EFFECT OF RECURRENT SELECTION ON GENERAL AND SPECIFIC COMBINING ABILITIES OF TWO RANDOM-MATING SORGHUM POPULATIONS

(Sorghum bicolor (L.) Moench)

A thesis submitted to the
Andhra Pradesh Agricultural University
in partial fulfilment of the requirements
for the award of the degree of

MASTER OF SCIENCE IN AGRICULTURE

By

Mohamoud Abdullahi Hashi

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College of Agriculture
Andhra Pradesh Agricultural University
Rajendranagar
Hyderabad 500 030

April, 1986

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<u>CERTIFICATE</u>

Mr Mohamoud Abdullahi Hashi has satisfactorily prosecuted the course of research and the thesis entitled "EFFECT OF RECURRENT SELECTION ON GENERAL AND SPECIFIC COMBINING ABILITY OF RANDOM-MATING SORGHUM (Sorghum bicolor (L.) Moench)" submitted is the result of original research work and is of sufficient high standard to its presentation to the examination.

I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any University.

Major Advisor

Date: 21 Apr 86

S.Z. Mukuru
Principal Breeder &
Program Leader
Sorghum, ICRISAT

<u>CERTIFICATE</u>

This is to certify that the thesis entitled "EFFECT OF RECURRENT SELECTION ON GENERAL AND SPECIFIC COMBINING ABILITY OF RANDOM-MATING SORGHUM" submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of Andhra Pradesh Agricultural University, Hyderabad, is a record as the bonafide research work carried by Mr Mohamoud Abdullahi Hashi under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of the investigations have been duly acknowledged by him.

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Chairman of the Advisory Committee
Dr. S.Z.Mukuru
Principal Breeder &
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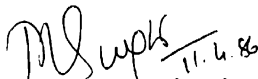Thesis approved by the Student Advisory Committee.

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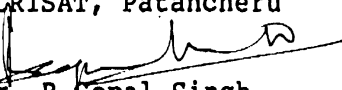   Professor & Head
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    Combining ability effects of 48 Fl hybrids obtained by
crossing 4 male-sterile lines with five cycles of recurrent
selection plus the original population, each from two random-
mating sorghum populations, were evaluated to determine the
effect of recurrent selection on GCA and SCA effects and to
estimate the progress made during the five cycles of recurrent
selection.

A randomized complete block design with three replications)f the 48 Fl hybrids was grown at ICRISAT Center during the 1984 rainy season (Kharif) and at Bhavanisagar, under irrigation, during the Summer season of 1985. The combining ability analysis followed a line x tester (A-lines) mating system.

Significant variations were observed among the A-lines and the cycles of the populations for all the characters studied. The cycles within populations showed larger variations for grain weight and panicle weight than the A-lines while the variations of the A-lines were larger for most of the yield components.

Five cycles of recurrent selection have been effective in increasing the grain yield of the two populations and resulted in simultaneous improvement of all the other traits in the desired direction except panicle length and 100-seed weight which remained unchanged.

Recurrent selection practised earlier for grain yield was effective primarily for general combining ability which indicated that the improvement of this trait involved largely additive effects, and a per cycle selection gain of about 17.9% and 22.9% was found for the US/R and RS/R populations, respectively.

Specific combining ability (SCA) did not appear to be important particularly for grain weight of these two populations.

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VI. SCA effects of the A-lines x Cycles for the characters studied in LT-2, Bhavanisagar 1985.

I. INTRODUCTION

The development of quantitative genetic theories and their
successful application to cross-pollinated crops, particularly to
maize, has drawn the attention of breeders in self-pollinated
crops to use population improvement procedures with some modi-
fications in recent years.

In sorghum, the discovery and use of genetic male sterile
alleles especially ms3 and ms7 made possible the development of
random-mating populations (Doggett, 1972; Gardner, 1972; Ross,
1974 and Ross et al. 1976).

The population improvement program at ICRISAT was initiated
with the introduction of a large number of populations from
different parts of the world, mainly from USA, East Africa and
West Africa. After their evaluation, the populations were merged
into new populations based on their geographic origin, height,
maturity and restoration behavior to cytoplasmic male sterility
(Bhola Nath, 1977). Initially a S_1 progeny recurrent selection
procedure was practiced to improve the population, but later, the
method was changed to S_2 progeny testing method (Hare, 1977).
Several populations are in different stages of recurrent
selection.

