorded and isolated on the plates from the rhizospheric soil. Of these, 11 strains were characterized as *P. fluorescens.* Among the 11 strains, PFSN 7 exhibited maximum inhibition of seedborne fungi and enhanced seed germination. The strain PFSN 7 was the most effective and therefore was used in further studies.

The seeds treated with *P. fluorescens* clearly indicated the complete inhibition of seed mycoflora over control. The results were similar in all cultivars. The seeds were completely free from fungal infection as in the fungicide treated seeds. The incidence of fungi was 32% on CSH 9, 33% on CSH 5 and 29% on SPV 86. However, *Alternaria tenuis, Aspergillus flavus, A. fumigatus, A. niger, Curvularia lunata, Fusarium moniliforme, F. o.xysporum, Penicillium citrinum, Rhizopus stolonifer,* and few others were recorded in the control. The treatment reduced the seed mycoflora incidence significantly.

An increase in seed germination in all the cultivars treated with *P. fluorescens* was recorded as compared to control, whereas it was similar when compared to fungicide treated seeds (Table 1). The variation in germination among the cultivars was not significant. The treatment of seeds with *P. fluorescens* increased seedling emergence by 20% in each cultivar over control. *Pseudomonas fluorescens* has been reported to improve plant growth either through suppression of pathogens or by stimulation of vegetative growth (Leeman et al. 1995). Enhanced seedling emergence by treatment of seed by spore suspension had been demonstrated in various crop plants (Gora et al. 1987).

The study confirms *P. fluorescens* as a seed treatment agent that offers a cheap, eco-friendly, biological alternative to fungicide for sorghum seed treatment.

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Maize Stripe Virus: A Disease of Sorghum Emerging in South India

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Introduction

During the growing season several foliar diseases of sorghum *(Sorghum bicolor)* affect grain and stover yields, stover quality and digestibility of the residues. While it is documented that foliar diseases of sorghum affect yields, no data were found in the literature on the effects of foliar diseases on crop residue yield and quality or the economic consequences for rural producers. Recently Rama Devi et al. (2000) indicated that diseased residues command much lower prices in the fodder market. Preliminary studies conducted at ICRISAT, Patancheru, India indicated that sorghum anthracnose *(Colletotrichum graminicola)* and maize stripe virus (MStV), a tenuivirus, reduce crop residue yield, quality and digestibility. Extensive on-farm surveys were conducted at various crop growth stages in India during 1999-2001 mainly to understand prevalence of foliar diseases, farmers' perceptions on sorghum diseases, feeding strategies and cropping pattern. In this article, we report the incidence and severity of MStV in farmers' fields and its likely effects on crop productivity based on the frequency of occurrence of MStV in inoculated and control plots.

Materials and Methods

Prevalence of MStV in farmers' fields. Maize stripe virus of sorghum was monitored in four states of India (Andhra Pradesh, Kamataka, Maharashtra and Tamil Nadu) from August 1999 to March 2001. The latitude and longitude of each of the fields surveyed were recorded using hand held global positioning system instrument (°1993 Magellan System Corporation, San Dimas, California, USA). A total of 939 sorghum fields were surveyed in 570 villages covering 202 farms in seven districts of Andhra Pradesh; 406 in 17 districts of Karnataka; 290 in 21 districts of Maharashtra and 41 in five districts of Tamil Nadu.

A total of 14 foliar, 5 panicle and one parasitic diseases of sorghum were identified using the identification keys of Williams et al. (1978) and Frederiksen and Odvody (2000). The incidence and severity of MStV in each field surveyed was recorded from an area of approximately 12 m^2 selected randomly at three different spots. Incidence (%) was calculated based on number of MStV plants out of the total plants counted and the severity (%) was based on individual plants damaged.

Prevalence of MStV in experimental plots. An experiment was conducted at ICRISAT, Patancheru research farm during the postrainy season 1999/2000 to understand the effect of MStV on grain and stover yields and digestibility under artificial inoculation. Three sorghum genotypes M 35-1, ICSV 93046 and ICSV 745 were planted in 8 rows, each of 4 m length in three replications. Four border rows were planted on either side of each plot to minimize insecticide drift from the control plot to the inoculated plots. Adult plant hoppers *(Peregrinus maidis)* feeding on MStV infected plants of CSH 9 were collected from early-sown ratoon and late-sown main crop of rainy season 1999/2000. Plant hoppers were collected using aspirators. Each plot was covered with nylon mesh nets (6 m wide x 4 m length x 2 m height); later, 4-5 viruliferous adult plant hoppers were slowly transferred into whorls of each plant from the aspirator using camel brush. All the plants in the 'inoculated' treatment were inoculated twice: first, 20 days after emergence and second, 10 days after first inoculation. Plants in control plots were not inoculated but carbofuran granules were placed in whorls at 20 days after emergence and sprayed with insecticide 10 days later. Plants were evaluated at weekly intervals for up to 9 weeks for MStV incidence and at maturity, disease severity was recorded on a 1-5 scale, where 1 = healthy, 2 = 75-100% panicle exertion and <25% stunting, 3 = 26-75% panicle exertion and 25-50% stunting, 4 = <25% panicle exertion and 51-75% stunting and 5 = no panicle exertion and >75% stunting. This scale was developed to

include two distinct symptom types of MStV (stunting and panicle exertion).

Measurement of stover and grain yields. At maturity, leaves, stems and panicles from infected and healthy plants from the central four rows in each plot were collected separately in cloth bags, dried in dryers for 3 days at 60°C and dry mass (kg plot^{-1}) was recorded. After threshing, grain yield (kg plot^{-1}) was recorded. Within the inoculated plot, stover and grain yields of infected and healthy plants were recorded separately and the data was converted to t ha^{-1} considering 133500 plants ha^{-1}. Similarly, the data from the control plots was recorded.

In vitro digestibility measurements. Digestibility was measured based on incubation of sorghum stover in an in vitro gas production test as described by Menke and Steingass (1988). All handling of rumen inoculum was carried out under continuous flushing of carbon dioxide. Portions of about 200 mg air-dried stover were accurately weighed (in triplicate) into 100 ml calibrated glass syringes, fitted with plungers as described by Menke and Steingass (1988) but modified as described by Blummel and 0rskov (1993). In vitro digestibility was calculated as 15.38 + (0.8453* ml of gas produced after 24 h) + (0.595* % crude protein) + (0.181* % ash) as described by Menke and Steingass (1988).

Table 1. Prevalence of maize stripe virus (MStV) of sorghum in four southern states of India, August 1999-March 2001.

State	Year[1]	No. of fields surveyed	No. of fields with MStV	MStV range (%)		MStV mean (%)	
				Incidence	Severity	Incidence	Severity
Andhra Pradesh	1	94	13	<I-30	25-100	9	86
	2	108	5	<1-10	48-80	3	84
Karnataka	1	221	42	<I-50	40-100	15	85
	2	185	73	<1-48	20-100	9	81
Maharashtra	1	45	1	<1	40	<1	40
	2	245	128	<1-100	<1-100	8	94
Tamil Nadu	1	17	2	<I-30	50-60	16	55
	2	24	11	<I-25	75-100	7	97

1. 1 = August 1999 to February 2000; 2 = August 2000 to March 2001.

Table 2. Mean cumulative incidence (%) of maize stripe virus on sorghum over 9 weeks at ICRISAT, Patancheru, India, post rainy season 1999/2000[1].

Genotype	Treatment	1	2	3	4	5	6	7	8	9
ICSV 745	Control	0	0	0	0	0	0	0	0	0
		(0)[2]	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
	Inoculated[3]	3.9	5.2	8.4	11.2	12.8	15.3	16.6	17.5	17.6
		(3.9)	(1.3)	(2.8)	(2.5)	(1.6)	(1.9)	(1.0)	(0.4)	(0.1)
ICSV 93046	Control	0	0	0	0	0.2	0.2	0.2	0.2	0.2
		(0)	(0)	(0)	(0)	(0.2)	(0)	(0)	(0)	(0)
	Inoculated[3]	5.8	13.1	23.2	29.6	31.3	35.2	36.4	37.4	37.7
		(5.0)	(5.0)	(5.0)	(4.6)	(1.3)	(1.8)	(0.7)	(0.3)	. (0.2)
M 35-1	Control	0	0	0	0	0	0	0.2	0.2	0.4
		(0)	(0)	(0)	(0)	(0)	(0)	(0.1)	(0.1)	(0.1)
	Inoculated[3]	2.5	4.2	9.5	18.3	19.4	21	22.9	24.8	25.8
		(2.5)	(1.7)	(5.0)	(5.0)	(0.8)	(0.8)	(1.3)	(0.9)	(0.4)
SEm±		1.0	2.1	3.7	5.0	5.3	5.9	6.2	6.5	6.5
		(0.9)	(0.8)	(1.0)	(1.0)	(0.3)	(0.4)	(0.2)	(0.2)	(0.1)

1. Mean of 3 replications.
2. Data within parentheses indicate mean weekly severity scores on 1-5 scale, where 1 = healthy, 2 = 75-100% panicle exertion and <25% stunting. 3 = 26-75% panicle exertion and 25-50% stunting, 4 = <25% panicle exertion and 51-75% stunting and 5 = no panicle exertion and >75% stunting.
3. Artificially infected by placing 4-5 viruliferous plant hoppers plant^{1}.

Results and Discussion

Prevalence of MStV. Among 14 foliar diseases observed, MStV emerged as the most destructive disease with a mean incidence of 6% with 85% severity in Andhra Pradesh, 12% incidence and 83% severity in Karnataka, 5% incidence and 67% severity in Maharashtra and 12% incidence and 76% severity in Tamil Nadu across two years. The fields infected with MStV varied in the four states: 9% in Andhra Pradesh, 28% in Karnataka, 45% in Maharashtra and 32% in Tamil Nadu. The incidence and severity of MStV varied from year to year and were higher in year 1 (August 1999 to February 2000) than in year 2 (August 2000 to March 2001) (Table 1). This variation could be due to weather factors, vector survival, cropping pattern, host specificity, etc. Monocropping and survival of vector on ratoon crop, on tillers, and on main crop probably aggravate the infestation and spread of MStV. Therefore, it is essential to understand that variability in distribution of MStV in the states surveyed does not imply that the disease is necessarily restricted to a particular zone or location. On-farm survey indicated the characteristic of MStV in reducing stover and grain yields. This was evident from the type of symptoms observed as well as from the incidence and severity. We observed that if the MStV infestation occurs at the vegetative stage the losses were higher than when the infestation occurrs in later growth stages.

Table 3. Effect of maize stripe virus of sorghum on mean stover and grain yields, ICRISAT, Patancheru, India, postrainy season 1999/2000.

Genotype	Treatment	Mean yield[1] (t ha^{-1}) Stover	Grain
ICSV 745	Control	5.90	5.48
	Inoculated[2]	4.59	4.67
ICSV 93046	Control	11.72	4.21
	Inoculated[2]	8.14	2.45
M 35-1	Control	8.83	3.64
	Inoculated[2]	8.26	3.20
LSD (P <0.05)		1.49	0.73

1. Based on population of 133500 plants ha^{-1}.
2. Artificially infested by placing 4-5 viruliferous plant hoppers plant^{-1}, and the yield from the inoculated treatment was recorded both from (i) plants infected at 37, 46, 52, 58, 65, 72, 79, 86 and 91 days after emergence; and (ii) uninfected plants.

Effects of MStV on stover and grain yield and digestibility under artificial inoculation. An experiment conducted at ICRISAT, Patancheru to better understand the effect of MStV on sorghum grain and stover yields under artificial inoculation revealed 37.7% mean cumulative incidence in ICSV 93046 followed by 25.8% in M 35-1 and 17.6% in ICSV 745 (Table 2). Disease severity was higher in initial 4 weeks than in later weeks indicating that the vegetative stage is more susceptible to MStV than the reproductive growth stage (Table 2). Mean grain and stover yields and digestibility varied with inoculated and control treatments in all the three genotypes (Tables 3 and 4). Our observation on yields is similar to Narayana and Muniyappa (1995).

We also observed that MStV occurs in different agro-ecological zones. It is currently not known if the virus occurs as distinct strains. Resistant sources for the virus or to the vector have so far not been identified and also the epidemiology of the disease has not been thoroughly investigated. As a result control measures are currently not available. Therefore, hot spots for MStV need to be identified in major sorghum-growing areas of India and in other countries, thus facilitating large-scale screening of sorghum genotypes for MStV resistance. To have better understanding of the disease and causal agent, there is a need to collect isolates from different ecological zones, maintain, purify, develop diagnostic tools to distinguish different isolates, develop screening techniques and identify broad-based resistance.

Table 4. Mean digestibility (%) of maize stripe virus infected and healthy sorghum plants'.

Genotype	Treatment	Leaf Healthy	Leaf Infected[2]	Stem Healthy	Stem Infected[2]
ICSV 745	Control	54.67	-	54.66	-
	Inoculated	58.67	59.33	54.33	55.00
ICSV 93046	Control	61.33	-	55.33	-
	Inoculated	60.67	60.00	53.00	60.00
M 35-1	Control	61.00	-	51.33	-
	Inoculated	61.33	60.67	50.00	60.00

1. Data arc means of three replications.
2. Plants infested at 37, 46, 52, 58, 65, 72, 79. 86 and 91 days after emergence were processed for digestibility and the values of infected plants were pooled.

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Entomology

Relative Susceptibility of Forage Sorghum Hybrids to Spotted Stem Borer *Chilo partellus*

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Introduction

Sorghum *(Sorghum bicolor)* is one of the most widely adopted forage crops in North India due to its high yielding ability and fast growth. It is mainly used as green chop, silage and hay. From sowing to harvest, this crop is attacked by more than 150 insect species, of which the spotted stem borer, *Chilo partellus,* is the most serious pest. Stem borer damage starts when the crop is two weeks old. In younger plants shot-holes caused by the early-instar larvae feeding in the leaf whorl are visible, while the older larvae leave the whorl and bore into the stem and damage the growing point, which results in deadheart formation. Feeding by the larvae inside the stem results in stem tunnelling, and reduction in plant vigor and fodder quality. Yield losses of about 40% have been reported in forage sorghum (Singh 1997). Though this pest can be effectively controlled by insecticides (Singh and Lodhi 1995), the expenditure involved is prohibitive and pesticide residues can also pose a hazard to livestock. The solution, therefore, lies in development of pest resistant varieties and their use to reduce insect damage.

Though forage sorghum hybrids are more prone to insect damage as compared to open-pollinated varieties, the demand for forage hybrids has gone up in recent years. This is because of their superiority, ie, multi-cut forage production as well as quick growth, high tillering, sweetness, and palatability to cattle. Very little emphasis has been given on screening forage sorghum hybrids against stem borer. This study was therefore conducted to evaluate the available forage sorghum hybrids for resistance to *C. partellus.*

Materials and Methods

Forty sorghum genotypes (consisting of 30 forage hybrids, five forage varieties, three resistant checks, and two susceptible checks) were sown during *kharif* (rainy) season 1996 at the Experimental Area of the Department

Table 1. Deadheart formation, leaf damage and stem tunnelling in forage sorghum genotypes by the spotted stem borer *Chilo partellus* at Hisar, India, rainy season 1996.

Genotype	Deadhearts[1] (%)	Leaf damage[2] (%)	Stem length tunnelled[3] (%)
FORAGE HYBRID			
AKFMS 1	62 (52)[4]	77 (61)	38 (38)
AKFSH 2	38 (38)	58 (50)	13 (21)
FS 103	60 (51)	76 (60)	35 (36)
FS 92079	43 (41)	65 (54)	20 (26)
FSH 13	41 (40)	60 (51)	24 (30)
FSH 93017	60 (51)	77 (62)	33 (35)
FX 13	63 (52)	78 (62)	38 (38)
GK 905	46 (42)	69 (57)	12 (21)
HD 16	52 (46)	72 (58)	20 (27)
HH 1	32 (34)	51 (46)	11 (20)
HH 2	62 (52)	76 (61)	39 (39)
ICI 583	62 (52)	76 (61)	27 (31)
ICI 584	62 (52)	76 (60)	32 (34)
Jumbo	63 (53)	79 (63)	37 (37)
MFSH 15	41 (40)	58 (50)	16 (24)
NFSH 701	50 (45)	67 (55)	27 (31)
NFSH 1255	49 (44)	71 (58)	27 (31)
NFSH 10659	30 (31)	58 (50)	11 (20)
Punjab Sudex	62 (52)	79 (63)	35 (36)
PSSG 333	56 (48)	75 (60)	34 (36)
PSSG 336	46 (43)	64 (53)	22 (28)
SSG 1001	62 (52)	75 (60)	38 (38)
VSSG 115	54 (48)	68 (56)	29 (33)
VSSG 121	23 (29)	53 (47)	15 (23)
855F	54 (48)	76 (60)	29 (33)
3055(A)	47 (43)	71 (57)	22 (28)
9595(H)	68 (55)	78 (62)	39 (39)
9596(H)	65 (54)	78 (62)	38 (38)
9597(H)	60 (51)	78 (62)	39 (39)
9598(H)	65 (54)	78 (62)	31 (38)
CONTROLS			
Forage variety			
HC 6	47 (43)	68 (56)	20 (26)
HC 136	51 (45)	60 (51)	35 (36)
HC 171	32 (34)	49 (44)	11 (20)
HC 260	46 (42)	67 (55)	21 (27)
SSG 59-3	27 (31)	64 (53)	13 (21)
Resistant			
IS 2205	17 (24)	49 (44)	4 (11)
IS 5469	16 (23)	47 (43)	3 (10)
IS 18551	28 (32)	60 (51)	11 (20)
Susceptible			
CSH 1	70 (57)	96 (78)	48 (44)
ICSV 1	68 (56)	92 (75)	45 (42)
SEm±	1.70	2.31	1.21
LSD at 5% t	4.78	6.50	3.42

1. Based on two counts, 30 and 45 days after emergence (60 plants per replication).
2. Based on 60 plants per replication at 50 days after emergence.
3. Based on ten stalks per replication at 80 days after emergence.
4. Angular transformed values are given in parentheses.

of Forage Research, CCS Haryana Agricultural University (HAU), Hisar, India. All genotypes were sown in a randomized complete block design with three replications and plot size of 7.5 m^2 (6 rows of 3 m length). Plant spacing was maintained at 50 x 10 cm. All the recommended agronomical practices, except insecticidal applications, were adopted to raise the crop.

Observations on deadhearts caused by *C. partellus* were recorded from 2nd and 3rd rows of each plot at 30 and 45 days after seedling emergence. Total number of plants in each row were also counted and the stem borer damage was expressed as a percentage of the total number of plants. Similarly, plants showing leaf injury (% plants infested) were also recorded in each plot at 50 days after seedling emergence. At harvest (80 days after seedling emergence), 10 stalks picked up at random from each plot were split open to record the stem length tunnelled by the borer.

Results and Discussion

There were significant differences in the parameters used for recording the stem borer damage. Deadheart incidence varied from 16 to 70% (Table 1). Among forage sorghum hybrids, VSSG 121 and NFSH 10659 suffered lowest damage (30% deadhearts) followed by HH 1 (32%) and AKFSH 2 (38%). The hybrids NFSH 10659, AKFSH 2 and VSSG 121 have earlier been reported to be less susceptible to *C. partellus* (Anonymous 1996). Resistant controls IS 5469 and IS 2205 showed minimum incidence of deadhearts. However, corresponding values in susceptible controls CSH 1 and ICSV 1, and the forage hybrid 9595(H) were maximum (>65%).

Plants with leaf damage varied from 47 to 96% (Table 1). Forage hybrid HH 1 (51%), followed by VSSG 121 (53%) showed minimum leaf damage, while Jumbo, Punjab Sudex, 9595(H). 9596(H), 9597(H) and 9598(H) showed maximum (>77 %) leaf infestation. However, minimum leaf damage was recorded in IS 5469 (47%) and IS 2205 (49%) and forage variety HC 171 (49%). Maximum leaf damage (92-96%) was recorded in the susceptible checks CSH 1 and ICSV 1.