Periodic assessment of the nature of the changes that have
occurred due to recurrent selection are made in a population
improvement program to decide the future course of the program.
In this study, the US/R and RS/R populations were evaluated after

five cycles of recurrent selection. The US/R population was synthesized from Purdue and Nebraska restorer lines and carries the male sterility gene, ms_3, while the RS/R population was made from East African restorer lines and contains ms_3 for male sterility. The objectives of this study were:

1) to estimate the GCA effects of the cycles of the populations and A-lines and the SCA effects of their crosses

2) to determine the change in GCA and SCA effects of the cycles of the populations.

II. REVIEW OF LITERATURE

Population breeding techniques as used in maize and other cross pollinated crops accomplish two important goals (Bhola Nath 1982):

a) The improvement of the mean performance of the population by increasing the gene frequency of the trait/traits under selection and

b) the maintenance of genetic variability by recombination of superior genotypes.

However, use of these techniques in self-pollinating crop species such as sorghum, requires certain modifications to overcome the difficulties of producing enough seed for testing and making the necessary intercrossings in each cycle.

2.1 CONVENTONAL METHODS OF SORGHUM BREEDING AND THIER LIMITATIONS

Sorghum bicolor (L.) Moench is a highly self-fertilized species with a small percentage of cross-pollination (Quinby et al. 1958). Breeding methods are strongly influenced by the pollinating characteristics of a species, thus most of the sorghum breeding programs rely almost exclusively on the pedigree and backcross methods (Doggett, 1970 and Gardner, 1972).

Doggett (1970) pointed out two major weaknesses of the pedigree breeding method. First, while it is suitable for characters of high heritability that are usually conditioned by

very few major genes, it is inadequate for quantitative characters like yield and quality that are generally under the control of, a fairly large number of genes that are highly sensitive to the environment. Second, it produces pure lines and puts too much stress on uniformity. While uniformity is required for quality and handling purposes like height for easy harvesting in the highly advanced and mechanized agriculture; it becomes more and more evident that uniformity as a whole may not always be desirable, particularly for resistance to diseases. A mutant form of a pathogen may break through the protection afforded by a particular resistance gene. The epidemic of Southern Corn Leaf Blight (Tatum 1971) illustrated this fact. This step by step procedure of the pedigree method is not only slow, but it generally limits the opportunities for desirable recombination among linked genes by the rapid approach to homozygosity (Gardner 1972).

2.2 THE DISCOVERY OF MALE STERILITY IN SORGHUM

The discovery of cytoplasmic male sterility and restorer genes in corn simplified seed production. This success attained with hybrid maize encouraged sorghum breeders to search for male sterility which would make possible the economical production of hybrid sorghum seed (Stephens 1937). Karper and Stephens (1936) reported several abnormals in sorghum, the presence of two antherless plants without lodicules but with as many as 6 pistils in the same flower in the progeny of a selfed dwarf sudangrass selection. The antherless plants were crossed as females to

several grain sorghums including Dwarf Yellow milo, Texas
Blackhull Kafir, Dwarf feterita and Sumac sorgo. They found the
character was recessively inherited, segregating 3 to 1 in the F2
generation. A year later, Stephens (1937) reported the
occurrence of a male-sterile plant in a plot of Texas Blackhull
Kafir at Texas. This male sterility which was later labelled as
ms2 (Stephens and Quinby 1945) was not successful, because this
gene was also responsible for high female sterility.

Webster (1965) reported a recessive male-sterile gene called
ms3 discovered in the 1940's in the Coes variety in Nebraska.
This gene, unlike ms2, does not have any female sterility, and
sets full seed after pollination. Andrews and Webster (1971)
reported a new factor for genetic male sterility ms7 controlled
at one locus which was discovered in 1963 at Samaru after seed of
Nigerian sorghum had been irradiated with Co60. Crosses were
made and the expression of the sterility remained stable in
different genetic backgrounds and in a range of climatic condi-
tions.

With the discovery of these genetic male-sterile alleles the
foundation was laid to sorghum to apply recurrent selection as
used in corn (Gardner 1972).

2.3   RECURRENT SELECTION

Recurrent selection, as defined by Allard (1960), is a
method of breeding designed to concentrate favorable genes
scattered among a number of individuals by selecting in each
generation among the progeny produced by intermatings of the

selected individuals (or their selfed progeny) of the previous generations.

Recurrent selection was first suggested by Hayes and Garber (1919) as a method of improving corn varieties, and East and Jones (1920) and Jenkins (1940) published detailed descriptions of this breeding scheme. Hull (1945) suggested that selection after each of several cycles of intercrossing was useful in improving specific combining ability; and it was after this that the method acquired the name recurrent selection.

Recurrent selection methods were developed primarily for the improvement of traits that are quantitatively inherited. It was realized that different methodologies were needed for the improvement of quantitative traits than those developed for qualitative traits (Sprague and Eberhart 1977). The basic premise of recurrent selection methods is to increase the frequency of desirable genes in a systematic manner and to enhance the opportunities of extracting superior genotypes. Success of recurrent selection methods is dependent on the original assemblage of genes in the breeding populations. If frequencies for genes that control the trait under selection differ among populations, response to selection, even though realized, may occur at varying rates in the different populations (Frey 1981).

2.4 TYPES OF RECURRENT SELECTION

Recurrent selection may be classified in various ways. Allard (1960) recognized four different types of recurrent selection distinguished by the way in which plants with desirable attributes are identified. These types are: (1) simple recurrent selection, (2) recurrent selection for general combining ability (3) recurrent selection for specific combining ability, and (4) reciprocal recurrent selection.

Simple recurrent selection was described by Sprague and Brimhall (1950), who studied oil content in the corn Kernel. In simple recurrent selection, plants are divided into a group to be discarded and a group to be propagated further on the basis of phenotypic scores taken on individual plants or their selfed progeny. Since test crosses are not made, the effective use of simple recurrent selection is restricted to characters with sufficiently high heritability that an accurate phenotypic evaluation of the character can be made visually or by simple tests. It cannot be used with much effectiveness in breeding for improved combining ability for yield or any other quantitative trait.

Recurrent selection for general combining ability is a direct outgrowth of early testing suggested by Jenkins in 1935 (Singh 1983). In this system, a number of plants which appeal to the breeder are selected from the source population. These S_0 plants are selfed and also crossed to a tester with a broad genetic base to identify the individuals with good general

combining ability. The individuals selected for general combining ability are propagated from the selfed seed intercrossed in all combinations, and a composite of the intercrossed seed is then used to establish a population for further selection.

Recurrent selection for specific combining ability was proposed by Hull in 1945 on the assumption that an important part of heterosis results from the nonlinear interactions of genes of different loci, from interactions between alleles at the same locus, or from both causes in combination. It involves determination of levels of specific combining ability by crossing the selected individuals on to a homozygous tester line; selection of the parents with high specific combining ability and intermating the selfed seed of the selected parents.

Reciprocal recurrent selection was proposed by Comstock, Robinson and Harvey in 1949. The objective of reciprocal recurrent selection is to improve two different populations in their ability to combine well with each other. The scheme involves two heterozygous source populations, A and B that are genetically unrelated. A number of plants from source A are self-pollinated and also crossed with a sample of plants from source B. In a similar fashion, a number of plants from source B are selfed and crossed with a sample of plants from source A. Selection is based on the experimental comparison of test-cross progenies in replicated yield trials. The plants selected are then interbred from S_1 progenies derived from the selfed seed of

the S_0 plants. The two resulting populations A and B serve as source populations to initiate the next cycle.

Penny et al. (1963) divided recurrent selection into two types: phenotypic recurrent selection and genotypic recurrent selection. Phenotypic recurrent selection includes those cases in which the phenotype of S_0 plants are the basis of selection, while genotypic recurrent selection is the genetic worth of the S_0 plants as evaluated in some type of progeny test. Progeny evaluation may be done on the basis of selfed-progeny performance or test-cross progeny performance. The test-cross progeny evaluation may be further sub-divided on the basis of the degree of heterozygosity or heterogeneity of the tester.

2.5 BREEDING SYSTEMS FOR POPULATION IMPROVEMENT

Several breeding schemes are available for population improvement through recurrent selection (Sprague and Eberhart 1977). They require the selection of plants with superior phenotypes in the breeding population and the intermating of the selected individuals to form a new population. These recurrent selection procedures will gradually increase the frequency of favourable alleles. Selection can be based on the phenotype of an individual (mass selection) or on the mean phenotype of families. When families are used, three phases are involved: (1) forming families, (2) evaluating these families and selecting those that are superior, and (3) intercrossing plants produced from remnant seed of the selected families (or selfed seed of the parents) to form the improved breeding population for the next

cycle of improvement. The choice of a selection method to be used in a crop depends upon the type of gene action involved in the inheritance of the trait under selection, the type of cultivars required for commercial production, and resources available to the breeder (Frey 1981). Generally, the systems can be divided into two main categories (Moll and Stuber 1974); (a) intrapopulation selection systems and (b) interpopulation selection systems. The first will tend to maximize improvement of the population itself and the inbred lines derived from it. This includes mass selection, half-sib family selection, full-sib family selection, S_1 and S_2 family selections. While the second will maximize improvement in the population cross and hybrids between lines from two different populations for characters controlled by genes with a relatively high level of dominance. It includes half-sib reciprocal recurrent selection, and full-sib reciprocal recurrent selection.