Stem length tunnelled by *C. partellus* in different sorghum genotypes ranged from 3 to 48%> (Table 1). Forage hybrids HH 1 and NFSH 10659 showed minimum stem length tunnelled (11 %), followed by GK 905 (12%), AKFSH 2 (13%), and VSSG 121 (15%). However, the resistant controls, IS 5469 and IS 2205 showed minimum stem length tunneled (3-4%), whereas maximum stem length tunnelled was recorded in the susceptible controls CSH 1 (48%) and ICSV 1 (45%), followed by the forage hybrids 9595(H) and 9597(H) (39%).

Amongst the forage hybrids, VSSG 121 not only showed minimum stem borer deadheart incidence, but

also showed comparatively less leaf infestation and stem tunnelling. Thus, this forage hybrid (VSSG 121) can be grown extensively and its parental lines may be used in breeding stem borer resistant cultivars for cultivation by the farmers.

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Fecundity and Longevity of Greenbug on Wild and Cultivated Grasses

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Introduction

Greenbug (*Schizaphis graminum*) is a major insect pest of sorghum (*Sorghum bicolor*) and small grains. Originally a pest of winter wheat (*Triticum aestivum*), this aphid became a serious and persistent pest of sorghum in the United States in 1968 (Harvey and Hackerott 1969). Greenbugs suck plant sap from the underside of leaves and inject toxin, resulting in reddish spots on leaves, which later turn yellow, brown and die (Teetes and Pendleton 2000. Eleven biotypes of greenbug (A through K) have been identified. Biotype I currently is dominant. Greenbugs infest 70 species of grasses in 44 genera (Michels 1986). Wild grasses are hosts when the growing seasons of wheat in winter and sorghum in summer do not overlap. Wild grasses also are thought to play a role in the development of new biotypes of greenbugs. Understanding the role of wild grasses in the survival of greenbugs could help limit damage caused by this serious insect pest of cereal crops.

Materials and Methods

Fecundity and longevity of greenbugs were assessed on barnyardgrass (*Echinocloa crusgalli),* Johnsongrass (*Sorghum halepense*), jointed goatgrass (*Aegilops cylindricum),* 'Arriba' western wheatgrass (*Agropyron smithii),* biotype I-resistant sorghum (LG35), biotype I-susceptible sorghum (RTx430), biotype 1-resistant wheat (GRS1201) and biotype 1-susceptible wheat (Custer). The experiment was done in August-October and November-December 2002 in a greenhouse at West Texas A & M University, Canyon, Texas, USA. Seed of each kind of grass was planted separately in 20.3-cm diameter plastic pots filled with Miracle-Gro® Enriched Potting Mix. Each pot was covered with a cylindrical, clear plastic cage with organdy cloth glued over the top to aerate the plants. Seedlings after emergence were thinned to three per pot. Plants, 35 days after emergence, were infested with greenbugs from a culture of biotype 1 maintained on susceptible sorghum Tx399 x RTx430 in the greenhouse. A single greenbug was enclosed in a 2.5-cm^1 clip cage. Three cages were clipped onto leaves of plants in each pot. Fifty-six pots were arranged in seven blocks in a randomized complete block design on benches in the greenhouse. The original greenbug in each clip cage was removed after it produced a nymph, which was retained. The date the nymph was born was recorded. The greenbug was allowed to mature and produce nymphs that were counted and removed daily. The number of nymphs produced by each greenbug and number of days each greenbug survived were recorded. Data were analyzed using the General Linear Model Procedure (P = <0.05) (SAS Institute 1999). Means were separated by using Tukey's HSD test at a probability of P = 0.05.

Results and Discussion

Total fecundities of the greenbugs were significantly different among the different kinds of grasses during August-October (F = 18.31; df = 7, 147; P <0.0001) and November-December (F = 21.39; df = 7, 148; P<:0.0001). During August-October, an average of only 8.5 nymphs was produced per greenbug on barnyardgrass, approximately seven times fewer than on Johnsongrass (57.8 nymphs per greenbug) (Table 1). During November-December, the average number of nymphs produced per

Table 1. Total fecundity and longevity per greenbug biotype I on different kinds of grasses during 2002 in Texas, USA[1].

Grass	Total fecundity (nymphs)		Longevity (days)	
	Aug-Oct	Nov-Dec	Aug-Oct	Nov-Dec
Barnyardgrass	8.5 ± 2.4 d	19.6 ± 4.0 d	12.6 ± 1.2 d	17.2 ± 1.4 c
Western wheatgrass	23.3 ± 3.7 cd	21.3 ±4.3 d	14.8 ± 1.1 cd	19.2 ± 2.4 bc
Jointed goatgrass	49.5 ± 4.3 ab	53.2 ±4.4 bc	17.5 ±1.2 bcd	21.1 ±1.6 bc
Johnsongrass	57.8 ±3.4 a	53.5 ± 5.3 be	32.1 ±2.0 a	28.4 ± 3.4 ab
Sorghum (LG35)	37.2 ± 3.6 bc	53.3 ±4.3 bc	19.9 ±1.6 bc	34.5 ± 2.6 a
Sorghum (RTx430)	47.1 ±4.6 ab	73.3 ± 3.8 a	23.4 ±2.1 b	35.9 ±1.9 a
Wheat (GRS1201)	47.4 ± 3.8 ab	47.2 ± 4.2 c	21.6 ± 1.7 b	22.5 ± 1.9 bc
Wheat (Custer)	55.3 ± 4.8 a	69.5 ± 3.3 ab	20.7 ±1.5 bc	25.2 ± 1.2 bc

1. Data is average ± SEm. Means followed by the same letter in a column are not significantly different (Tukey's HSD, $P = 0.05$).

greenbug on barnyardgrass (19.6) was three times less than on susceptible sorghum RTx430 (73.3). Fecundities of the greenbugs differed significantly on susceptible versus resistant sorghum and wheat during November-December.

Average longevities of the greenbugs differed significantly during August-October ($F = 13.34$; df = 7, 147; $P < 0.0001$) and November-December ($F = 10.5$; df = 7, 148; $P < 0.0001$). In August-October, greenbugs survived fewest days on barnyardgrass (12.6), less than half as many days as on Johnsongrass (32.1) (Table 1). In August-October, average longevities of the greenbugs were not significantly different between susceptible and resistant sorghum or between susceptible and resistant wheat. In November-December, greenbugs on barnyardgrass survived the fewest days (17.2), half as many as on susceptible sorghum RTx430 (35.9). Average longevities of the greenbugs were not significantly different among grasses of the genus *Sorghum* during November-December. In November-December, greenbug longevities did not differ significantly on the two wheat lines or jointed goatgrass, a wild relative of wheat.

Biotype I greenbugs survive and reproduce well on different grasses. Among the wild grasses evaluated, Johnsongrass and jointed goatgrass were better hosts of greenbug than was barnyardgrass or western wheatgrass. Johnsongrass belongs to the genus *Sorghum* and jointed goatgrass is a close relative of wheat. The mechanism of resistance in sorghum LG35 and wheat GRS 1201 might be antixenosis because no symptoms of damage were seen on either resistant line.

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Workshop Highlights

Summary Proceedings of the All India Coordinated Sorghum Improvement Project - Annual Group Meeting 2003

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Sorghum *(Sorghum bicolor)* is the most important dryland cereal food, feed and forage crop in India. Presently, it is grown in many states of India from Tamil Nadu in the South to Uttaranchal in the North. The food types are grown during both the rainy *(kharif)* season (roughly 4.9 million ha, mostly in the southwestern states) and the postrainy *(rabi)* season (approximately 5.07 million ha, mostly in Maharastra and the adjoining areas of Karnataka and Andhra Pradesh). In addition, about 4.0 million ha of forage sorghum are grown primarily in the northwestern regions of the country. Being a dryland crop grown with minimum purchased inputs, utilization of sorghum is important for the economy of the country, especially for the rural poor farmers and the urban poor migrant labor force, both of which have limited purchasing power.

The Indian Council of Agricultural Research (ICAR) is the national agency leading sorghum research and development. While the National Research Centre for Sorghum (NRCS) at Hyderabad works on basic and strategic issues, the All India Coordinated Sorghum Improvement Project (AICSIP) coordinated largely by NRCS scientists works on all applied aspects including extension. AICSIP is supported by several scientists at 16 centers throughout the country, and annual work plans are reviewed during group meetings held annually.

The XXXIII Annual Meeting of the Sorghum Group was conducted at Surat in Gujarat during 1-3 April 2003 under the auspices of the Gujarat Agricultural University (GAU). Dr SN Shukla, Assistant Director General (FFC) represented the Council and provided guidance for improving the quality of research, discussions and reporting. Other special guests included Dr SV Singh, Director, Millet Directorate and Dr DN Singh, Additional Commissioner (Crop Production), Ministry of Agriculture, New Delhi. A total of 240 participants including those from ICRISAT, private seed industry, non-governmental organizations (NGOs) and the host University participated actively. Progress reports were presented and discussed throughout the meetings.

The group noted that many challenges remained. In spite of drought, progress has been noted in adapting hybrids to the west central zone of the country. However, much work is needed in the adoption of dual purpose sorghums in the southern zone and fodder sorghums in the northern zone. A new work plan for 2003-04 was prepared. One of the major concerns of the group was the slow spread of high-yielding varieties bred by the public sector institutions because of inadequate seed supply.

The group felt strongly that there is a need to diversify the genetic base of current breeding stocks, which are bred primarily for high grain yield. Grain quality parameters, especially nutrition, are very important in the improvement of our stocks. For the first time, nutritional assessment of both grain and the stover was made by comparing elite stocks at two different locations. The group came up with a new set of criteria for advancement of test materials, which will be finalized soon considering the needs of each zone.

Disciplinary Highlights

Germplasm. Germplasm was displayed to the participants, and awareness was created to demonstrate the importance of evaluation, documentation, and conservation of germplasm. New germplasm has been introduced into various sorghums for specific uses and over 100 new accessions are now being used.

***Kharif* sorghum improvement.** Three hybrids yielding up to 8-15% more than checks were identified. All these are from the private sector. Some varieties were excellent for specific traits.

***Rabi* sorghum improvement.** A few new varieties were identified that were deemed superior to CSV 216 (Phule Yashoda).

Forage sorghum improvement. Lack of improvement over checks was noted, but some entries showed better quality or disease resistance than the checks.

Sweet sorghum improvement. Two new varieties NSSH 104 and RSSV 9 were identified.

Agronomy. Mulching significantly improves yield under *rabi* conditions. *Kharif* soybean *(Glycine max)* followed by *rabi* sorghum is a sustainable and profitable system on deep soils.

Physiology. CRS 6 and RSP 1 were identified as drought tolerant varieties under *rabi* conditions, especially for shallow to medium-deep soils.

Entomology. Cruiser (Syngenta) was identified as an effective insecticide against shoot fly and costs Rs 900 ha^{-1}. C 43 and RS 29 are resistant to shoot bug and aphids, but are *kharif* types, while these insects are serious problems during the *rabi* season.

Plant pathology. Disease problems were negligible during 2002/03 crop season because of drought. However, sorghum downy mildew in Rajasthan, and smut in Gujarat were reported for the first time. Grain mold was much less during the past dry monsoon. In those places where grain mold was considerable, *Fusarium* dominated among mold-causing fungi.

Front-line demonstrations. Countrywide demonstrations showed that recent cultivars have the potential for a 30% increase in grain yield.

Major Changes Implemented or to be Undertaken

- The *kharif* sorghum region was divided into 3 zones for testing and release purposes, with differential weightage for traits proposed for each zone.
- Commitment to preserve germplasm at centers, depositing novel germplasm at the National Bureau of Plant Genetic Resources (NBPGR) was obtained.
- Specialization at centers based on comparative advantages at each region or station was planned.
- Commitment for making new crosses and using appropriate size populations for selection was obtained.
- A controlled vocabulary of technical terms used by sorghum workers (to be consistent with the usage of technical words and concepts) is needed.
- The responsibility of breeder seed production of forage sorghum was shifted from the forage program to AICSIP.

Major Concerns for Sorghum Program

- The ratio of *rabi* to *kharif* sorghum area is increasing, but efforts on *rabi* sorghum are still much less than those for *kharif* sorghum.
- Similarly for *kharif,* the efforts to breed sorghum for Zone I and III where dual-purpose sorghums are required are not adequate; most efforts are concentrated on Central Zone (Zone II).
- There is a definite improvement in the number of trials successfully conducted but quality concerns remain.
- Timeliness of reporting and consistency still needs much attention.
- The program is still loaded with trials as in the past.
- The number of crosses made is few; yet, very small F_2 populations are used for selection, and inter-disciplinary research is mostly cosmetic.

Linkages

Forage program. Forage sorghum breeding and quality research should be linked with the National Diary Development Board (NDDB) and this program will be finalized during the Forage Group Workshop at Trivandrum in May 2003.

Other millet programs. Where ICAR-supported staff members are present for all millet crops research [pearl millet (*Pennisetum glaucum*) and small millets] at any station, more coordination is needed. Also, creation of the Society for Millet Research was agreed upon. Participants suggested merging of existing separate societies for each millet crop with this new society.

The workshop was a successful event, and the future looked bright with many challenges and promises. The coordinating team thanked ICAR, GAU, and all individuals, participants and guests for making the meeting successful.

Genetic Enhancement and Breeding

Pearl Millet Male-sterile Population NCD_2A_4 and its Counterpart Maintainer Population NCD_2B_4

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The pearl millet (*Pennisetum glaucum*) population NCD_2B_4 is a d_2 dwarf population developed as a maintainer of the A_4 cytoplasmic-nuclear male-sterility system (Hanna 1989). NCD_2A_4 is the male-sterile counterpart of NCD_2B_4 in the A_4 cytoplasmic background. Both populations were developed at ICRISAT, Patancheru, India. NCD_2B_4 was derived from NCD_2 by three cycles of recurrent selection for male-sterility maintenance ability of male-sterile line 81 A_4(Rai et al. 2000). In each cycle, 123 to 392 plants of NCD_2 were selfed as well as testcrossed onto $81A_4$; of these, 76 to 131 testcrosses that were fully male-sterile were selected. In each cycle, S_1 progenies of the NCD_2 plants that produced these male-sterile testcross hybrids were recombined by hand to produce the seed of the next cycle bulk. The frequency of male-sterile testcrosses increased from 36% for the C_0 cycle to 88% for the C_1 and 100% for the C_2 cycle. The NCD, C_3 bulk produced by recombining 116 S_1 progenies of those plants from NCD_2 C_2 that produced fully male-sterile testcross progenies was designated as NCD_2B_4 maintainer population.

Initially, the NCD_2 C_0 bulk was crossed onto $81A_4$ to produce the topcross F_1 hybrid. During the 1994 postrainy hot summer (hereafter referred to as 'dry') season, 20 male-sterile plants of this hybrid were crossed with bulk pollen from 160 plants of the NCD, C_1 bulk to produce NCD_2A_4-BC_1, Two subsequent backcrosses were made on about 50 male-sterile plants of backcross populations using the bulk pollen from more than 200 plants of the C_2 and C_3 cycle bulks of NCD_2. Five additional backcrosses were made with the NCD_2C_3 bulk (ie, NCD_2B_4) crossed onto male-sterilc plants of the advancing backcross populations. The NCD_2A_4-BC_8 produced as the final backcross generation was designated as NCD_2A_4.

Comparison of male-sterility of NCD_2A_4-BC_3 with a commercial male-sterile line with the A_1 cytoplasm (841 A_1) used as a control showed that both had similar and low frequency of pollen shedders (0.2 to 1.0%) in the 1998 rainy season and 1999 dry season at Patancheru (Table 1). Further evaluation of a completely male-sterile version NCD_2A_4 (=NCD_2A_4-BC_8) during the 2000 dry season showed that it had no pollen shedders, while 841 A_1 had up to 0.1 % pollen shedders.

Evaluation of the four cycle bulks of NCD_2B_4 in a yield trial conducted at Patancheru during the rainy and dry seasons of 1996 showed that there was no significant difference between the C_0 bulk of NCD_2 and its final C_3 bulk (ie, NCD_2B_4) for grain yield and other agronomic traits (Table 2). Although not evaluated in a replicated trial, after eight generations of backcrossing, NCD_2A_4 and NCD_2B_4 plants, as expected looked phenotypically similar in observation plots. In a replicated trial for two seasons at Patancheru, NCD_2B_4 had a mean grain yield of 183 g m^{-2}, with plant height of 1.5 m and 53 days to 50% flowering. NCD_2B_4 has long panicles (33 cm), produces mostly one main panicle $plant^{-1}$ and has small seeds (7.1 g

Table 1. Pollen shedders in pearl millet male-sterile NCD_2 populatioas (NCD_2A_4-BC,and NCD_2A_4) at Patancheru, India.

Male-sterile population/line	Season	Total plants	Pollen shedders (%)
Experiment 1			
NCD_2A_4-BC_3	Rainy 1996	1431	1.0
	Dry 1997	1067	0.2
841 A_1 (control)	Rainy 1996	1119	1.0
	Dry 1997	1333	0.2
Experiment 2			
NCD_3A_4	Dry 2000	750	0.0
841 A_1 (control)	Dry 2000	838	0.1

Table 2. Mean grain yield and agronomic traits of four cycle bulks of NCD_2 in pearl millet during 1996 rainy and dry seasons, Patancheru, India.

Cycle bulk	Grain yield (g m^{-2})	Time to 50% flowering	Plant height (m)	Panicle length (cm)	No. of tillers $plant^{-1}$	1000-seed mass (g)
C_0	196	53	1.5	34	1.1	7.3
C_3	145	58	1.4	34	1.1	6.7
C_2	180	56	1.5	34	1.1	7.1
C_3[1]	183	53	1.5	33	1.2	7.1
SE±	5.6	0.2	0.02	0.4	0.02	0.13

1. C_3bulk = NCD_2B_4.

1000-seed mass). The seed is light gray and hexagonal in shape. Both populations have mixed anthers of purple and cream color.

Seed of NCD_2A_4 and NCD_2B_4 will be maintained and distributed upon request in germplasm quantities by ICRISAT, Patancheru under the terms and conditions of the ICRISAT Breeding Materials Transfer Agreement.

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ICMR 98001: A Restorer Stock of A_5 Cytoplasmic-nuclear Male Sterility in Pearl Millet

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ICMR 98001 pearl millet (*Pennisetum glaucum*) restorer stock is a highly male-fertile inbred line in the A, cytoplasmic background. This line was developed at ICRISAT, Patancheru, India from one of the several pollen-fertile plants identified in a topcross hybrid produced by crossing Large-seeded Genepool-1 (LSGP-1) developed at ICRISAT, Patancheru (Rai et al. 1999) with male-sterile line $81A_5$ that possesses the A_5 cytoplasm. LSGP-1 was developed by random mating 959 large-seeded (>10 g 1000-seed mass) germplasm accessions from 23 countries (Rai et al. 1999). The line 81 A_5 was developed by seven generations of backcrossing of a d_2 dwarf maintainer line 81B (Anand Kumar et al. 1984) into the A_5 male-sterility-inducing cytoplasm identified from one of the 67 pollen-sterile plants of LSGP-1 (Rai and Rao 1998).

During the 1995 postrainy hot summer (hereafter referred to as 'dry') season, 81 A_5 was crossed using the bulk pollen from 140 plants of LSGP-1. Of the 645 plants of the resulting topcross hybrid grown at Patancheru during the 1995 rainy season, six were pollen-fertile. Two generations of head-to-row evaluation, using seeds from open-pollinated panicles of the pollen-fertile plants in the A_5 cytoplasmic background, concomitant with selection for high levels of pollen fertility, was followed by one generation of selfing of pollen-fertile plants to produce six S_1 progenies, one S_1 from each of the six rows. Six fertile plants in each S_1 were selfed to produce S_2 progenies and also testcrossed onto $81A_5$. During the 1997 dry season, it was observed that all plants in one S_2 progeny were pollen-fertile and they had 65-95% selfed seedset. Similarly, all the plants in the corresponding testcross were pollen fertile and they had 75-95% selfed seedset. Further selfing in this S_2 produced S_3 progenies. An additional selfing in this S_3 produced S_4 progenies and testcrossing of those selfed plants onto 81 A_5 produced testcross hybrids.