For mass selection, individual plants are evaluated and selected phenotypically i.e. no information other than their own phenotype is used as a criterion for selection (Hallauer and Miranda 1981). Mass selection is the easiest of all methods and requires the fewest resources and only one generation per cycle. The system is very effective for characters of high heritability. It is useful if the population is highly heterogeneous and permits a large germplasm pool to be sampled (Bhola Nath 1982).

Half-sib family selection is a simple system to use in sorghum population in which genetic male-sterility has been incorporated (Gardner 1972). Male-sterile plants in the

populations are tagged at the time of flowering and are permitted to open-pollinate. Each head is harvested and threshed separately, the seed from one head forming one entry in a yield trial. Remnant seed is saved. The best entries are chosen from the yield trial results and remnant seed of these entries is bulked and sown. This population forms the recombination phase. Again male-sterile plants are tagged and harvested individually to form the next cycle of evaluation.

Full-sib family selection may offer more promise than mass selection for sorghum improvement . The plant population density of families being evaluated should be the same as that recommended for sorghum production. Such families can be easily formed by crossing selected male-fertile plants on to selected male-sterile ones. These are evaluated (yield trials) and the selected families can be recombined using bulked remnant seed. Crosses of male-fertile to male-sterile plants are then made and the cycle repeated (Gardner 1972).

S_1 family selection is one of the most effective selection schemes for sorghum . Heads of male-fertile plants can be bagged at flowering time to insure selfing, or they can be tagged to be sure that male-fertile (and not male-sterile) heads are harvested at maturity. Selected plants are harvested and threshed separately, each head forming an S_1 family. These families are entered into yield trials. Remnant seed from the selected families, based on yield trials, is sown, and seeds from male-sterile heads are selected to insure recombination. Seeds from

male-sterile heads are than bulked and sown. Male-fertile heads of good plants are identified for testing to begin the next cycle (Gardner 1972).

The mechanics of S_2 family selection are similar to those described for S_1 progeny selection except that another generation of inbreeding is accomplished before evaluation in replicated trials. S_2 family selection helps to work with heterogeneous material, where characters are segregating; it is much easier to select in S_2 than in S_1. Hence; this system is effective in eliminating undesired genes from the population (Bhola Nath 1977).

Half-sib reciprocal recurrent selection as originally proposed by Comstock et al. (1949) is the most promising in sorghum because it gives a better evaluation of males to be selected (Gardner 1972). A male-fertile plant in one population can be crossed to several male-sterile plants in the opposite population and seed can be bulked to form the half-sib family.

Full-sib reciprocal recurrent selection was designed by Hallauer and Eberhart (1970). In this system randomly selected pairs of S_0 plants from two populations are selfed and crossed reciprocally to produce full-sib progenies. Selection among S_0 plants in each population is based on the performance of the full-sib progenies in replicated yield trials. S_1 progenies from selected S_0 plants within each population are intermated to form two new populations for the next selection cycle. The use of full-sib RRS in sorghum would give a poorer evaluation of males

to be selected and it is impossible to maintain the male-sterile genotypes and reproduce the hybrids (Gardner 1972).

Several techniques have been developed by different geneticists and breeders to more effectively identify the genetically superior individuals or families selected in the various recurrent selection schemes used for population improvement. Eberhart (1970) presented the detailed discussion about this. These include: (a) increase the additive genetic variance, (b) increase the selection intensity, (c) increase the number of generations per year, (d) improve field-plot techniques, (e) improve field designs and use of irrigation, pest control, and freedom from weed to control environmental variation (f) improve statistical procedures for better estimation, and (g) test in several environments for better evaluation of genotypes.

2.6 RECURRENT SELECTION IN SORGHUM

The concept of population improvement can be easily visualized as appropriate to the breeding behaviour of a cross-pollinating species. At first it may seem less applicable to sorghum, a primarily self-pollinating species (Hare 1977). However, it may be noted that cross-pollination has been an effective means of introgression in cultivated sorghum landraces as evidenced by the variability they contain and that cross pollination does occur in related species of sorghum (Doggett and Majisu 1968). There are several available genes for male-sterility (Ross et al. 1971) which operate as single recessives, independent of the genetic background. He indicated the best of

these are ms3 and ms7 and these are commonly employed in sorghum population improvement.