Evaluation during the 1998 dry season at Patancheru showed that all plants in one S_4 progeny and its corresponding testcross were pollen-fertile and they had 90-100% selfed seedset. A S_5 progeny ($ICMA_5R$-1) produced from this S_4 progeny was designated as ICMR 98001. It was evaluated in a yield trial along with three other restorer stocks during the rainy season in 1998 and 1999 at Patancheru. ICMR 98001 gave a mean grain yield of 201 g m^{-2} compared to 264 g m^{-2} for an A_1-system restorer line (ICMR 356) of a commercial hybrid ICMH 356. In this trial, ICMR 98001 grew 1.6 m tall, produced 1.4 panicles $plant^{-1}$, and took 54 days to 50% flowering (6 days later than ICMR 356). ICMR 98001 has short (21 cm), cylindrical and compact panicles with tufted tip. It has hairy leaf blade and leaf sheath, and yellow anthers. It is a prolific pollen producer with plants having 85-100% selfed seedset. The seed is small (7.2 g 1000-seed mass), gray in color, hexagonal in shape and has spiny outer surface.

Seed of ICMR 98001 will be maintained and distributed in germplasm quantities on request by ICRISAT, Patancheru, under the terms and conditions of ICRISAT Breeding Materials Transfer Agreement.

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DRSB-2: A High-yielding Forage Pearl Millet Variety

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DRSB-2 is a high-yielding fodder pearl millet (*Pennisetum glaucum*) composite developed at the Indian Grassland and Fodder Research Institute (IGFRI), Regional Research Station, Dharwad, Karnataka, India. It is an open-pollinated variety yielding very good green fodder, dry matter and crude protein. It is also resistant to two pathotypes (predominant in South India) of downy mildew pathogen (*Sclewspora graminicola)* in field plots as well as in vitro. It is a tall variety, with comparatively higher number of synchronous tillers, sweet in taste, increased leaf to stem ratio, reasonably good seed yield with adaptability to both normal and late sowings. The variety was superior to the national check UUJ IV M (Raj Bajra Chari) in the All India Coordinated Regional Project (AICRP) trials (AICRP 1994, 1995, 1996). Based on the excellent performance over the local check DFB-1 (Dharwad Fodder Bajra-1) in station trials, regional multilocational trials and large-scale farm trials, the variety DRSB-2 was released for northern transitional zone (Zone 8) of Karnataka by the State Agricultural University, Dharwad in 2001 and State Varietal Release Committee of Karnataka in 2002.

Origin and Development

DRSB-2 is a selection from landrace germplasm from Togo (Africa) with accession number IP 9294 and identity P-3301 within the ICRISAT germplasm collection. The accession IP 9294 was a mixture of plants differing in flowering, early vigor and growth rate, as germplasm of pearl millet is maintained by cluster bagging and for sibbing phenotypically similar plants to maintain vigor. From this original population early flowering types with good early vigor and growth rate were selected. The selected plants were inter-mated to develop the population, which was advanced further by selection and multiplication in isolation until varietal distinctness, uniformity and stability was achieved.

Performance

Yield. The yield potential of forage pearl millet composite DRSB-2 is on an average 35-0 t ha^{-1} green fodder, 7-8 t ha^{-1} dry matter and 0.7-0.8 t ha^{-1} crude protein. DRSB-2 surpassed the control DFB-1 by 22.5% in green fodder yield, 36.4% in dry fodder yield and 21.3% in crude protein over five years in on-station trials (Table 1). Similarly, in multilocational testing for three years and large-scale farm trials for two years, it excelled the control in green fodder yield by 13% and 25%,

Table 2. Performance of forage pearl millet DRSB-2 in Agronomic trials at Dharwad, Karnataka, India[1].

	Green fodder yield (t ha^{-1})		Dry fodder yield (t ha^{-1})	
Entry	DI	D2	DI	D2
DRSB-2	38.2	36.2	20.6	18.3
DFB-1	27.3	24.9	14.8	12.4
Increase (%)	40.2	45.4	39.2	47.4
CD at 5%				
G	10.5		7.3	
D	7.4		5.2	
G x D	NS		NS	

1. D1 = Normal sowing (21 June 1997); D2 = Late sowing (07 July 1997); G = Genotype or entry; D = Date of sowing; NS = Not significant.

Table 1. Performance of forage pearl millet DRSB-2 in varietal trials in India[1].

	Station trials[2]			National trials[3]		
Entry	GFY	DFY	CPY	GFY	DFY	CPY
DRSB-2	35.4	7.9	0.7	37.2	7.6	0.7
Control[4]	28.9	5.8	0.6	31.7	7.1	0.6
Increase (%)	22.5	36.4	21.3	17.2	6.6	10.1

1. GFY = Green fodder yield (t ha^{-1}); DFY = Dry fodder yield (t ha^{-1}); CPY = Crude protein yield (t ha^{-1}).
2. In Dharwad, Karnataka; values are averages of five years.
3. At 17 locations; values are averages of three years.
4. Local control: DFB-1 in station trials; National control: UUJ IV M in national trials.

Table 3. Reaction of pearl millet forage varieties to downy mildew at Dharwad, Karnataka and ICRISAT, Patancheru, India.

Description	Variety	Infection (%)
Field reaction (Dharwad) (natural)	DRSB-2	0
	DFB-1	0
Field reaction (ICRISAT) (artificial, Patancheru pathotype)	DRSB-2	10.0
	Susceptible control	95.5
Greenhouse conditions (ICRISAT and Dharwad) (Jalna pathotype)	DRSB-2	5.1
	DFB-1	11.8
	Susceptible control	92.2

Table 4. Ancillary and quality parameters of pearl millet forage varieties during rainy season at Dharwad, Karnataka, India[1].

Variety	PH (cm)	NT	LL (cm)	LW (cm)	LS	DF	SC (cm)	DM (%)	Payability (%)	Oxalate (%)	Brix (%)
DRSB-2	245.9	11	85.3	3.3	1.2	52	2.7	16	76.9	3.2	7.5
DFB-1	182.5	6	61.5	3.9	0.6	64	3.3	12	71.6	5.2	4.8
CD at 5%	12.6	2.51	8.7	0.4	0.3	2.0	0.8	2.0	NA	0.8	1.1
CV (%)	12.6	6.48	8.0	10.8	9.7	10.6	9.1	11.2	NA	11.1	10.0

1. Data are averages of 3 years.
PH = Plant height; NT = Number of tillers plant^{-1}; LL = Leaf length; LW = Leaf width; LS = Leaf to stem ratio; DF = Days to flowering; SC = Stem circumference; DM = Dry matter; NA = Data not available.

respectively. The composite was also superior to the national check UUJ IV M (Raj Bajra Chari) in AICRP trials by 17.2% for green fodder, 6.6%' for dry fodder and 10.1% for crude protein content (Table 1). Seed yield is about 2.0-2.2 t ha^{-1} and production is simple and cost-effective. Farmers can multiply and maintain this composite without extra expenditure on recurrent seed purchase as required for hybrids.

Agronomic performance. The performance of DRSB-2 was assessed in timely sown (2nd to 3rd week of June) and late-sown (1st to 2nd week of July) conditions. DRSB-2 was found adapted to both these conditions, providing better yield than the control DFB-1 (Table 2).

Reaction to pests and diseases. Downy mildew is a serious threat to pearl millet. DRSB-2 was tested both in greenhouse and field conditions against different pathotypes of downy mildew pathogen and was found resistant to pathotypes present at Jalna and Patancheru with less than 10% disease incidence (Table 3).

Quality. DRSB-2 was superior to the control for crude protein content (9.9%) and dry matter content (16%), lower in oxalate content (3.2%), an anti-nutritional factor in pearl millet, and more palatable than the control DFB-1 (Table 4).

Plant and seed characters. DRSB-2 is tall, with a good number of synchronous tillers, moderate culm thickness and sweet taste (brix 7.5%) (Table 4). The leaf sheath has light purple pigmentation at the nodal region and leaves are dark green in color with drooping leaf attitude. Leaves are long resulting in a high leaf to stem ratio of 1.2. The variety is early maturing with 50-52 days to 50% flowering and takes only 90 days to maturity in the *kharif*rainy) season. The panicle is candle shaped with bristles below the level of seed apex. The seed is deep gray in color and globular in shape.

Acknowledgment. The authors are grateful to RP Thakur, Senior Scientist and VP Rao, Senior Scientific Officer, Crop Improvement, ICRISAT, Patancheru, India for facilitating greenhouse and field screening of the material for reaction to downy mildew.

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Development of Populations with Improved Fodder Potential in Pearl Millet

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Introduction

Pearl millet (*Pennisetum glaucum*) grows well in marginal soils, where fodder crops are often cultivated. It has a great potential as a fodder crop due to high forage yield, heavy tillering, leafiness and succulent stems. The green fodder is highly nutritious because of high fat and protein content but free from cyanide at all stages of growth (Burton and Powell 1968). Though several varieties and hybrids with improved forage potential are under cultivation in other countries (southeastern United States, Latin America, Mediterranean region, South Africa, southern parts of former USSR, Pakistan and Australia), improvement in India exclusively for fodder purpose has only been attempted recently. Concerted efforts made at the Indian Grassland and Fodder Research Institute (IGFRI), Regional Research Station, Dharwad, Karnataka, India has resulted in the development of several composites (DRSB-1 to DRSB-11). This study reports the performance of these populations in comparison to existing fodder varieties, Raj Bajra Chari (UUJ IV M) and DFB-1, for yield and other fodder-related attributes.

Materials and Methods

The composites were derived from high-yielding genetic stocks through sib mating followed by half-sib selection in segregating populations after hybridization. The material was selected based on early vigor, growth rate, plant height, tillering, free from pubescence and other leaf traits contributing to better fodder yield and quality. The entries were evaluated during the rainy season in 1998, 1999 and 2000. Trials were conducted in randomized complete block design with three replications. The crop was raised in plots of 4 m x 3 m and spaced at 10 cm between plants and 30 cm between rows. The fodder yield and associated traits, quality parameters and palatability were assessed at flowering stage when 50% of the plants were in bloom. Crude protein and oxalate contents were determined by standard methods (Gupta et al. 1988). Palatability was assessed as percentage of the known quantity of fresh sample that was actually consumed by ten cows in four hours.

Results and Discussion

All the newly developed composites flowered early as compared to checks and were either superior or comparable for fodder yield (Table 1). Their superiority was due to more tillers per plant and/or increased plant height (tallness). Dry matter is very important in forage crops as it determines the proportion of fodder that is available for the animal. While some of the new composites recorded significantly higher dry matter content, others have maintained the proportions observed in the checks. Seed yield is often considered an important constraint in the maintenance and spread of new varieties in fodder crops. The new composites were comparable to the existing varieties for seed yield during the rainy season at Dharwad. Considering all these features, DRSB-1, DRSB-2, DRSB-5 and DRSB-10 were superior to checks for green fodder yield and dry matter as these varieties were early flowering and had more tillers.

Apart from yield, quality is of utmost importance in fodder for its acceptance and utilization by the animals. Leafiness is one of the important quality attributes that improves the intake and protein content of the fodder (Paroda 1975). New populations were superior to checks for leafiness as indicated by higher leaf-stem ratio with broader and longer leaves (Table 2). Stems in some populations were moderately thin (as indicated by stem circumference) and juicier with sweet taste due to high brix, an indicator of total soluble solids. The most important anti-nutritional factor in pearl millet is oxalate (Gupta 1969). New populations had low oxalate. The populations DRSB-1, DRSB-2, DRSB-4, DRSB-5, DRSB-10 and DRSB-11 were superior for fodder quality, being more leafy with moderately thin and juicy sweet stems making it more palatable and nutritious due to high protein and low oxalate content.

Downy mildew is the most important disease affecting pearl millet and the best approach to manage the disease

Table 1. Performance of pearl millet populations for fodder yield and its components during rainy season 1998-2000 at Dharwad, Karnataka, India.

Population	Pedigree	Days to flowering	Plant height (cm)	No. of tillers $plant^{-1}$	Green fodder yield ($t\ ha^{-1}$)	Dry matter (%)	Grain yield ($t\ ha^{-1}$)	Resistance to downy mildew pathotype
DRSB-1	IP 9294 x Giant Bajra	55	346	11	38.1	0.23	2.09	Jalna
DRSB-2	Selection from IP 9294	52	343	12	39.9	0.22	2.20	Jalna
DRSB-3	IP 5549 x IP 9294	60	321	9	28.2	0.19	1.68	Jodhpur, Jalna
DRSB-4	Selection from IP 13237	55	300	12	36.9	0.20	1.98	Jalna
DRSB-5	IP 9294 x IP 14188	55	333	11	38.9	0.22	2.06	Jalna
DRSB-6	Selection from IP 14188	58	355	9	30.7	0.19	1.62	Patancheru, Jalna
DRSB-7	Selection from IP 14305	60	334	9	28.6	0.18	1.80	Patancheru, Jodhpur, Jalna
DRSB-8	Selection from IP 17395	58	330	9	31.2	0.19	1.92	Jalna
DRSB-9	IP 9294 x IP 14305	56	382	11	35.8	0.22	2.00	Jalna
DRSB-10	IP 13237 x IP 17395	55	335	12	37.9	0.22	2.12	Patanacheru, Jalna
DRSB-11	IP 14188 x Giant Bajra	55	343	12	35.3	0.21	1.98	Jalna
Raj Bajra Chari		62	305	8	25.0	0.20	1.90	Jalna
Giant Bajra		64	378	8	30.2	0.20	2.02	Jalna
DFB-1		66	293	7	23.3	0.18	1.68	Jalna
CD at 5%		2.0	12.6	2.5	7.9	0.01	0.32	
CV(%)		10.2	12.8	6.5	12.8	4.3	7.2	

Table 2. Performance of pearl millet populations for fodder quality attributes during rainy season 1998-2000, Dharwad, Karnataka, India.

Population	Stem circumference (cm)	Brix (%)	Leaf length (cm)	Leaf width (cm)	Leaf-stem ratio	Crude protein (%)	Payability (%)	Oxalate content (%)
DRSB-1	2.9	7.0	101	3.4	1.00	9.1	76	3.28
DRSB-2	3.0	7.5	110	3.2	1.20	9.9	77	3.21
DRSB-3	3.0	5.1	98	3.8	0.70	7.8	69	5.00
DRSB-4	3.2	6.2	87	3.5	1.10	8.6	74	3.48
DRSB-5	3.0	7.0	106	3.1	1.20	9.5	78	3.90
DRSB-6	3.2	7.9	92	3.0	0.90	7.6	68	4.61
DRSB-7	3.4	8.0	99	3.6	0.72	7.8	69	4.80
DRSB-8	3.6	8.1	77	3.6	0.68	8.0	67	5.10
DRSB-9	3.2	8.0	104	3.3	0.91	9.2	71	3.92
DRSB-10	3.2	6.8	108	3.3	1.10	9.7	77	3.90
DRSB-11	3.3	7.6	104	3.2	0.86	9.0	75	3.62
Raj Bajra Chari	3.4	5.0	89	2.9	0.68	8.0	68	4.78
Giant Bajra	3.4	5.1	97	3.1	0.70	9.0	71	5.10
DFB-1	3.3	4.8	77	3.4	0.65	7.8	72	5.00
CD at 5%	0.5	1.6	8.7	0.5	0.18	0.6		1.2
CV (%)	9.6	10.5	8.0	10.8	12.1	6.9		10.4

is to grow resistant varieties. All the test composites were resistant to Jalna pathotype. Some composites exhibited resistance to more than one pathotypes; eg, DRSB-6 (Jalna, Patancheru), DRSB-7 (Jalna, Patancheru and Jodhpur), DRSB-10 (Jalna, Patancheru), and DRSB-3 (Jalna and Jodhpur). Thus these can be safely recommended to farmers of different regions, especially Karnataka, Maharashtra, Andhra Pradesh and Rajasthan. Further, they could form useful source material for developing pearl millet varieties resistant to multiple pathotypes.

These superior populations with high yield potential and good fodder quality could be extensively tested for commercial release and are potential sources of new germplasm for use in breeding programs. All these composites are at various levels of testing in the All India Coordinated Research Project and Regional Multi-Location Trials. The composite DRSB-2 was released in 2002 in Karnataka for northern transitional zone. The open-pollinated varieties are better suited than hybrids for forage purpose owing to technically easy and cost-effective seed production by the farmer. Because of diverse genetic base, they maintain growth and vigor and ensure the crop against diseases and pests.

Acknowledgment. The authors are grateful to RP Thakur, Senior Scientist and VP Rao, Senior Scientific Officer, Crop Improvement, ICRISAT, Patancheru, India for facilitating greenhouse and field screening of the material for downy mildew.

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Stover Quality and Grain Yield Relationships and Heterosis Effects in Pearl Millet

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Introduction

Pearl millet (*Pennisetum glaucum*) is the most drought tolerant of all domesticated cereals and can yield grain under rainfall as low as 200 to 250 mm (Bidinger and Hash, in press) making it the only reliably productive cereal in the driest rainfed regions of the arid and semi-arid tropics. In these regions, crop-livestock production systems are highly integrated and the stover from pearl millet plays a very crucial role in feeding the livestock. Kelley et al. (1996) observed that farmers rejected several pearl millet cultivars (improved only for grain yield) because of too poor fodder value of the stover. Considering the growing demand for more and better quality fodder for livestock, crop improvement programs have now become multidimensional, targeting the whole plant rather than one single trait. Nearly 70% of the Indian pearl millet area (>9 million ha) is sown to more than 72 hybrids and improvement in the quantity and/or the nutritional quality of the stover of these hybrids could make tremendous impact on livestock productivity in the region. The objective of the current research was to assess heterosis in top-cross hybrids for stover quality traits and to investigate genotypic variability in stover quality traits and their relationships with grain and stover yield.

Material and Methods

Field trial. Forty-two top-cross hybrids developed by crossing seven populations of diverse origin on each of six fodder-type male-sterile lines, plus the respective parental populations and three released dual-purpose cultivars (2 open-pollinated varieties and a hybrid) as checks, were evaluated at ICRISAT, Patancheru, India during the 2002 rainy season at a high fertility level [120 kg nitrogen (N) and 18 kg phosphorus (P) ha^{-1}]. The trial was planted in 4-row plots of 4 m length in randomized complete block design replicated three times with 75 cm spacing between the rows and 10 cm spacing between plants within the rows. Panicles were harvested at maturity and dried at 55°C for 24 h and threshed to determine grain yield. For stover yield, plants were

Table 1. Grain yield (GY) (t ha^{-1}), stover yield (SY) (t ha^{-1}), stover crude protein (CP) (%), stover in vitro digestibility (IVD) (%) and heterosis effects (Δ) (%) in 42 top-cross hybrids of pearl millet and GY, SY, CP and IVD in 7 pollinator populations used in producing these hybrids.

Genotype	GY	ΔGY	SY	Δ SY	CP	Δ CP	IVD	Δ IVD
ICMA 01222 x HHVBC Tall	3.36	-8.4	3.86	-10.7	4.8	-21.6	41.1	-7.3
ICMA 01222 x RC-B-2	3.52	24.4	4.14	11.3	4.8	1.3	41.8	4.2
ICMA 01222 x ICMV 91059	3.64	0	3.86	-25.2	4.5	-21.2	43.4	-6.2
ICMA 01222 x SDMV 93032	3.61	19.5	4.77	18.4	5.9	8.5	45.9	2.1
ICMA 01222 xMC 94	3.60	9.4	3.45	3.0	4.7	-6.2	41.1	-4.8
ICMA 01222 x ICMS 7704	3.65	18.9	4.43	-19.9	4.2	6.0	44.1	-1.6
ICMA 01222 x ICMV-IS 94206	3.72	1.9	4.29	-3.2	4.3	29.6	40.8	2.2
Mean	3.59	9.4	4.6	-3.8	4.6	-0.5	42.6	-1.6
ICMA 98555 x HHVBC Tall	3.53	-3.8	4.31	-0.2	6.3	3.0	43.5	-1.9
ICMA 98555 x RC-B-2	3.35	18.4	3.64	-2.2	5.2	8.2	39.1	-2.6
ICMA 98555 x ICMV 91059	3.91	7.4	3.74	-27.5	5.7	-0.5	43.1	-6.9
ICMA 98555 x SDMV 93032	3.45	14.2	4.11	2.0	5.1	11.1	45.0	0.1
ICMA 98555 x MC 94	3.59	9.1	3.47	3.6	5.2	2.6	41.3	-4.3
ICMA 98555 x ICMS 7704	3.65	18.9	4.05	-26.8	4.0	1.8	41.8	-6.8
ICMA 98555 x ICMV-IS 94206	3.89	6.6	4.78	7.9	4.5	35.5	42.8	7.1
Mean	3.62	10.1	4.01	-6.2	5.1	8.8	42.4	-2.2
ICMA 91777 x HHVBC Tall	3.54	-3.5	4.09	-5.3	4.4	-26.9	40.0	-9.7
ICMA 91777 x RC-B-2	3.20	13.1	4.37	17.5	4.9	2.5	40.9	2.0
ICMA 91777 x ICMV 91059	3.20	-12.1	4.44	-14.0	5.2	-1.3	43.7	-5.5
ICMA 91777 x SDMV 93032	3.31	9.6	4.58	13.7	4.2	-7.9	42.8	-4.8
ICMA 91777 x MC94	3.65	10.9	5.29	57.9	4.8	-4.0	39.6	-8.2
ICMA 91777 x ICMS 7704	3.72	21.2	4.37	-21.0	4.3	8.1	40.7	-9.2
ICMA 91777 x ICMV-IS 94206	3.43	-6.0	3.97	-10.4	3.9	17.0	38.5	-3.6
Mean	3.43	4.7	4.44	5.5	4.5	-1.8	40.9	-5.6
ICMA 98333 x HHVBC Tall	3.75	2.2	3.18	-26.4	6.0	-1.0	42.1	-5.0
ICMA 98333 x RC-B-2	3.27	15.6	3.10	-16.7	4.6	-2.5	40.5	1.0
ICMA 98333 x ICMV 91059	3.82	5.0	3.53	-31.6	5.8	0	41.5	-10.3
ICMA 98333 x SDMV 93032	3.44	13.9	3.62	-10.2	4.4	-3.5	42.4	-5.6
ICMA 98333 x MC 94	3.66	11.3	3.12	-6.9	5.2	3.8	42.9	-0.7
ICMA 98333 x ICMS 7704	3.83	24.8	3.38	-38.9	4.9	22.7	41.7	-7.1
ICMA 98333 x ICMV-IS 94206	3.96	8.5	3.89	-12.2	4.1	23.0	42.0	5.2
Mean	3.68	11.6	3.40	-20.4	5.0	6.1	41.9	-3.2
ICMA 00888 x HHVBC Tall	2.85	-22.3	3.24	-25.0	5.2	-13.7	43.3	-2.3
ICMA 00888 x RC-B-2	3.15	11.3	3.40	-8.6	5.1	6.5	43.0	7.1
ICMA 00888 x ICMV 91059	3.10	-14.5	3.77	-26.9	6.0	4.9	46.0	-0.6
ICMA 00888 x SDMV 93032	3.01	-0.3	3.56	-11.7	5.9	29.7	43.5	-3.3
ICMA 00888 x MC 94	3.50	6.4	3.53	5.4	5.4	6.2	44.4	2.9
ICMA 00888 x ICMS 7704	3.92	27.8	3.72	-32.7	5.6	41.8	42.4	-5.6
ICMA 00888 x ICMV-IS 94206	3.50	-4.1	3.65	-17.6	4.4	32.5	. 43.3	8.3
Mean	3.29	0.6	3.55	-16.7	5.4	15.4	43.7	0.9
ICMA 01777 x HHVBC Tall	3.66	-0.3	3.71	-14.1	4.1	-32.5	41.6	-6.1
ICMA 01777 x RC-B-2	3.91	38.2	4.18	12.4	4.9	3.6	41.7	3.7
ICMA 01777 x ICMV 91059	3.70	1.7	3.89	-24.6	3.9	-31.5	44.8	-3.2
ICMA 01777 x SDMV 93032	3.46	14.6	3.87	-4.0	5.6	22.1	46.7	4.0
ICMA 01777 x MC 94	3.78	14.9	3.59	7.2	4.7	-6.4	42.5	-1.5
ICMA 01777 x ICMS 7704	3.84	25.1	4.74	-14.3	4.0	1.8	45.5	1.4
ICMA 01777 x ICMV-IS 94206	3.91	7.1	2.93	-33.9	3.6	8.4	39.9	-0.2
Mean	3.75	14.5	3.84	-10.2	4.4	-4.9	43.2	-0.3

continued

Table 1. *continued.*

Genotype	GY	Δ GY	SY	Δ SY	CP	Δ CP	IVD	Δ IVD
HHVBC Tall	3.67		4.32		6.1		44.3	
RC-B-2	2.83		3.72		4.8		40.2	
ICMV 91059	3.64		5.16		5.8		46.3	
SDMV 93032	3.02		4.03		4.6		44.9	
MC 94	3.29		3.35		5.0		43.1	
ICMS 7704	3.07		5.53		4.0		44.9	
ICMV-IS 94206	3.65		4.43		3.4		40.0	
Pollinator mean	3.31		4.36		4.8		43.4	
JBV2 9 (check)	3.27		3.76		6.0		42.3	
JBV3 (check)	3.27		3.68		4.0		44.3	
ICMH 451 (check)	3.54		4.16		5.2		42.2	
SED[1]	0.24		0.54		0.6		1.8	
SEm±	0.17		0.38		0.4		1.3	
Mean	3.51		3.96		4.9		42.6	
CV (%)	8		17		14		5	
LSD	0.47		1.06		1.1		3.6	

1. Statistical variables relate to overall ANOVA on all treatments.

harvested at soil level and a sample of 5 plants from each plot was oven-dried at 50°C for three days (8 h a day) to determine dry stover yield and quality. Heterosis effects were estimated as value of the top-cross hybrid minus value of the pollinator divided by value of the pollinator. Significant heterosis effects were assumed with differences between lop-cross hybrid and pollinator greater than the least significant difference value from overall analysis of variance.

Stover analysis. Stover quality assessments were based on a combination of conventional laboratory analysis and Near Infrared Spectroscopy (NIRS) using a FOSS 5000 Forage Analyzer with WINSI II software package. Seventy-two stover samples from the total of 165 were selected for NIRS calibration-validation procedures using WINSI II software features and analyzed for protein and in vitro digestibility by conventional laboratory techniques. Thirty-six of these stover samples were used to develop NIRS calibration equations for protein and in vitro digestibility to blind-predict these measurements for the remaining 36-stover samples. Agreement between conventionally analyzed crude protein and in vitro digestibility and NIRS-predicled values were R^2 = 0.92 and 0.89, respectively. Calibration equations were then developed based on all 72 samples and used for the prediction of crude protein and stover digestibility of the entire set of stover samples.

Conventional in vitro digestibility measurements were based on incubation of stover in an in vitro gas production test as described by Menke and Steingass (1988). Rumen microbial inoculum for in vitro incubation was collected from two rumen-cannulated bullocks (local Indian breed) kept on a diet based on stover. Accumulating gas volumes were recorded after 24 h of incubation and in vitro digestibility was calculated as 15.38 + [0.8453 x gas (ml) produced after 24 h] + [0.595 x crude protein (%)] + (0.181 *% ash) as described by Menke and Steingass (1988). Conventional crude protein measurements were obtained by N determinations by Technicon Auto Analyzer and multiplication of N% by 6.25.

Results and Discussions

Grain yield, stover yield, stover crude protein content and in vitro digestibility of stover of the 42 top-cross hybrids, the 7 pollinators and the 3 checks of pearl millet and heterosis for traits are presented in Table 1. Significant genotypic differences (P <0.05) were observed for all the traits. Grain yield ranged from 2.83 to 3.96 t ha^{-1} and stover yield ranged from 2.93 to 5.53 t ha^{-1} . Stover crude protein content and stover in vitro digestibility ranged from 3.4 to 6.3% and from 38.5 to 46.7%, respectively. Significant (P <0.05) positive as well as negative heterosis effects were observed for grain yield, stover yield and stover crude protein content but not for in vitro digestibility where only negative heterosis effects were significant. As pointed out by Bidinger et al. (2003) selection history played a large role in heterosis effects on grain and stover yields in pearl millet. Parental material selected for grain yield through increasing harvest index resulted in heterosis for higher grain yield but lower stover yields while lines which were selected

for increased biomass yields/growth rates and neutral effects on harvest index resulted in hybrids with higher grain and stover yields (Bidinger et al. 2003). We observed positive (although rarely significant) heterosis trends in 32 hybrids for grain yield, in 12 hybrids for stover yield, in 27 hybrids for crude protein and in 14 hybrids for in vitro digestibility (Table 1).

Ruminants need a minimum of 7% of crude protein in their diet (Van Soest 1994) to utilize the potentially digestible organic matter. Cereal crop residues are deficient in crude protein since their mean protein content is approximately only half of that required. The response in livestock productivity to incremental increases of 3.5 to 7% in protein content of the diet is substantial. The observed genotypic variation in stover crude protein (3.4 to 6.3%) is therefore nutritionally relevant, and increasing crude protein content of stover by crop improvement could be a very relevant option to pursue. However, this option would require absence of strong competitive associations between stover crude protein content and grain yield and other desirable traits. Stover crude protein content and grain and stover yield tended to be inversely associated but the relationships did not attain (nor approach) significance levels (Figs. la and lb). These findings suggest that stover with high crude protein content can be selected without sacrificing the grain yield. Crude protein content in pearl millet stover is also affected by N fertilizer application; Blummel et al. (2003) observed mean stover crude protein content of 3 and 4.4% under low (9 kg N ha^{-1}) and high (90 kg N ha^{-1}) fertilizer application, respectively. The N application rate in our work was even higher (120 kg N ha^{-1}) which might explain the very large range in crude protein values observed. More work appears to be warranted to investigate the variation in protein content and the relationships between stover protein content and grain and stover yield under low input systems.

Stover organic matter digestibility - besides stover intake - will determine livestock productivity in stover-fed animals. Organic matter digestibility in the animals is an estimate of how much of the fodder can be used (digested) by the animal for productive purposes and is

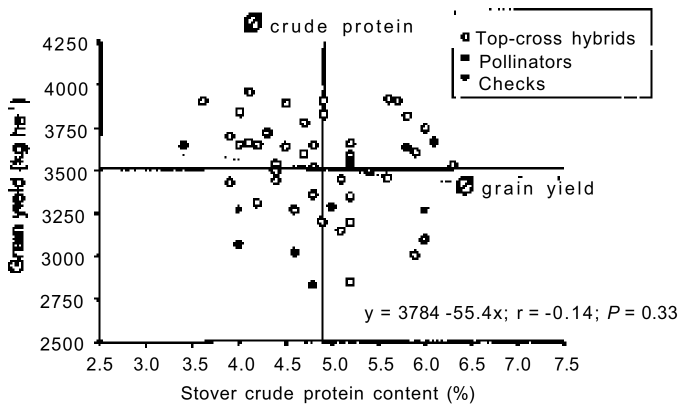

Figure la. Relation between stover crude protein content and grain yield in 52 genotypes of pearl millet.

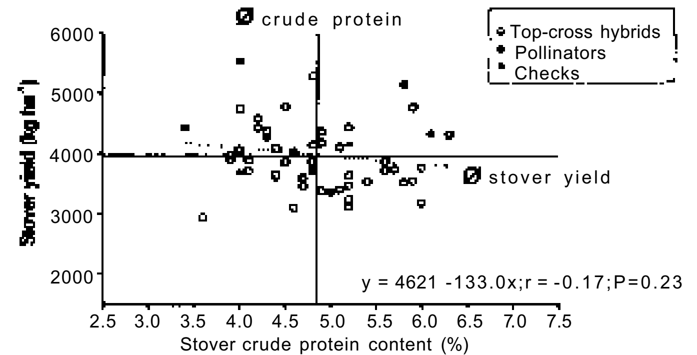

Figure lb. Relation between stover crude protein content and stover yield in 52 genotypes of pearl millet.

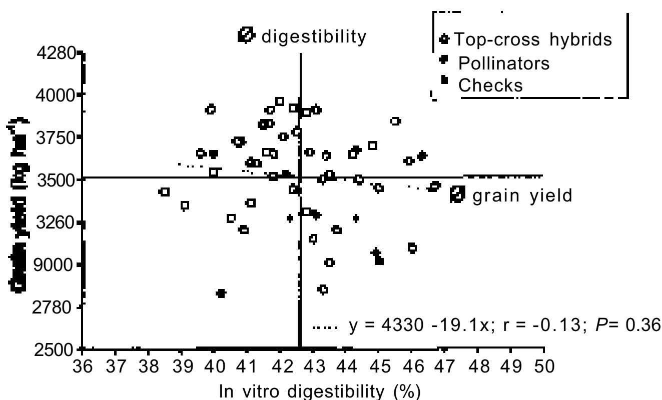

Figure 2a. Relation between in vitro digestibility and grain yield in 52 genotypes of pearl millet.

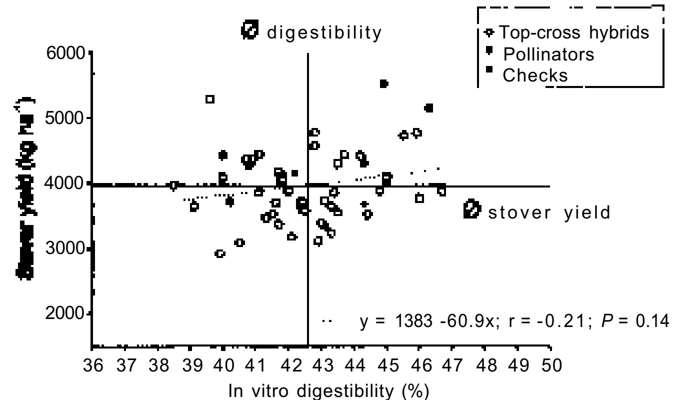

Figure 2b. Relation between in vitro digestibility and stover yield in 52 genotypes of pearl millet.

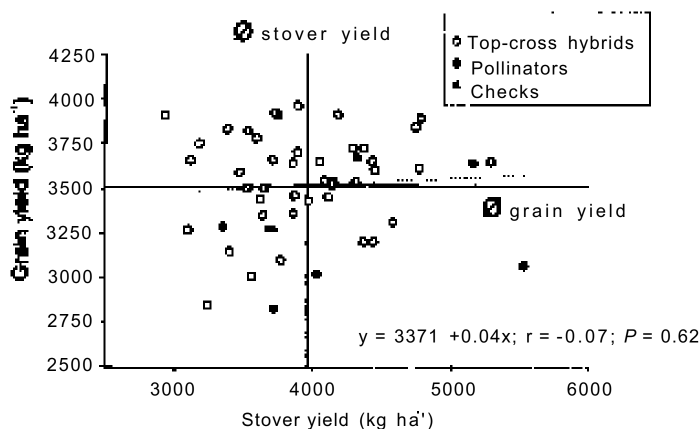

Figure 3a. Relations between stover yield and grain yield in 52 genotypes of pearl millet.

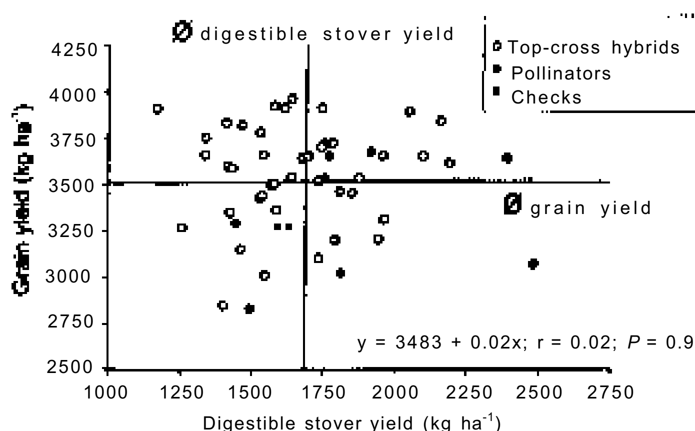

Figure 3b. Relations between digestible stover yield and grain yield in 52 genotypes of pearl millet.

commonly predicted by in vitro incubation in rumen inoculum in the laboratory. We observed genotypic differences of about 8 units in in vitro digestibility of stover. Differences of this magnitude will have substantial effects on livestock productivity (Van Soest 1994). In vitro digestibility of stover and grain and stover yield seem to be compatible traits, ie, stover in vitro digestibility and grain and stover yields were not significantly associated (Figs. 2a and 2b).

Mixed crop-livestock farmers in the semi-arid tropics require stover of good quality but they also need stover quantity. Stover yield and grain yield were not related (Fig. 3a) and improvement for grain yield will not automatically affect stover yield in either positive or negative way. Stover yield measurements should, therefore, be included in genotype evaluations. Overall stover value will be a product of stover quantity and stover quality. Digestible stover yield was calculated as the product of total stover yield and its in vitro digestibility and was found to vary from 1.3 to 2.5 t ha^{-1}. No relationship was observed between these two variables (Fig. 3b) suggesting that high stover value and high grain yield are not mutually exclusive traits.

Conclusions

Significant and nutritionally relevant cultivar differences exist in pearl millet stover quality and these were largely independent of grain and stover yield. Highest grain yields were observed for top-cross hybrids but some open-pollinated cultivars were superior in dual-purpose usage in that they provided excellent stover value and good grain yield at the same time.

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Biotechnology

Development of CT-based Microsatellites in Pearl Millet

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Introduction

Pearl millet (*Pennisetum glaucum*) is a monocot species belonging to the *Poaceae* family and has a relatively small diploid genome (2n = 2x = 14) with a DNA content of 1C = 2.36 pg (Martel et al. 1997). Pearl millet is a highly cross-pollinated crop. It demonstrates the highest levels of tolerance to drought and heat found in domesticated cereals and, consequently, is grown on more than 26 million ha in the arid and semi-arid regions of Africa and India.

Simple sequence repeats (SSRs), or microsatellites, consist of 2-5 nucleotide sequences such as (GA)n, (ATT)n or (ATGT)n that are tandemly repeated. Such repeated sequences are found throughout eukaryotic genomes and provide the basis for a polymerase chain reaction (PCR)-based marker amplification strategy. Microsatellites can be isolated directly from total genomic DNA libraries, or from libraries enriched for specific microsatellites.

Microsatellites as sequence tagged site markers demonstrate high levels of DNA polymorphism, and their co-dominant inheritance allows for the detection of several different alleles at a locus. Such features are essential for effective discrimination between closely related lines (Akkaya et al. 1992). SSR markers are analyzed by a rapid, technically simple, and inexpensive PCR-based assay that requires only small quantities of DNA. They occur universally in plants and are both abundant and uniformly dispersed in plant genomes (Akkaya et al. 1995). In contrast to animals, in which GT dinucleotides are most frequent, predominance of AT repeats seems to be a common feature of plant genomes. The SSR markers are currently used in soybean *(Glycine max)* (Akkaya et al. 1995), barley (*Hordeum vulgare)* (Liu et al. 1996), rye *(Secale cereale)* (Saal and Wricke 1999), sugarcane *(Saccharum qfficinarum)* (Cordeiro et al. 2(K)0) and wheat *(Triticum aestivum)* (Roder et al. 1998). The SSRs also serve as a tool for the identification of genotypes, tagging of important traits, and in population genetic studies. Plant SSRs are reported to exhibit high levels of polymorphism with as many as 37 alleles at individual loci in barley (Saghai-Maroof et al. 1994) and 26 alleles in soybean (Rongwen et al. 1995). In most plant species the level of detected polymorphism is shown to be 10 times higher than with RFLP markers (Akkaya et al. 1992, Senior and Heun 1993).

To date, collections of 20 and 24 SSR markers have been developed for pearl millet (Allouis et al. 2001; Qi et al. 2001). They represent the marker system of choice because of their ease of application, low cost, and utility in assessment of allelic variation. The availability of a collection of SSR markers to the pearl millet research community would establish millet as a more powerful genetic model, and allow millet breeders to readily integrate marker-assistance to their selection strategies.

Materials and Methods

Genomic DNA of pearl millet line IBMV 840 was extracted with the Qiagene DNAesy kit. Genomic DNA (40 ug) was digested with the restriction enzyme *Smal,* and then size-selected on 1% agarose gel in IX TBE buffer for 3 h at 1.5 v cm^{-1}. Following electrophoresis, fragments in the size range of 400-800 bp were extracted and the DNA purified using the Gene Clean II (Bio 101 Inc., LaJolla, California, USA).

Purified DNA fragments (0.7 µg) were ligated to Smal-digested pUC19 vector in the presence of *Smal.* Following transformation of competent *Escherichia coli* DH5 (Life Technology) cells, the size selected library was screened by colony hybridization at 45°C using ^{32}P-labelled poly $(CT)_{15}$ in 6x SSPE, 5x Denhardt's solution, 1% SDS, with three post hybridization washes in 0.5x SSC, and 0.1% SDS. Putative positive colonies were re-plated and a second round of screening was carried out to confirm the hybridization results. A total of 34 clones were identified using this procedure and their inserts were sequenced. Primer pairs were designed to amplify the microsatellite from those clones containing >10-CT repeats using the OLIGO 6 (Molecular Biology Institute, Co. Cascade, Colorado, USA) program software. The SSR marker names, sequences, repeat length, melting temperature, expected size and nature of polymorphism used in this study are shown in Table 1.

Genomic DNA of pearl millet lines was extracted with the Qiagene DNAesy kit. A total of 65 SSR primers were assayed using 15 millet lines chosen to represent a range of diversity. The PCR reaction mixtures (25 ul total volume) consisted of 10 mM Tris-HCl, pH 8.8 at 25°C, 50 mM KCl, 2.0 mM $MgCl_2$, nucleotides dATP, dTTP, dCTP, and dGTP (200 uM each), 0.2 uM primer, 30 ng

template DNA, and 1.5 units of *Taq* DNA polymerase (Promega). Amplifications were carried out in a MJ Research PTC-100 thermocycler programmed for 32 cycles of 1 min at 94°C, 1 min at 53°C, 1 min at 72°C, and ending with 5 min at 72°C.

To refer to the informativeness of microsatellites, we employed the term polymorphism information content (PIC). The PIC value was calculated according to the formula:

$$PIC_i = 1 - P_{ij}^2$$

where p_{ij} is the frequency of the j_{ih} microsatellite allele for clone *i*. This value is referred as heterozygosity and gene diversity (Anderson et al. 1993).

Results and Discussion

The screening of a partial genomic library of *P. glaucum,* consisting of about 40,000 clones with an average size of 400 bp, with a dinucleotide repeat oligonucleotide probe $(CT)_{15}$ identified 80 positive clones. Over 50% (46 out of 80) of the positive clones were discarded as false positives during the second screening. Of the 34 remaining clones, sequence analysis determined that 18 contained microsatellites with at least 10 CT repeats and sufficient flanking sequence to design primers, while the remainder contained short repeats (2-9) and were discarded. The primers that contain the short repeats generally produced monomorphic PCR products or displayed very low PIC value (Qi et al. 2001).

Assuming an average insert size of 400 bp, the library contained 16,000 Kbp of genomic DNA. This gave an estimate of one microsatellite motif per 888 Kbp. This estimate is roughly similar to those obtained from maize (*Zea mays*) (Taramino and Tingey 1996), but much lower than those reported in the genome of barley (Liu et al. 1996). Based on these findings, it appears that GA/CT repeats are abundant and easily detected in millet. Our results are consistent with reports from other plant species (Lagercrantz et al. 1993, Wang et al. 1994). Although most of the primer pairs produced a maximum of two bands per genotype, two (CTM-26 and CTM-60) primer pairs produced more bands than expected according to the diploid constitution of this pearl millet, probably implying the duplication of some loci; in fact, Devos et al. (2000) reported that the pearl millet genome carries at least one, and probably two duplications between linkage groups 1 and 4.

All primer pairs that amplified microsatellite loci in line IBMV 840 were examined for polymorphism among 15 lines of pearl millet (Fig. 1) to obtain an estimate of SSR length polymorphism associated with each locus. All loci displayed one or more alleles. The number of alleles found for each of these loci varied from 1 to 9. The polymorphisms detected for CTM 9 are shown in Figure 1. Of the 18 microsatellites developed as part of this work, 15 primer pairs were polymorphic and three pairs were monomorphic (Table 1). The PIC values for the 18 CTM loci were calculated based on screening of 15 lines (Table 1, Fig. 1). PIC values of microsatellite markers varied from 0 to 0.88 with an average of 0.44 (Table 1).

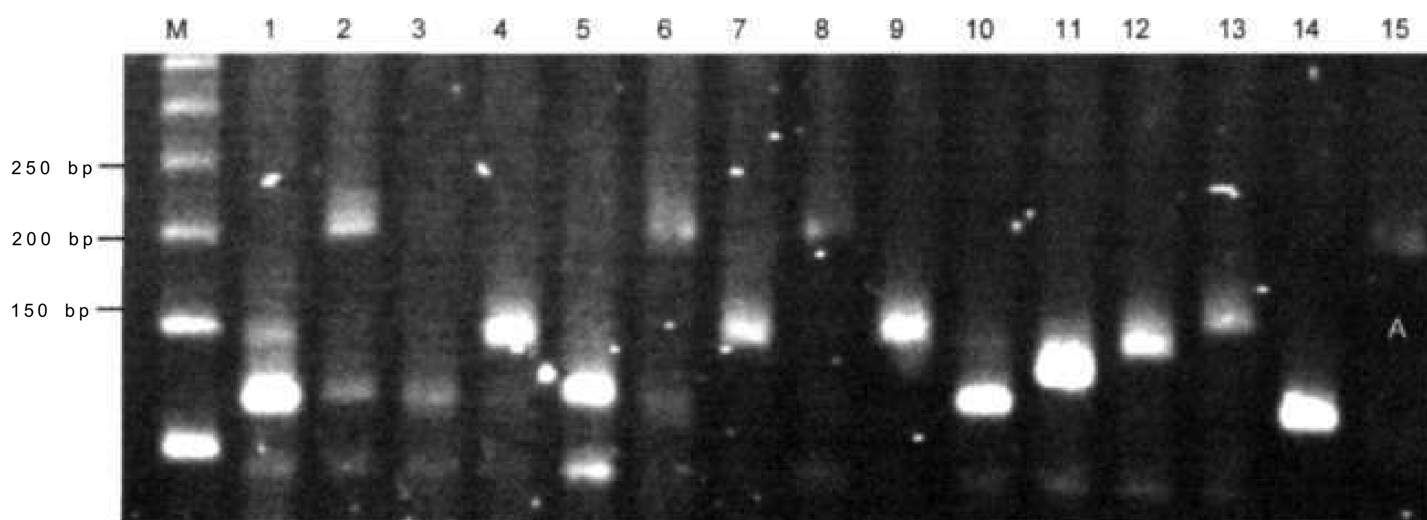

Figure 1. PCR amplification of pearl millet genomic DNA from 15 lines [Lanes: 1 = 81B, 2 = 94m59648CBR, 3 = 293B, 4 = 5173B, 5 = c4241A5. 6 = 086R1, 7 = BmreB, 8 = PI 164421, 9 = PI286892,10 = PI 536327,11 = PI307713, 12 = PI511036,13 = PI561619, 14 = PI 583799. 15 = 85DB; and lane M contains a 50-hp size marker (Promega Corp.)]. (Note: Two microsatellites, (A) PSM 2202 (Qi et al. 2001) and (B) CTM9. were assayed. The DNA samples were fractionated in 12% non-denaturing acrylamide gels stained with ethidum bromide.]

Table 1. SSR marker names developed for pearl millet line IBMV 840, primer sequences, repeated type and length, melting temperature, expected size and number of alleles.

Marker[1]		Primer sequences	Repeat type and length (bp)	Tm^2 (°C)	Expected size (bp)	Number of alleles[3]
CTM1	F	5'-TCTGGGG ATTGGCTGGAATTACA/	$(CT)_{29}$	53	222	3 (0.23)
	R	AAGTTGGGTAACGCCAGGGTTTTC-3'				
CTM2	F	5-GGTGATTAAAATCGAGGGTT/	$(CT)_{13}$	53	255	3(0)
	R	AGC AACTTGAGCAGCGG-3'				
CTM3	F	5-GTCCATCGTCGCCGACGAA/	$(CD)_{12}$	53	195	4(0)
	R	GGATTTGCTAGTTGTGGGCT-3'				
CTM8	F	5'-GCTGC ATCGGAGATAGGGAA/	$(CT)_8$	53	210	4 (0.47)
	R	CTCAGCAAGCACGCTGCTCT-3'	$(CT)_{11}$			
CTM9	F	5'-GCCTCCTCTTGATACCATATT/	$(CT)_{20}$	52	219	8 (0.85)
	R	TAGCCTTGGCTGCTATATTC-3'				
CTM10	F	5'-GAGGCAAAAGTGGAAGACAG/	$(CT)_{22}$	54	235	6 (0.60)
	R	TTGATTCCCGGTTCTATCGA-3'				
CTM11	F	5'-GACCGATCTTCTTTGCTGTTG/	$(CT)_{21}$	54	230	1(0)
	R	TCTATCGTACGTTAACCTCA-3'				
CTM12	F	5-GTTGCAAGCAGGAGTAGATCGA/	$(CT)_{12}$	53	189	4 (0.46)
	R	CGCTCTGTAGGTTGA ACTCCTT-3'				
CTM21	F	5'ATGCCTCCCACCCCACGTCG/	$(CT)_{24}$	53	260	5 (0.49)
	R	CGTCGCACTAGCCACAGTCA-3'				
CTM25	F	.V-GCGAAGTAGAACACCGCGCT/	$(CT)_{34}$	53	225	6 (0.59)
	R	GCACTTCCTCCTCGCCGTCA-3'				
CTM26	F	5'-GCAAGTGATCCATGACATTACGA/	$(CT)_{10}$	53	188	6 (0.59)
	R	ACTTGCT AGCTGCTGCTCTTG-3'				
CTM27	F	5-GTTGCAAGCAGGAGTAGATCGA/	$(CT)_{71}$	53	255	4 (0.33)
	R	CGCTCTGTAGGTTGAACTCCTT-3'				
CTM55	F	5'CGTCTTCTACCACGTCCT/	$(CT)_{25}$	54	140	4 (0.33)
	R	CATAATCCCACTCAACAATCC-3'				
CTM56	F	5'-GCGTTGTTTCGGTGACCAC/	$(CT)_{15}$	53	165	5 (0.50)
	R	GCGTATCTTTAAATTGCCTTTGTT-3'				
CTM57	F	5'-TGGTGGCAATGCAAGCTACAG/	$(CT)_{13}$	53	172	5 (0.53)
	R	AGCGAGACGATCGACAGGG-3'				
CTM58	F	5'TACGTGCTACAAGAATGG/	$(CT)_{24}$	53	155	5 (0.56)
	R	GCTGGCTAGGACACAA-3'				
CTM59	F	5'-TCCTCG ACATCCTCCA/	$(CD_{11}$	54	183	8 (0.87)
	R	GACACCTCGTAGC ACTCC-3'				
CTM60	F	5'-AAGCCCCGATCACATCAA/	$(CT)_{23}$	53	218	9 (0.88)
	R	AGCCGAGCCTCATCCC-3'				

1. F = Forward; R = Reverse.
2. Tm = Melting temperature.
3. Polymorphism information content (PIC) values are given within parentheses.

The degree of polymorphism detected by these primer pairs did not correlate with the number of repeats in the microsatellites. Although the relationship between the degree of polymorphism and the number of repeats has been reported in some species (Saghai-Maroof et al. 1994, Fisher et al. 1998), theoretically the number of repeats is correlated with the mutation rate, and not with the degree of polymorphism (Xu et al. 2000). Polymorphism may correlate with the product of the mutation rate and the generation term of the locus. More recently evolved microsatellites would have fewer polymorphisms because of fewer occasions for mutation, even if they have longer repeats.

Based on the effectiveness of SSR marker-based mapping efforts in maize, sorghum *(Sorghum bicolor),* soybean and other crops, it is reasonable to assume that these SSR markers will be adopted readily by pearl millet breeding programs and will greatly enhance selection efforts. The development of such a marker collection is ideally suited for practical application to the breeding of pearl millet as will be demonstrated by their integration into ongoing efforts for pedigree assessment, quantitative trait loci (QTL) identification, and cytoplasmic male-sterility (CMS)-restorer identification.

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Genetic Enhancement of Pearl Millet for Downy Mildew Resistance - A Project Summary

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Objectives

The proposed research aimed at fine-mapping and isolating genes underlying downy mildew resistance in pearl millet (*Pennisetum glaucum),* a key agronomic trait affecting crop adaptability and yield. Disease resistance is of importance for both subsistence farmers and breeders in Africa and India. The isolated genes will provide a resource for future crop improvement, and allow elucidation of the resistance mechanisms. This may lead, in the long run, to the design of new strategies for the adaptation of pearl millet varieties to their often harsh and highly variable growth habitats, while maintaining yields. The development of an efficient transformation procedure for pearl millet will underpin the trait study and provide the necessary resources for complementation testing of the isolated genes. In addition, the establishment of pearl millet transformation technology in Africa will form the basis for further genetic enhancement of this crop for the benefit of sub-Saharan Africa.

Activities

Isolation of *dm* genes [carried out through a collaboration between the John Innes Centre (JIC), Norwich, UK; the University of Parma (UP), Italy; and Savanna Agricultural Research Institute (SARI), Nyankpala, Ghana].

1. Identification of F_2 plants heterozygous for a single quantitative trait locus (QTL) for downy mildew resistance as starting material for the generation of a fine-mapping population (JIC):

To fine-map a QTL, it is necessary to develop **a** population in which only the target QTL is segregating. This can be achieved by backcrossing the QTL into a suitable (ie, in the case of downy mildew, a susceptible) background, and generating a cross between the resultant near-isogenic lines (NILs). In the absence of NILs, one can select lines from the population in which the QTL analysis has been conducted and that contain only a single QTL and are heterozygous for this QTL.

QTL data, including genotypic data and disease scores, had been generated in the crosses PT 732B x P1449-2 and ICMP 451 x H 77/833-2 by a pearl millet collaborative network, funded by the Department for International Development (DFID), UK. The network includes ICRISAT (Patancheru, India), the Institute of Grassland and Environmental Research (IGER) (Aberystwyth, UK), the University of Wales (Bangor, UK) and JIC (Norwich, UK). The population PT 732B x P1449-2 was shown to segregate for resistance against *Sclerospora graminicola* isolates (causing downy mildew) from Niger. The population ICMP 451 x H 77/833-2 was segregating for resistance against isolates from Niger, Mali and Nigeria. The F_2 plants that were heterozygous for a single resistance QTL were identified, and corresponding F_3/F_4 seed was obtained from ICRISAT. The selected lines were field tested for downy mildew in Ghana (see sub-activity 3).

2. Identification of F_3 plants that are heterozygous for the target QTL (JIC):

As the F_2 genotypes identified in sub-activity 1 were heterozygous for a single downy mildew resistance QTL, and thus were segregating in the F_3/F_4 seed obtained from ICRISAT, it was necessary to identify F_3/F_4 plants that were heterozygous for the critical region. For each line, 10 to 15 F_3/F_4 plants were grown and plants that were heterozygous for chromosome segments carrying a QTL were selected using molecular markers. These plants were grown to maturity and selfed to produce large fine-mapping populations of some 2,000 seeds. A total of 21 populations with a minimum of 1,000 seeds were generated. These populations cover five QTL regions in two crosses. The aim was to select two mapping populations, based on the resistance levels of the parental

lines in Ghana, for further analysis. Seeds of all populations have been stored in the seedstore at JIC.

3. Field screening of selected lines for downy mildew resistance in Ghana (SARI):

F_4 seed, corresponding to the lines selected under sub-activity 1, were planted in June 1999 in the downy mildew nursery at Bawku, Ghana by SARI. The trial was carried out in duplicate. The number of infected plants was scored 20 and 30 days after planting and at dough stage. All plants were heavily infected with downy mildew. As the plants were either homozygous or heterozygous for a single QTL only, we concluded that none of the individual QTL provided significant resistance to Ghanaian *S. graminicola* isolates.

4. Selection of mapping populations for fine-mapping (JIC):

None of the lines tested displayed significant resistance to Ghanaian downy mildew isolates (see sub-activity 3). Hence, we decided to target the resistance QTL on LG 1 and LG 4, which had previously been identified in the PT 732B x P1449-2 cross as being effective in Niger, for fine-mapping and isolation of the underlying genes. The rationale for this decision was that the QTL on LG 4 was detected in both PT 732B x P1449-2 and ICMP 451 x H 77/833-32 crosses, and thus was effective to downy mildew isolates in Niger, Nigeria and Mali. The fine-mapping population segregating for the LG 4 QTL consisted of 2,200 seeds, and is referred to as POP1. This population was analyzed by JIC. The QTL at the top of LG 1 was selected because it coincides with a QTL effective against *S. graminicola* isolates from Patancheru, India in the cross P7-3 x 843B, which is being analyzed in a different research project by JIC. This population, referred to as POP2, consisted of 1,000 seeds and was sent to UP for further mapping.

5. Identification of informative plants in the fine-mapping population (JIC and UP):

To fine-map a gene, it is necessary to first identify plants that carry a recombination event in the target region ('informative plants'). This is done most efficiently by genotyping the population with co-dominant polymerase chain reaction (PCR)-based markers flanking the region of interest.

POP1 (JIC): As reported under sub-activity 4, POPI was selected to segregate for the QTL on LG 4. However, this QTL was located at the end of LG 4 in the population PT 732B x P1449-2, and no distal flanking PCR-based markers were available that could be scored reliably in POPI. Therefore, an attempt was made to isolate microsatellites from bacterial artificial chromosome (BAC) clones that had been selected using distally located restricted fragment length polymorphism (RFLP) markers. This was complicated by the fact that the distal region of LG 4 in pearl millet is duplicated on LG 1: Although a microsatellite was isolated that was polymorphic between PT 732B and P1449-2, it mapped to LG 1. No microsatellites were obtained for LG 4.

In the meantime, RFLP analysis had also shown that the F_2 plant from which POP 1 had been generated was, although heterozygous for the marker proximal to the QTL and for a distally located marker, contained a homozygous P1449-2 interstitial segment. Because it was possible that the downy mildew QTL was contained on the homozygous segment, POP1 needed to be screened for downy mildew resistance as a matter of urgency to determine whether it was segregating for the disease resistance locus.

Because of lack of a distally located selective marker, 552 POP1 progeny were screened with the sequence-tagged-site (STS) marker PSM305 and the RFLP marker PSM84. PSM84 was located distal to PSM305, but its location relative to the downy mildew resistance gene was not known. One hundred and fifty plants that displayed a recombination event between PSM305 and PSM84 were selected for disease screening. These plants were grown to maturity and selfed. A number of RFLP markers with known location on LG 4 were mapped on POP1.

POP2 (UP): Two RFLP markers, PSM280 (=PSM464) and PSM858, were available that flank the target QTL on LG 1 in the cross PT 732B x P1449-2. However, the STS markers, derived from these RFLPs, failed to uncover polymorphisms between PT 732B and P1449-2 in a preliminary screen carried out by JIC. UP therefore directed its efforts towards the development of single nucleotide polymorphism (SNP) markers. Sequencing of the PT 732B and P1449-2 alleles for STS marker PSMP461 revealed a few basepair differences that were exploited for the development of allele-specific dominant markers. The dominant PT 732B and P1449-2 SNP markers can be used in combination to obtain a full classification of the POP2 progeny at that locus (Fig. 1).

The STS primers for the marker PSMP858 gave good amplification from the variety P1449-2, but weak amplification from PT 732B, probably due to the presence of a primer-template mismatch in PT 732B. Therefore, the clone PSM858, which had previously been end-sequenced only, was sequenced further. New primers were developed, and the amplification products from PT 732B, P1449-2 and three lines, two of which

were homozygous PT 732B (A2 and A3) and one that was homozygous P1449-2 (B) for markers at the top of LG 1 were sequenced. Exploiting the sequence differences between the alleles, two primer pairs were developed, F2 858/R 858 and F2 858/R2 858, that gave differential amplification of the A and B genotypes.

The F_4 seeds from POP2, obtained from JIC (see sub-activity 4) were sown and transplanted. Of the 52.4% surviving seedlings, 376 plants (74.3%) grew to maturity and were selfed. Genomic DNA was extracted from leaves of 1-month-old seedlings, and the plants were genotyped using the developed allele-specific markers for the loci *Xpsmp858* and *Xpsmp461.* Genotypic data was obtained at both loci for 357 lines, and 107 plants were identified that carried a recombination event between *Xpsmp858* and *Xpsmp461.* Approximately 150 seeds of 168 F_5 families were sent to SARI for field testing. All remaining seed was sent to JIC.

6. Field screening of F_4 families of the cross PT 732B x P1449-2 for downy mildew resistance (SARI):

The results obtained under sub-activity 3 had indicated that selected lines derived from the crosses PT 732B x P1449-2 and ICMP451 x H 77/833-2 and carrying only a single resistance QTL were not resistant to *S. graminicola* isolates from Ghana. It was therefore decided to test about 130 F_4 families from the cross PT 732B x P1449-2, and to use the phenotypic data in a QTL analysis to determine the presence of potential resistance QTL effective in Ghana. The screen was conducted in 2000 in duplicate by SARI. The disease incidence in the population varied from 0 to 100%. Using the software package QTL cartographer, a single QTL explaining about 40% of the variation was identified at the top of LG 1. However, this QTL was identified in only one of the replicate trials. It may correspond to the QTL under study in POP2. Interestingly, P1449-2 was completely disease free, while PT 732B was moderately susceptible. The population was also scored for plant height. A QTL for plant height, explaining about 35% of the variation and corresponding to the dwarfing gene *d2,* was identified on LG4.

7. Further evaluation of the lines PT 732B and P1449-2 (SARI):

Although the QTL study had identified only a single QTL in the cross PT 732B x P1449-2, and this in only one of the replicates, the parental varieties P1449-2 and PT 732B, which had been included in the trial, had shown no infection and moderate infection levels, respectively, when tested in the field in Ghana (see sub-activity 6). A hybridization program was, therefore, initiated with the aim of introgressing the resistance from PT 732B and P1449-2 into Manga nara, a local variety. The hybridization products and the parents were tested in the field in 2001 for resistance to downy mildew. Neither PT 732B nor the derivative from PT 732B displayed increased resistance compared to the control Manga nara. P1449-2, however, remained disease free throughout the trial, and is likely to provide a good source of resistance for the improvement of local cultivars.

8. Glasshouse screen of POP1 for downy mildew resistance [JIC in collaboration with Centre for Arid Zone Studies (CAZS)]:

The disease screen was carried out by Wendy Breeze, CAZS, University of Wales, Bangor, UK. The screening was conducted in triplicate on the 150 selected families, using a *S. graminicola* isolate from Niger. The population was segregating for disease resistance, and therefore the downy mildew resistance gene had to be located proximal to *Xrgc903,* the LG 4 marker that was homozygous for the P1449-2 allele in POP1 (see sub-

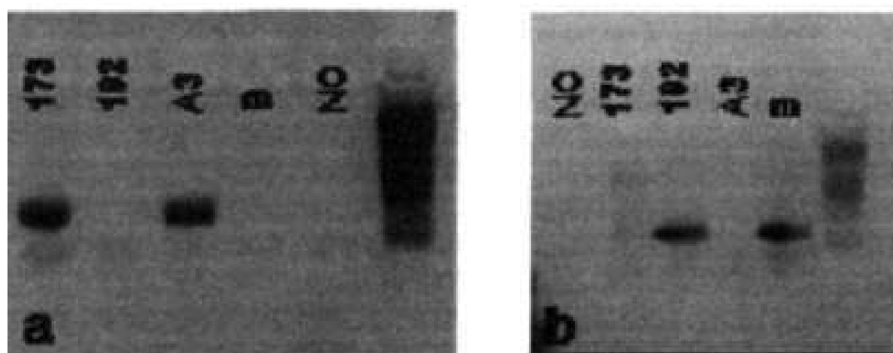

Figure 1. *Dominant SNP markers for locus Xpsmp46J using primer sets (a) SNP1/SNP5; and (h) SNP4/SNP5. (Note: The lines A3 and B are controls and are homozygous PT 732B and homozygous P1449-2, respectively, for markers at the top of LG 1; NO = No DNA control; 173 and 192 are* F_5 *lines from POP2.)*

activity 5). However, because the infection levels showed a continuous distribution, it was not possible to score the plants qualitatively as homozygous resistant, homozygous susceptible or heterozygous. To obtain an approximate position, we only considered F_3 families that displayed infection levels of <20% and >80% over the three replicates. The former were classified as homozygous resistant, and the latter as homozygous susceptible families. Scoring only those families that could be unambiguously identified as homozygous resistant or homozygous susceptible, the resistance gene *Dm2* was tentatively assigned to a 4 cM linkage interval. Rescreening of a subset of the F_3 families supported this location.

9. Saturation of the QTL region in POP1 with amplified fragment length polymorphism (AFLP) markers (JIC):

To saturate the *Dm2* region with more markers, an AFLP analysis was done on the parents, PT 732B and P1449-2, and on five homozygous susceptible and five homozygous resistant plants. One hundred and twenty-eight primer combinations yielded seven fragments that were polymorphic between the two parents, and between the resistant and susceptible lines. All fragments mapped proximal to *Xpsm84.* Six of these fragments have been cloned and sequenced.

10. Determination of the genetic/physical ratio in the QTL target regions (JIC):

BAC clones were isolated from several regions of pearl millet LG 1 and LG 4 using RFLP markers PSM280 (LG 1), PSM858 (LG 1) and RGR1963 (LG 4). The BAC end-clones, isolated from PSM280 and PSM858 co-mapped with the corresponding RFLP markers. Hence, no conclusions could be drawn on the ratio of physical/genetic distance at the top of LG 1. In contrast, four markers from LG 4, spanning a genetic distance of 5 cM and closely linked to *Dm2,* mapped to the same BAC. Restriction mapping further showed that three of these markers, which spanned 4.1 cM, were located on the same 15 kb fragment, giving a ratio of physical to genetic distance of less than 4 kb/cM. Chromosome walking, however, was hampered by the large amount of retroelements present in the pearl millet genome. Approximately 50 to 60% of BAC ends are highly repetitive, and cannot be used for the identification of overlapping BAC clones.

11. A comparative approach to isolating *Dm2* (JIC):

The publication of a draft of the rice *(Oryza sativa)* genomic sequence in January 2002, and the increasing availability of genomic information of specific chromosome regions from the Rice Genome Project (RGP)-led public sequencing effort (completion of the draft sequence was announced in December 2002), offered an alternative approach to isolating *Dm2.* Comparative genome analysis between pearl millet and rice had previously shown that the *Dm2* region corresponded to a region on rice chromosome 8. Rice genes, annotated on the sequenced BACs from the target region were used in BLAST searches against monocot EST (expressed sequenced tag) databases. Homologous ESTs were aligned, and primers were designed against conserved sequences. So far, five polymorphic markers have been mapped, and these more precisely delineate the region in rice that is orthologous to *Dm2.* Further fine-mapping of this region is being carried out by Sebastien Faure, a PhD student funded by the John Innes Foundation at JIC.

12. Mapping of the dwarfing gene *d2* (JIC):

One of the parents of POP1, PT 732B, was known to carry the recessive dwarfing gene *d2.* POP1, which was segregating for a large segment of LG 4 containing *Dm2* was also segregating for height. Plant height was scored as a quantitative trait by SARI in POP1, and QTL analysis had shown that the majority of the variation could be explained by a QTL on LG 4 (see sub-activity 6). Under glasshouse conditions in UK, the dwarf parent PT 732B was about 70% shorter compared to the tall parent P1449-2; and F_2 progeny of POP1 were scored qualitatively for tall or dwarf phenotype. They fell into two distinct height classes, with means comparable to the height of the parents. Twenty-three percent of the progeny were dwarfs, indicating that a single recessive gene, *d2,* was responsible for the difference in plant height between PT 732B and P1449-2 ($\chi^2_{3:1}$= 1.39, NS). Integration of the phenotypic data with the mapping data provided a map position for *d2.*

13. Field screen of POP2 for downy mildew resistance (SARI):

Seed of 168 F_5 families of POP2 was obtained from UP. Due to the low germination rates obtained, insufficient plants were available to conduct a meaningful field trial.

14. Generation of new markers in the downy mildew target regions using representational difference analysis (RDA) (UP).

The starting materials for RDA were two NILs in a background of 843B that differed for a downy mildew QTL at the top of LG 1, effective in India (see sub-activity 4). This QTL maps to the same interval as the

QTL in P0P2. The NILs were grown in the glasshouse; DNA was extracted and used as template for the optimization of the RDA protocol. DNA of the elite parent 843B was used as driver. DNA from the resistant NIL was used as tester. After the first cycle of subtraction-amplification, a faint band was detected. However, this band disappeared after a second round of subtraction-amplification. Despite several attempts, no enrichment of sequences with differentia] presence in the resistant and susceptible NILs could be obtained.

Development of transformation technology for pearl millet (carried out through a collaboration between CSIR Bio/Chemtek, Pretoria, South Africa; and University of Hamburg (UH), Germany).

1. Assessment of the regenerability of selected pearl millet lines (CSIR and UH):

Eight pearl millet genotypes, selected because of sensitivity to downy mildew, origin (inbreds and landraces) and agricultural importance, were assessed for their tissue culture amenability using different explants and culture media. The use of immature embryos proved more efficient than immature inflorescences due to the higher number of explants per donor plant and lower glasshouse requirements. For the leaf base cultures, only a small percentage produced proliferating callus. A range of different media was tested. The number of regenerants per embryo varied from 2 to 80. In addition to a system for regeneration of plants from immature embryos on solid medium, a liquid culture system was established from callus derived from immature embryos. This provided a second source for somatic embryogenic callus and gave 6-fold higher regeneration rates in a 2-fold shorter regeneration time.

2. Optimization of transformation technology (CSIR and UH):

Transformation was done with a Particle Inflow Gun (PIG) by CSIR and a BioRad Helium Gun by UH. To establish transformation technology in pearl millet, 5125 precultured immature zygotic embryos from the varieties 842B, Manga nara and Bongo nara (CSIR) or 2165 scutella from immature embryos from 841B, 7042, Manga nara and Bongo nara (UH) were bombarded with vector constructs containing the marker genes *uidA* and *bar.* Five transgenic plants, one derived from 842B (CSIR), two from Bongo nara (UH), one from Manga nara (UH) and one from 7042 (UH) were obtained. This corresponds to transformation efficiencies of 0.02% and 0.18%, respectively. Integration of the *uidA* and *bar* genes in the pearl millet genomic DNA was confirmed by Southern analysis.

3. Integration of broad spectrum resistance genes into pearl millet (CSIR and UH):

Because no downy mildew resistance genes had, as yet, been isolated, work was focused on the introduction of broad spectrum resistance genes that may be effective in improving resistance to downy mildew. Three genes with putative antifungal properties were used for bombardment. These include the hydrolytic enzyme β-1,3-glucanase, the antifungal peptide *Leapep20* and a defensin-like protein *ZmES4.* The *bar* gene was used as a selectable marker.

Screening for and analysis of putative transformants is ongoing. So far, two transgenic plants have been identified that carry the *Leapep20* gene construct. Southern blot hybridization experiments have shown that in one transformant the *Leapep20* construct has been integrated as a single copy, while multiple copies have integrated in a second transformant (Fig. 2). Expression analysis of the *Leapep20* gene in these transformants is in progress.

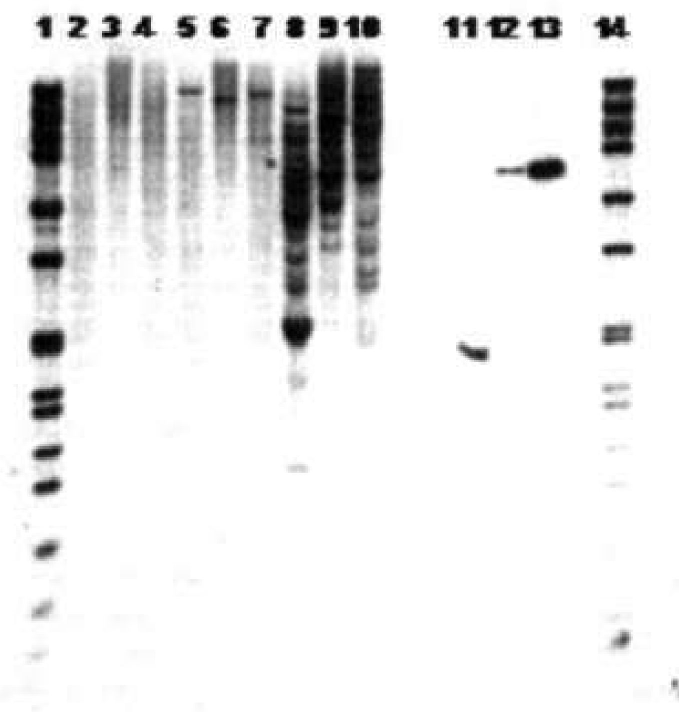

Figure 2. Southern blot of Leapep20 transformants LI and L2. [Note: Lanes 1, 14: Marker; Lanes 2, 3, 4: genotype 7042; Lanes 5, 6, 7: T_0-L1; Lanes 8, 9, 10: T_0-L2; Lanes 11, 12, 13: Plasmid control.
Lanes 2, 5, 8, 11: Excising cassette (EcoRl + Hindill);
Lanes 3, 6, 9, 12: Linearizing vector (EcoRI);
Lanes 4, 7, 10, 12: Linearizing vector (Hindlll).]

Conclusions

The project has successfully established a transformation system for pearl millet. Although transformation efficiencies are currently low, work will continue towards improving the technology. A year's funding to achieve this objective and to analyze the putative transformants generated during the EU project has been secured through the DFG Germany/South African bilateral funding scheme (UH and CSIR).

Considerable progress has also been made towards the isolation of a downy mildew resistance gene. The *Dm2* gene has been located to a 4 cM interval. The publication earlier this year of the rice genomic sequence presented us with a tool to exploit our molecular markers to delineate the orthologous region in rice, which can then be used as a source for further markers or even candidate genes. It has also been shown that recombination in the vicinity of *Dm2* is high, with a genetic to physical ratio of 5 kb/cM. We are therefore optimistic that we will be able to isolate the first downy mildew resistance gene over the next year. The research is being continued at JIC through a John Innes Foundation Studentship until September 2003.

The collaborative project has also led to the testing of new genotypes in Ghana. One such line, P1449-2, was infection-free during two years of testing in the downy mildew nursery in Ghana. The use of this line in the breeding program for the improvement of local varieties is currently being explored. The nutritional composition and functional properties of the new pearl millet lines will be determined for their industrial potential by small- and medium-scale food entrepreneurs in Ghana.

Agronomy

Screening Pearl Millet Germplasm for Tolerance to Soil Salinity

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Introduction

Saline soils account for up to 580 million ha worldwide and are widespread in arid and semi-arid regions (Rengasamy 2002). Pearl millet (*Pennisetum glaucum)* is often grown in saline soils and is known to be relatively better in tolerance to salinity than other crops, particularly maize (*Zea mays)* or legumes (Ashraf and McNeilly 1987, Dua 1989). However, a well-focused search can lead to the identification of genotypes with superior tolerance. Since pearl millet is usually grown rainfed with minimum input, it is all the more important to genetically improve the adaptation of this crop to soil salinity. The improved salinity tolerant lines together with cultural management options provide greater scope for improving the crop productivity in these saline soils.

Most crop species are sensitive to salt stress during all stages of plant development, including seed germination, vegetative growth and reproductive growth. Variation in whole-plant reaction to salinity provides the most efficient initial screening for salinity tolerance (Shannon 1984, Ashraf and McNeilly 1987, Ashraf and McNeilly 1992). Therefore, the objective of this study was to screen a wide range of improved hybrid parents and germplasm lines of pearl millet for relative ability to produce more biomass under salinity during pre-anthesis stage.

Materials and methods

One hundred entries of pearl millet comprising popular varieties, hybrids and progenies were grown in a greenhouse at 20-28°C in a randomized complete block design (RCBD) with three replications. There were two salinity treatments: (1) Control: irrigated with deionized water; and (2) Saline: irrigated with 250 mM NaCl solution (EC 23.4 dS cm^{-1}), once at the time of sowing and later irrigated with deionized water. Plastic pots (12.5 cm diameter) were sealed at the bottom and filled with 1.2 kg of Alfisol mixed with diammonium phosphate at 0.25 g pot^{-1}. Sixteen seeds of each entry were sown on 29 March 2003 in four equally spaced hills in each pot and irrigated with deionized water or saline solution to

field capacity previously estimated for the soil. To avoid waterlogging during subsequent irrigations, the water needed was determined by regular weighing of representative pots. A maximum of four plants pot^{-1} were retained after thinning at 10 days after sowing (DAS) in the control. However, thinning was necessary in few saline pots, as most of them did not have the required four plants pot^{-1}. One plant per pot was sampled at 18, 25, 32 and 39 DAS. While sampling, plants were always reserved for later sampling dates; for example, if there were two plants pot^{-1} they were reserved for the third and fourth sampling. Each sampled plant was separated in root (extractable) and shoot, oven-dried at 60°C for 3 days and the dry mass then recorded. The total plant biomass for each sample was subjected to ANOVA as a two factor RCBD and the genotypic means were obtained. All the four individual sample genotypic means of total biomass produced under saline condition and the four calculated ratios of total biomass under saline condition as that of the control were used for clustering the entries into different classes using Numerical Taxonomy and Multivariate Analysis System (NTSYSPC), version 2.1 from Exeter Software, New York, USA. A similarity/ dissimilarity matrix was obtained based on Euclidean distances and thus the entries were grouped on the basis of UPGMA (unweighted pair-group method of arithmetic average).

Results and Discussion

The pearl millet genotypes emerged in 6 to 9 DAS in the pots irrigated with saline water whereas those in the control pots emerged within 3 to 4 DAS. However, many test entries did not emerge in the saline pots, but wherever emergence occurred, the number of seedlings were few (data not shown). Differences among the genotypes and genotype x salinity interactions existed at all stages of sampling for both absolute and relative weights (Table 1). Cluster analysis on the basis of absolute and relative biomass for four growth stages indicated about 4 major groups with a similarity coefficient of 40%. Eight entries with a skewed performance at one or two stages were excluded and grouped separately. The pots where one or two plants emerged were harvested at the fourth, or third and fourth sampling time and the sparse population in these pots permitted them to grow with relatively more vigor and less competition. Thus, though these ranked the least at the early stages (as the mean values were 0), their later performance was high. However, the rest of the genotypes can be grouped into highly sensitive, sensitive, tolerant and highly tolerant entries based on the group means of the total biomass and relative biomass in all four sampling periods (Tables 2 and 3). Almost all the entries that emerged poorly under irrigation with saline water were classified as highly sensitive. However, it is quite possible that some of the entries of this category might have the capacity to produce higher shoot dry mass at later stages if emerged successfully. Such a condition can be expected to prevail where saline water irrigations are practiced (Francois et al. 1994). Most of the highly tolerant entries such as IP 3757 are either previously documented to be tolerant or grown in Rajasthan, India where the soils are often saline (CZI 9621 bred by the Central Arid Zone Research Institute and RIB 3135-18 bred by the Rajasthan Agricultural University). From most of the populations, at least one highly tolerant progeny and one sensitive or highly sensitive progeny were identified. Some of the B-lines currently in use for hybrid development such as ICMB-00888, ICMB-91444, ICMB-93333 and ICMB-98222 also fall under the salinity tolerant category.

These experiments are being repeated to confirm the salt tolerance reaction of the 100 test entries. Also, determination of various ionic compositions of the plant tissues is being carried out to delineate the mechanisms of salt tolerance. The same material is being tested at the International Center for Biosaline Agriculture (ICBA), Dubai, UAE as part of a collaborative project on salinity tolerance.

Table 1. Analysis of variance and its significance for salinity treatments, pearl millet entries and their interactions for the total dry matter $plant^{-1}$ of samples at different days after sowing (DAS).

Source of variation	Mean sum of squares and significance level[1]			
	14 DAS	25 DAS	32 DAS	39 DAS
Salinity levels (S)	16.03***	96.12***	249.66***	48768***
Pearl millet entries (G)	0.012***	0.097***	0.29**	1.07*
S x G	0.012***	0.087**	0.30**	115*
Residual	0.007	0.059	0.20	0.82

1. * = Significant at P = <0.05; ** = Significant at P = <0.01; *** = Significant at P = <0.001.

Table 2. Cluster group means of total biomass (g plant^{-1}), the ratio of total biomass under 250 mM saline condition as that of control on 18,25,32 and 39 days after sowing (DAS) and the comparative reaction of the tested pearl millet entries.

Pearl millet entries	18 DAS		25 DAS		32 DAS		39 DAS		
	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	Reaction[1]
30	0.004	0.014	0.008	0.008	0.018	0.013	0.158	0.055	Highly sensitive***
23	0.018	0.060	0.043	0.054	0.105	0.080	0.739	0.306	Sensitive***
29	0.023	0.069	0.071	0.085	0.218	0.157	1.197	0.487	Tolerant ***
10	0.036	0.102	0.242	0.283	0.485	0.342	0.974	0.373	Highly tolerant*
8	0.025	0.059	0.103	0.108	0.289	0.223	1.951	0.759	Highly tolerant* (needs confirmation)

1. Pair-wise analysis of means by multivariate analysis showed that the clusters listed with *** were different at 0.001 level of probability and * were different at the 0.05 level.

Table 3. Pearl millet entries grouped on the basis of pre-anthesis total biomass production under 250 mM saline water irrigated condition and the ratio of biomass under salinity as that of control.

Group	Entries
Tolerant	RCB-2-S1-33-1-3-2-2, ICMR 312-S1-17-2-3-1-2. MC 94 C2-S1-3-2-2-2, IP 3732,ICMV 91059-S1-17-3-3-1-2, MC 94 C2-S1-33-1-3-2, ICMR 312-S1-17-3-2-1-2, SDMV 90031-S1-60-1-1-2, ICMB 01222, MC 94 C2-S1-3-2-1-1, ICMB 98777, ICMR 356, MC 94 C2-S1-66-1-2-2, ICMP-451, CZI 98-11, ICMB 94555, ICMB 95111, AIMP 92901-SI-520-1-3-1, ICMB 95333, ICMR 312-S1-22-1-3-2-1, ICMB 02111, ICML 22, RCB-2-S1-43-3-4-2, ICMR 312-S1-22-1-3-2-1, ICMS 7704-S1-51-5-1-2. MC 94 C2-S1-36-1-3-2, 841 B, J 104 Selection, RIB 335/74 (RHB 30 Pollinator)
Highly tolerant	RCB-2-S1-24-2-3-1-2, ICMS 8511-S1-17-2-1-2. ICMB 93333, MC 94 C2-S1-3-1-1-2, HTP 94/54 (HHB 146 pollinator), ICMV 91059-S1-11-3-3-3-2, MC 94 C2-S1-89-4-2-2, ICMB 98222, RCB-2-S1-40-1-1-2-2, IP 3757, RCB-2-S1-19-2-2-1-2, ICMS 8511-S1-14-2-2-2, CZI 9621, RIB 3135-18 (RHB 121 pollinator), ICMV 91059-S1-4-2-3-2-2, ICMB 91444, SDMV 90031-S1-26-3-1-2, ICMB 00888

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Strip-till Establishment of Pearl Millet

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Introduction

Soil conserving tillage practices are becoming increasingly common in the southeastern United States. The techniques are not equally applicable to all crops. Various growers have reported difficulties in establishing stands of pearl millet (*Pennisetum glaucum*) with minimum tillage. These experiments were conducted to identify potential difficulties and limitations expected in strip-till establishment of pearl millet.

Materials and Methods

In all experiments, the experimental pearl millet hybrid 'Tifgrain 102' was planted in rows spaced 0.9 m apart at the rate of 2.8 kg ha^{-1}. Prior to planting pearl millet, bahiagrass (*Paspalum notatum*) or rye (*Secale cereale*) was mowed to a height of 15 cm, and sprayed with glyphosate at 1.1 kg ai ha^{-1} approximately 5 days prior to planting. For strip tillage plots, subsoiler shanks were set to a depth of 35 cm, and seed was dropped behind fluted coulters. Soil was firmed over the seed by rollers with a chain drag. Weeds were controlled by glyphosate applications from hooded sprayers.

For conventional tillage plots, soil was turned to a depth of 25 cm, and seed was planted with a grain drill. Weeds were controlled by glyphosate applications from hooded sprayers and by cultivation. Plots were fertilized by broadcast application of fertilizer (5-10-15 NPK) at 280 kg ha^{-1}.

Two experiments were conducted in 2001. In the first experiment, stand establishment in perennial bahiagrass pasture was evaluated. The experiment was planted in a field that had been divided into two replications each of Tifton 9, which tends toward a sod-forming growth habit, and Tifton 23, which has an upright growth habit. The test was arranged in a strip-plot design with bahiagrass cultivar as the main plot, and with tillage treatment (one or two passes with the subsoiler) as subplots. Seedlings were counted on 20 June, 21 days after planting within ten sub-samples (1 m length in each of four, two-row beds) within each replication. Seedling counts for each two-row sub-sample were averaged prior to analysis.

In the second experiment, treatments consisted of strip-till planting in rye stubble, with comparisons between either one or two passes with the subsoiler shank, or conventional tillage. The experiment was arranged in a strip-plot design with seven replications. Seedlings were counted (21 days after planting) on 20 June 2001 in ten sub-samples consisting of 1 m of two-row beds within each replication. Seedling counts for each two-row bed sub-sample were averaged prior to analysis.

In 2002, season-long comparisons were made between pearl millet grown by strip tillage in rye stubble (second year minimum tillage) and conventional tillage. Plots (eight two-row beds x 25 m length) were arranged in a randomized complete block design with four replications. Within each tillage treatment, transects were established and stand counts (seedlings m^{-1}) were taken on 16 July within ten pre-determined and marked sub-sections of each plot. Each tillage treatment had 10 subplots (3 m x 2 rows). Percentage foliage affected by bacterial stripe (*Acidovorax avenae*) was assessed on 10 August. Foliar necrosis due to chinch bug (*Blissus leucopterus leucopterus*) was assessed on 26 August. After cross-pollination, ten panicles were bagged in each subplot. On 6 September, numbers of lodged and standing culms were counted. Weed populations by species was determined within subplots. All plant biomass within the subplots was harvested on 18 September, and pearl millet and weed biomass was separated, dried and weighed.

Results and Discussion

In 2001, although the bahiagrass cultivars differed in their growth habit, pearl millet stand establishment did not differ between Tifton 23 (3.5 plants m^{-1}) and Tifton 9 (3.4 plants m^{-1}) ($LSD_{p=0.05}$= 1.2). Stand establishment was affected by tillage treatment. Greater seedling stands were obtained after two passes with a subsoiler shank (3.8 plants m^{-1}) compared to one pass (3.0 plants m^{-1}) ($LSD_{p=0.05}$ = 0.5).

In the comparison of conventional and strip tillage in rye stubble, stand was affected by tillage treatment. The conventional tillage had greater stands (6.9 plants m^{-1}) compared to either strip-tillage treatment of two subsoiler passes (4.8 plants m^{-1})or one subsoiler pass (4.2 plants m^{-1}) in rye stubble ($LSD_{p=0.05}$ = 0.9).

Although statistical comparisons between the two experiments conducted in 2001 cannot be made, trends could be observed from these experiments that were planted on the same day, with the same methodology and in fields a few hundred meters apart. Planting after two passes of a subsoiler shank through perennial grass

Table 1. Comparisons of tillage practices for pearl millet planting at Tifton, Georgia, USA in 2001.

Treatment	Stand (seedlings m^{-1})	Bacterial stripe (%)	Lodged culms (%)	Weed:millet biomass	Grain yield (kg ha^{-1})
Conventional	9.8	4.1	46.8	0.14	1906
Strip tillage	7.3	5.6	65.4	0.53	2041
$LSD_{p=0.05}$	0.7	1.2	8.1	0.14	NS[1]

1. NS = Not significant.

resulted in better stands than a single pass, probably due to more effective soil disruption that resulted in better seed-soil contact. A numerical improvement was observed in stands after two subsoiler passes in rye stubble compared to one pass, but the difference was not significant. The crown and root system of the rye was less dense than that of the perennial bahiagrass. When planting into a rye base, a single pass of a subsoiler shank was adequate. Stand establishment in conventionally tilled plots was superior to that in the strip-tilled plots. Differences in stand establishment based on the prior crop was previously observed when pearl millet was minimum-tilled into canola *(Brassica rapa)* or wheat (*Triticum aestivum*) residue (Wilson et al. 1999).

In 2002, tillage treatment affected most of the test parameters. As in 2001, better stands were obtained in conventional tillage compared to strip-tillage plots (Table 1). This observation contrasts with the results of Spitalniak et al. (1995), who found better emergence in strip-tilled plots. Early season foliar blight predominantly consisted of bacterial stripe, and severities were greater in strip-tilled plots than in conventional tillage plots. Later season foliar necrosis was predominantly due to chinch bug damage, which averaged 38.2% and did not differ between treatments. Lodging was considerably greater in the strip-tilled plots.

The ratio of weed:millet biomass was greater in the strip-tilled plots. The two most common grass weeds were Texas panicum (*Panicum texanum*) and large crabgrass (*Digitaria sanguinalis*). Biomass of these weeds averaged 582 and 376 kg ha^{-1} in strip-tilled plots, and 222 and 90 kg ha^{-1} in conventional tillage plots, respectively. We observed that chinch bug populations tended to be greater within crabgrass-infested plots. The greater weed infestations in these strip-tilled plots probably served as a refuge for the chinch bugs, resulting in the high level of lodging in this test.

Grain yield did not differ between the tillage treatments; however, these yields were determined by hand harvest. Combine yields would likely differ due to the high level of lodging. Stand establishment difficulties in strip-tilled plots encountered by farmers were confirmed. Establishment was most difficult in the conversion of a perennial grass pasture, and better when strip-tilling into rye stubble. Particular attention must be given to address the greater potential for problems resulting from diseases, grass weeds and chinch bugs in strip-tilled pearl millet.

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Physiological Basis of Yield and Influence of Diurnal Temperature on Growth and Development in Finger Millet

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Introduction

Finger millet (*Eleusine coracana*) is mostly cultivated in marginal lands in India over a wide range of geographical areas and agro-ecological diversity. The productivity of finger millet is low in the hills of the Garhwal region when compared to other parts of India. Absence of significant corelation of various component characters with yield at high altitude (Bandyopadhyay 1999) suggested that low grain yield is perhaps associated with

sensitivity of certain physiological processes to environment resulting in production of less number of grains per unit area (Magrin et al. 1993). The random pattern of development of fewer seeds by florets and/or the failure of realizing total yield potential in finger millet is presumed to be associated with poor floret site utilization (FSU) either due to inadequate supply of assimilate to sustain seed growth at all pollinated sites (Hampton 1988), disorder in physiology related to pollination and fertilization process (Howe and Westley 1986), defects in developmental morphogenesis of shoot apex in the early stages of crop growth (Rahman and Wilson 1978), genetical causes (Marshall and Ludlam 1989) or cytological causes. Research in other crops did elucidate the differences in final grain yield due to both environmental conditions (Fischer 1985) and genetic improvement (Slafer et al. 1994). An understanding of the climatic factors controlling flowering and seed production helps not only in identifying high productive environment for finger millet cultivation around higher hills in the Garhwal region, but also for selecting superior high-yielding adaptable genotypes that induce stability into a production system. In this study, finger millet cultivars were examined to explain the physiological basis of yield and the influence of environmental factors on yield components.

Materials and Methods

Cultivars TNAU 874 from Coimbatore and GPU 45 from Bangalore were sown on 12 June 2000 and 11 June 2001 at an altitude of >2100 m above mean sea level at Ranichauri (30° 15' E and 78°2' N) in the Garhwal region. On the basis of flowering behavior, individual plants of the two cultivars were classified into three groups: early (M_1)(105 days), intermediate (M_2)(112 days) and delayed (M_3)(119 days). Eighty-one randomly selected plants were considered within each group for each cultivar for recording observations on the following physiological characters: IOO-seed mass (SW) (g); average mass of head (AWH) (g); number of fingers per head (NFH); number of florets per finger (SPF); number of florets per spikelet (FSP); Number of seeds per spikelet (SSP); days to flowering (DF); and days to maturity (DM).

FSP and SSP were used for estimating FSU (%) on individual plant. Four derivatives (in degree days) from day and night temperatures were recorded during the study period: (1) night thermal time during (pre-flowering) vegetative phase (NTV); (2) night thermal time during grain-filling (post-flowering) stage (NTM); (3) cumulative value of diurnal temperature differences during vegetative phase (DTV); and (4) cumulative value of diurnal temperature differences during grain-filling stage (DTM).

Average values of two cultivars for respective flowering groups of individuals and for two years were subjected to statistical analysis. Significant differences in mean values between populations for individual characters were compared using t-test. The observed value of AWH for individual flowering groups, were compared with theoretically determined expected value of AWH separately to substaintiate the physiological basis of yield through Chi-square (x^2) analysis. The theoretical value of expected AWH was obtained through physiological model by employing the formula:

$$NFH \times SPF \times SSP \times SW$$

Three sets of correlation and path analysis were computed for the two cultivars in different flowering groups. In the first set, NFH, SPF, FSP, SSP, FSU and AWH were considered to determine relative influence of individual component characters on AWH. To examine the influence of environment on FSU and SSP two separate correlation and path analyses were performed. In the second set, NTV, DTV and FSU were considered to observe the relative influence of environment on FSU and in the third set, NTM, DTM and SSP were considered for studying the effect of environment on SSP.

Results and Discussion

Significant variation was observed in most of the characters recorded among the three flowering groups of finger millet cultivars (Table 1). It was apparent that AWH gradually tended to decline with delay in flowering. A high coefficient of variation (CV) was registered (above 33%) in AWH irrespective of different groups of flowering individuals. On the contrary, SSP and FSU recorded high CV within intermediate (M_2) and delayed (M_3) flowering groups. It was, therefore, suggested that the productivity and stability of cultivars was impaired perhaps due to the expression of non-adaptable deleterious genes (Fasoula and Fasoula 1997). The comparison between actual and expected values of AWH showed no substantial differences, substantiating the physiological basis of yield.

Correlation coefficient (Table 2) revealed that both FSU and SSP had direct positive significant relation with AWH across early, intermediate and delayed groups of flowering. Path analysis suggested that predominant influence of FSU appeared in the early flowering (M_1) group as indicated by the presence of maximum positive direct effect of FSU on AWH, while SSP had lower values. It was therefore presumed that AWH was mostly affected by the supply of insufficient assimilates to sustain the seed growth at all pollinated sites perhaps due to increase in SSP and due to greater competition for assimilates.

Table 1. Statistical analysis of some physiological characters in finger millet populations in the Garhwal region, India, 2000 and 2001[1].

Population[2]	SW	NFH	AWH	FSU	SPF	FSP	SSP	DF	NTV	DTV	DM	NTM	DTM	AWH[3]	Chi-square analysis
Mean															
T_1	0.24	7.40	4.14	76.35	69.12	4.32	3.30	105.97	1658.7	807.67	63.59	857.33	422.82	4.05	0.02
T_2	0.26	6.88	2.15	34.50	60.60	4.91	1.68	112.09	1735.8	873.79	66.87	518.50	784.60	1.79	0.07
T_3	0.23	6.62	0.52	10.43	64.02	5.10	0.53	119.14	1823.9	940.18	78.04	572.01	799.85	0.51	0.00
G_1	0.30	8.13	4.92	58.48	62.01	5.21	3.06	105.95	1657.1	805.74	63.17	851.66	419.49	4.62	0.02
G_2	0.27	9.22	2.09	23.61	60.88	5.53	1.30	111.90	1732.9	872.60	67.12	520.62	788.06	1.97	0.07
G_3	0.23	6.18	0.37	9.81	57.28	5.18	0.50	119.12	1823.5	939.98	78.00	572.01	799.85	0.40	0.00
t-test															
T_1-T_2	+	–	+	+	+	+	+	+	+	+	+	+	+	–	–
T_1-T_3	–	+	+	+	+	+	+	+	+	+	+	+	+	–	–
T_2-T_3	+	–	+	+	+	+	+	+	+	+	+	+	+	–	–
G_1-G_2	+	+	+	+	–	+	+	+	+	+	+	+	+	–	–
G_1-G_3	+	+	+	+	+	–	+	+	+	+	+	+	+	–	–
G_2-G_3	+	+	+	+	+	+	+	+	+	+	+	+	+	–	–
T_1-G_1	+	+	+	+	+	+	+	–	–	–	–	–	–	–	–
T_2-G_2	–	+	–	+	–	+	+	–	–	–	–	–	–	–	–
T_3-G_3	–	–	+	+	+	–	–	–	–	–	–	–	–	–	–
CV (%)															
T_1	28.68	23.67	46.66	13.19	23.22	11.52	14.75	1.53	1.54	1.83	2.45	2.44	3.16	–	–
T_2	12.73	29.24	92.23	66.97	19.98	6.94	65.42	1.54	1.51	1.58	2.47	2.49	2.49	–	–
T_3	18.26	29.76	72.52	36.73	11.16	7.00	41.52	1.37	1.36	1.39	2.14	2.11	2.14	–	–
G_1	14.98	31.37	51.19	22.92	13.61	7.61	23.17	1.25	1.57	1.60	2.65	2.62	2.65	–	–
G_2	15.00	24.68	77.39	55.69	8.80	6.91	53.27	1.46	1.50	1.44	2.41	2.41	2.39	–	–
G_3	19.98	37.56	81.16	60.75	11.75	8.10	58.07	1.41	1.43	1.40	2.14	2.11	2.14	–	–

1. SW = 100-seed mass; NFH = Number of fingers per head; AWH = Average mass of head; FSU = Floret site utilization; SPF = Number of florets per finger; FSP = Number of florets per spikelet; SSP = Number of seeds per finger; DF = Days to flowering; NTV = Night thermal time during vegetative phase; DTV = Cumulative value of diurnal temperature differences during vegetative phase; DM = Days to maturity; NTM = Night thermal time during grain-filling stage; DTM = Cumulative value of diurnal temperature differences during grain-filling stage.
   + = Significant; – = Not significant.
2. Cultivars: T = TNAU 874, G = GPU 45. Subscript: 1 = Early flowering individuals; 2 = Intermediate flowering individuals; 3 = Late flowering individuals.
3. Theoretical determination of expected value of AWH estimated through physiological model.

Table 2. Path coefficient analysis of major yield component characters of finger millet within three flowering groups of two cultivars[1].

Flowering group[2]	Components[3]	FSU	NFH	SPF	FSP	SSP	Correlation coefficient of AWH[4]
M_1	FSU	0.60	0.00	0.07	-0.35	-0.09	0.24*
	NFH	0.00	0.35	0.00	-0.00	0.00	0.36**
	SPF	0.13	0.00	0.32	0.26	-0.00	0.19*
	FSP	-0.28	0.00	0.11	0.74	-0.02	0.31**
	SSP	0.45	0.00	0.12	0.13	-0.12	0.48**
M_2	FSU	-0.44	0.01	0.00	0.01	1.22	0.81**
	NFH	-0.01	0.33	0.02	-0.02	0.08	0.41**
	SPF	-0.01	0.04	0.16	0.00	0.03	0.23*
	FSP	0.13	0.11	-0.00	-0.06	-0.22	-0.04
	SSP	-0.43	0.02	0.00	0.01	1.23	0.84**
M_3	FSU	-1.51	0.01	0.00	0.01	2.16	0.63**
	NFH	-0.05	0.46	0.09	-0.00	0.09	0.56**
	SPF	-0.07	0.07	0.13	0.02	0.05	0.20*
	FSP	0.17	0.01	-0.02	-0.01	0.03	0.10
	SSP	-1.49	0.01	0.00	-0.00	2.20	0.72**

1. Test cultivars TNAU 874 and GPU 45.
   Diagonal values are direct effect and off-diagonal values are indirect effect within individual flowering groups.
2. M_1 = Early flowering plants; M_2 = Intermediate flowering plants; M_3 = Delayed flowering plants.
3. FSU = Floret site utilization; NFH = Number of fingers per head; SPF = Number of florets per finger; FSP = Number of florets per spikelet; SSP = Number of seeds per spikelet.
4. AWH = Average mass of head; * = Significant at 5% level. ** = Significant at 1% level.
   Residual effects for M_1, M_2 and M_3 are 0.4806, 0.1390 and 0.1933, respectively.

Pollination and fertilization process was most effective in increasing the sink capacity per plant with exposure to favorable climatic condition. High residual effect on the contrary suggested that the association of five characters (Table 2) was not sufficient to explain the total variability in AWH among the finger millet cultivars. Incorporation of more number of characters would be required to explain the variability more precisely. For intermediate (M_2) and delayed (M_3) flowering groups, SSP had the major positive direct and indirect effect on AWH (Table 2), while the relative importance of FSU gradually declined. This suggested that the physiological processes associated with pollination and fertilization were impaired with exposure to unfavorable suboptimal low temperature condition, which in turn reduced the competition for sharing the assimilates, to sustain effective seed growth at all pollinated sites. The residual effect also suggested that with the advent of stress environment approximately 80 to 90% variability of AWH could be explained through the six characters of finger millet cultivars. The association between FSU with DTV and NTV and between SSP with DTM and NTM was not significant (Table 3). This and high residual effect suggested that the dynamics of the environment influence on FSU and SSP could not be explained using the night and diurnal temperature variation.

It was apparent from the present investigation that the physiological basis of yield in finger millet cultivars remained similar across different flowering groups. The variability of AWH could be better explained in intermediate (M_2) flowering group of cultivars, where SSP appeared as the major component character that contributes to yield. The influence of FSU in early flowering (M_1) group, however, explained that variability in AWH and reduced contribution of SSP to yield could be due to increase in competition to sustain the seed growth at all pollinated sites.

Table 3. Path coefficient analysis of major environmental factors on FSU and SSP within three groups of finger millet[1].

Factor	NTV	DTV	FSU	R^2
M_1				
NTV	0.001	0.004	0.005	
DTV	0.000	0.022	0.022	1.00
M_2				
NTV	-0.012	0.028	0.016	
DTV	-0.002	0.087	0.085	0.99
M_3				
NTV	1.004	-1.001	0.003	
DTV	1.005	-1.000	0.005	1.00
	NTM	DTM	SSP	R^2
M_1				
NTM	0.002	-0.029	-0.027	
DTM	0.000	-0.063	-0.062	0.99
M_2				
NTM	-2.983	3.003	0.020	
DTM	-2.977	3.010	0.032	0.91
M_3				
NTM	-0.093	0.007	-0.086	
DTM	-0.088	0.008	-0.079	0.99

1. Diagonal values are direct effect and off-diagonal values are indirect effect within individual flowering groups.
   NTV = Night thermal time during vegetative phase; DTV = Cumulative value of diurnal temperature differences during vegetative phase; FSU = Floret site utilization, NTM = Night thermal time during grain-filling stage; DTM = Cumulative value of diurnal temperature dilcrcnces during grain-filling stage; SSP = Number of seeds per finger.
   M_1 = Early flowering plants; M, = Intermediate flowering plants; M_1 = Delayed flowering plants.

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Pathology

Effect of Head Blast on Grain Mass and Grain Color in Finger Millet

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Head blast caused by *(Pyricularia grisea),* is a serious disease of finger millet (*Eleusine coracana*) in Karnataka, India. Most of the popular varieties are susceptible to the disease. The disease is known to affect ear heads and grain, so much so, even the grain of resistant varieties is affected. In this study, 15 genotypes comprising five each of resistant, moderately resistant and susceptible groups were assessed for yield loss in Bangalore, Karnataka, India. These fifteen genotypes were raised in a randomized complete block design with three replications. At maturity, infected and healthy ear heads in each group were harvested separately, threshed, and grain mass and number of black grain were assessed. Loss due to head blast was assessed by harvesting blast affected and healthy plants separately in each genotype. Loss in 1(X)0-grain mass and ear head mass were assessed in relation to healthy plants of each genotype. The incidence of black grain was assessed in each ear head.

The results are presented in Table 1. The extent of loss in 1000-grain mass in head blast affected ear heads ranged from 3 to 6% in resistant genotypes, 9 to 16% in moderately resistant group, while it ranged from 24 to

Table 1. Effect of head blast on 1000-grain mass, ear head mass, and incidence of black grain in finger millet.

Genotype	Loss in 1000-grain mass (%)	Loss in ear head mass (%)	Incidence of black grain (%)
Resistant			
GE 632	6	10	15
GE 669	6	9	2
GE 676	3	8	8
GE 696	3	14	3
GE 705	5	7	8
Moderately resistant			
GE 637	14	15	14
GE 639	16	13	11
GE 692	13	6	19
GE 710	10	8	16
GE 728	9	15	23
Susceptible			
GE 635	30	33	24
GE 649	25	35	34
GE 651	27	50	37
GE 688	35	47	32
GE 712	24	37	27
SEm±	0.0604	0.0274	0.2653
CD at 5%	0.1831	0.0831	0.8047

35% in susceptible genotypes. In fact, the average annual loss in yield of finger millet due to blast has been reported to be 28% (Viswanath et al. 1997). The trend was similar with the loss in total ear head mass which ranged from 7 to 14% in resistant, 6 to 15% in moderately resistant, and 33 to 50% in susceptible groups. Similarly, the incidence of black grain ranged from 2 to 15% in resistant, 11 to 23% in moderately resistant, and 24 to 37% in susceptible groups. Black grains were also seen in apparently healthy ear heads. Thus, it is imperative to take note of these parameters, in addition to looking for the extent of the incidence of neck blast, while choosing lines resistant to blast.

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Components of Slow Blasting Resistance in Finger Millet

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Introduction

Finger millet (*Eleusine coracana*) is a staple food crop in southern Karnataka, India and is grown over an area of 1 million ha with production of 1.5 million t. The crop is damaged by blast, caused by *Pyricularia grisea,* especially during the rainy season. The disease causes 28% loss annually (Viswanath et al. 1997). The economic returns of the crop do not permit application of fungicides. Among the released cultivars only two varieties, GPU 26 and GPU 28, possess good level of resistance to blast and thus farmers have limited choice. Moreover, the pathogen being highly variable (Hegde 1996), a broad-based resistance could be useful. The slow blasting resistance or partial resistance is a phenomenon wherein the resistance is governed by many genes, each gene adding for resistance. Such resistance is unlikely to break down as mutation against all these genes in the pathogen is unlikely. Preliminary studies indicated the existence of such genotypes in finger millet (Sunil 2002). In this study, the early events of infection by the blast pathogen and the components of resistance to blast are reported.

Materials and Methods

From the initial field screening of 100 finger millet genotypes during the rainy season (August-November) 1999, 25 genotypes were selected for intensive screening at the University of Agricultural Sciences, Bangalore, Karnataka, India during the rainy season 2000. These were screened in four independent replicated field trials sown on different dates. Based on the host reaction **to**

blast, eight genotypes were selected for this study. These were GEs 632, 637, 669, 674, 676, 705, 718 and 728 along with two susceptible checks GE 649 and GE 712. These lines were raised in the field in a plot size of 2.5 m x 3 m for each genotype, which was replicated thrice. There were 250 hills per plot. The disease was allowed to develop from natural infection. To study the components of resistance, five plants were randomly selected in each replication. Three leaves from each plant from middle canopy were chosen to record size of the lesion and number of conidia per lesion. At the crop maturity stage, the length of the neck lesion and the incidence of finger blast were recorded from five randomly selected plants in each replication.

The early events of infection by *P. grisea* were studied under laboratory conditions using two resistant genotypes (GE 669 and GE 705) as well as two susceptible genotypes (GE 649 and GE 712). These genotypes were raised in pots in a greenhouse. About 12 mm length bits from fully unfolded leaves (3rd to 5th from top) were cut and placed on a sponge sheet soaked with sterile water amended with 2 ppm cytokinin. A drop of conidial suspension 4 x 10^3 conidia ml^{-1} was placed on each leaf disc, which was placed on a sponge sheet in a petri dish. The petri dishes were incubated at room temperature and exposed to 16-h light and 8-h dark periods. Three leaf discs per genotype were sampled at 30 min and 3, 6, 12 and 18 h after incubation. They were fixed in a solution of absolute alcohol-glacial acetic acid (3:1) mixture. These discs were stained with lactophenol-cotton blue and observed under microscope for infection process; conidial germination, germtube formation and appresoria formation were observed.

Results and Discussion

The conidia germinated quickly on the leaf surface of the susceptible genotypes compared to that on resistant genotypes at 30 min after inoculation (Table 1). However, at the end of 6 h the extent of germination was around 90% regardless of the nature of the host genotype. The behavior of the fungus with regard to the production of appresorium was similar. The differences in germtube length on susceptible and resistant genotypes were significant *(P* - 0.05) and indicative of the critical stage where host resistance comes into operation to the invading fungus. Similarly, there was a significant difference in the diameter of the appressorium formed on the resistant genotype as well as the speed of development and enlargement of lesion and production of conidia.

There was a significant reduction in the size of the lesions on the resistant genotypes compared to that on the susceptible genotype. The maximum leaf lesion size was 56.45 mm^2 in the susceptible genotype GE 712, while it was as low as 21.40 mm^2 in the resistant genotype GE 669 and 22.50 mm^2 in GE 676 (Table 2). Infact, the size of the lesion is considered as an important component in horizontal resistance to blast in rice *(Oryza saliva)* (Villareal et al. 1981). There was a reduction not only in lesion size but also the production of conidia in slow blasting genotypes. As against a conidial number of 35500 $lesion^{-1}$ in the susceptible check GE 712, the conidial production in resistant genotypes GE 669 and GE 676 were as low as 6000 $lesion^{-1}$ and 6800 $lesion^{-1}$, respectively. The rate and amount of conidial production are important components that add to the level of partial resistance (Sun et al. 1990).

Table 1. Early events of infection by *Pyricularia grisea* in finger millet.

	Conidial germination[1] (%)				Appresorium formation[2] (%)			Germtube $length^{-1}$ (µm)	Appresorium $diameter^2$ (µm)
Genotype	30 min	1 h	3 h	6 h	6 h	12 h	18 h	18 h	18 h
Susceptible									
GE 649	60.5	65.0	91.5	90.0	71.6	80.0	88.3	13.7	12.5
GE 712	58.4	60.0	90.0	91.9	65.0	78.4	93.4	15.3	13.5
Resistant									
GE 669	54.9	55.8	86.8	88.3	68.4	76.5	91.6	7.7	9.0
GE 705	51.0	58.4	85.0	92.7	55.2	71.6	88.3	8.3	9.3
SEm±	0.50	0.41	0.39	0.44	0.29	0.27	0.24	0.10	0.01
CD at 5%	1.60	1.32	1.26	1.41	0.93	0.88	0.78	0.35	0.01

1. Mean of 30 conidia from each leaf disc.
2. Mean of 30 observations from 3 leaf discs.

Table 2. Components of resistance to blast in finger millet.

Genotype	Size of leaf lesion[1] (mm^2)	No. of conidia per lesion[1]	Length of neck lesion[1] (cm)	Finger blast incidence[2] (%)
GE 632	24.60 abd	7000 a	0.76 a	11.81 a
GE 637	26.90 abd	9400 b	1.40 b	10.23 acd
GE 669	21.40 a	6000 a	0.50 a	2.24 b
GE 674	31.40 bd	15700 c	2.30 c	9.75 cd
GE 676	22.50 abd	6800 a	0.87 ab	8.85 d
GE 705	24.10 abd	7100 a	0.85 ab	2.85 b
GE 718	41.80 c	19200 d	1.09 ab	9.65 c
GE 728	29.10 d	10200 b	1.00 ab	9.14 c
GE 649	54.60 e	27800 e	4.97 d	59.99 e
GE 712	56.45 c	35500 f	6.10 e	68.77 f

1. Mean of 15 lesions or neck lesions from 3 replications. Figures followed by the same letter do not differ significantly {P = 0.05).
2. Mean of 15 plants from 3 replications. Figures followed by the same letter do not differ significantly (P = 0.05).

Unlike in other diseases, the critical stage in blast is the neck infection, intensity of which indicates the economic loss. Here again, genotypes with high level of partial resistance to blast showed significantly low level of neck and finger infection. As against a neck lesion length of 6.1 cm in the susceptible check GE 712, the neck lesion length was 0.5,0.85 and 0.87 cm in GEs 669, 705 and 676, respectively (Table 2). The incidence of finger infection was also very low in the above genotypes.

It appears that resistance of the host to the pathogen is expressed only just at about or immediately after penetration as seen in these studies. Such observations have been noted in rice blast also (Koga 1989). Thus, the genotypes GEs 676, 705, 718, 728 and 632 were found to possess a good level of partial resistance to blast in finger millet.

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Publications

Book Review

Anilkumar TB, Mantur SG and Madhukeshwara SS. 2003. Diseases of finger millet. Bangalore, India: All India Coordinated Small Millets Improvement Project, Indian Council of Agricultural Research. 126 pp.

The manual "Diseases of finger millet" compiled and edited by the Technical Project Leader (Millets Pathology), and colleagues in the project coordination cell, of the All India Coordinated Small Millets Improvement Project (AICSMIP), Indian Council of Agricultural Research (ICAR) is an updated and much needed compilation. Diseases, especially blast (caused by *Pyricularia grisea)* has emerged as a major threat to sustainable production of finger millet crop worldwide. The intractable nature of several foliar diseases with blast of finger millet presents a range of exasperating complexities rarely seen in any single plant disease.

The manual provides a comprehensive record of past and current knowledge on the nature of foliar and panicle diseases caused by fungi, bacteria and viruses, the damage caused by them and current research on how to control them. The book begins with fascinating historical account and geographical distribution of small millets and their diseases in India and Africa. A review of pathogen taxonomy and population biology is especially helpful for scientists to understand the relationships among different phases of blast disease. Information on infection processes of some other diseases will be helpful in developing a suitable resistance breeding strategy in finger millet. Other useful additions for the reader include an extensive list of available references on finger millet diseases.

The popularity of the book would have been further enhanced with correct and uniform reference citation style, proper scientific and technical editing, inclusion of disease cycle drawings of few important diseases and use of quality paper and printing.

In general, plant pathologists, breeders, geneticists and anyone interested in diseases affecting finger millet production will value this comprehensive reference book.

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ICRISAT Publication

Sharma HC Taneja SL, Kameswara Rao N and Prasad Rao KE. 2003. Evaluation of sorghum germplasm for resistance to insect pests. Information Bulletin no. 63. Patancheru 502 324, Andhra Pradesh. India: ICRISAT. 184 pp. ISBN 92-9066-458-4. Order code IBE 063. HDC US$246.00, LDC US$ 82.00, India Rs 3,887.00.

Sorghum is one of the most important cereal crops in the semi-arid tropics. Nearly 150 insect species have been reported to damage this crop worldwide, causing an estimated loss of more than US$1,000 million annually. Of these, sorghum shoot fly (*Atherigona soccata*), stem borers (*Chilo partellus, Busseola fusca* and *Diatraea* spp), sorghum midge *(Stenodiplosis sorghicola),* and head bugs (*Calocoris angustatus* and *Eurystylus oldi)* are the major pests worldwide. Host-plant resistance is one of the most effective means of controlling insect pests in sorghum. ICRISAT holds 36,700 accessions of the sorghum germplasm from all over the world. Therefore, extensive screening of the sorghum germplasm was undertaken, and several stable sources of resistance to the key insect pests have been identified. This information bulletin lists the reactions of the sorghum germplasm accessions to the key pests. This list can be made use of while selecting lines with resistance to the target pests for use in sorghum improvement.

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Information for ISMN Contributors

Publishing objectives

The International Sorghum and Millets Newsletter (ISMN) is published annually by the Sorghum Improvement Conference of North America (S1CNA) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). It is intended as a worldwide communication link for all those interested in the research and development of sorghum [*Sorghum bicnlor* (*L.*) MoenchJ, pearl millet [Pennisetum *glaucum* (L.) R. Br.], and minor millets, and their wild relatives. Though the contributions that appear in ISMN are reviewed and edited, it is expected that the work reported will be developed further and formally published in refereed journals.

What to contribute?

- Contributions should be current, scholarly and well justified on the grounds of new information.
- Results of recently concluded experiments, newly released varieties, recent additions to germplasm collections, registration notes for newly developed trait-specific breeding lines/germplasm, etc.
- Genome maps and information on probe-availability and sequences, and populations synthesized for specific trails being mapped.
- Short reports of workshops, conferences, symposia, field days, meetings, tours, surveys, network activities and recently launched or concluded projects.
- Details of recent publications, with full bibliographic information and 'mini reviews' whenever possible.
- Personal news (new appointments, awards, promotions, change of address, etc.).

Deadline for submission: 15 August

How to format contributions

- Keep the items brief up to **6 pages (double-spaced) including data tables and figures.**
- Table should be separated from the text and placed upright (not landscape). Supply only the essential information; round off the data-values to just one place of decimal; use suitable units to keep the values small (eg, tons instead of kg).
- Keep the list of references short - not more than five references, all of which should have been seen in the original by the author. Provide all the details including author/s, year, title of the article, full title of the journal, volume, issue and page numbers (for journal articles), and place of publication and publishers (for books and conference proceedings) for every reference. **Cite references as in this issue.**
- Black-and-white photographs are welcome. Send disk-files whenever you submit line figures and maps.
- Express all quantities only in SI units. Spell out in full every acronym you use.
- Give Latin name of every crop, pest, or pathogen at the first mention.
- Submit one hard copy of the manuscript in the correct format to the Scientific Editor of the respective region at the address given below. Also send the manuscript MS Word file as email attachment.
- Include full address of all authors, and provide telephone, fax and e-mail of the **corresponding** author.

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