Nordquist et al. (1973) described the first registered random-mating grain sorghum populations and credited O.J. Webster with the initiation of the first planned random-mating sorghum population developed about 1960 in Nebraska. Jowett used cytoplasmic male-sterility to apply recurrent selection to sorghum (Doggett and Jowett, 1963 and 1964). Gilmore (1964) suggested methods of utilizing both cytoplasmic and genetic male sterility for this purpose. In 1966 Webster did three cycles of recurrent selection in a bulk population using cytoplasmic male sterility (Doggett and Eberhart 1968). He also set up a further bulk population using the Coes genetic male sterile, ms3. Several populations were developed in East Africa by Doggett and Jowett, in West Africa by Andrews, in USA by Gardner, Nordquist, Ross, Axtell and Oswalt, in Australia by Downes, and in ICRISAT by Bhola Nath and Doggett (Hare 1977).

Doggett (1972) using the male-sterile gene, ms3, developed eight populations at Serere, Uganda, and applied three selection systems namely (1) female choice, in which selection involved only male steriles, (2) alternate selection; in which selfed male-fertile plants were selected in alternate generation with male-sterile plants, and (3) S_1 testing, in which male-fertile plants were selfed and tested in replicated trials. He observed a 20% increase in grain yield over three cycles under the female choice mass selection, and an average of 25% yield increase per cycle under S_1 testing.

Obilana and El-Rouby (1980) used recurrent mass selection for improving yield of two random-mating populations of sorghum, B and Y composites. They observed 38.4% and 40.4% increased grain yield over three cycles of selection and the selection response per cycle was 12.8% and 13.5% in the two populations.

Foster et al. (1980) studied the response to mass selection in an inbred population of grain sorghum and found that the mean response to selection per cycle expressed as a percentage of the control mean, ranged from 0.25 in the population selected for earliness to 3.40 in the population selected for increased seed weight.

Jan-orn et al. (1976) predicted expected gains from mass selection of individual fertile plants, mass selection of individual sterile plants, S_1 family selection, half-sib family selection, and full-sib family selection in the NP_3R sorghum random-mating population. They concluded that S_1 family selection would be the most effective for improving grain yield, but mass selection could effectively improve highly heritable traits such as days to flower and plant height.

Eckebil et al. (1977) predicted gains in yield from S_1 progeny tests in three grain sorghum random-mating populations by selecting the highest 20% of the families in each generation. Their results were 16.3, 10.2 and 8.7 q/ha per cycle for NP_5R, NP_3R, and NP_7BR populations respectively.

Bhola Nath at ICRISAT (Hare 1977) reported yield increases ranging from 21-36% in six populations out of eight which he evaluated. The plant height of all the populations was reduced and the grain colour improved from brown to white. There was almost no change in maturity.

Parasit (1981) studied the effect of recurrent S_1 selection on maturity, plant height, and grain yield and its components in two populations, US/R and US/B. The per cycle selection gain for grain yield ranged from 13 to 19 per cent in the US/R population and 7 to 14 per cent in the US/B population.

2.7 COMBINING ABILITY AND GENE ACTION

Studies on general and specific combining ability are useful to understand the nature of genetic variance. They help the breeder to choose suitable parents for developing either hybrids or varieties.

The concepts of general and specific combining ability were introduced by Sprague and Tatum (1942). General combining ability was defined as the average performance of a line in a hybrid combination, while specific combining ability referred to those cases in which certain hybrid combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved.

Genetically, general combining ability is associated with genes which are additive in their effects while specific combining ability is attributed primarily to deviations from the

additive scheme caused by dominance and epistasis (Rojas and Sprague 1952).

Falconer (1981) states that the mean value obtained from a cross between line P and line Q can be expressed as Mean (PQ) = general combining ability (P) + general combining ability (Q) + specific combining ability (PQ). The specific combining ability in statistical terms is an interaction component. He suggested that differences due to general combining ability are a result of both additive genetic variance in the base population and additive by additive non-allelic interactions. Differences due to specific combining ability were, on the other hand, attributable to non-additive genetic effects such as dominance deviations, additive by dominance, and dominance by dominance, and so forth.

The diallel analysis (Griffing 1956) and/or the line x tester (L x T) analysis proposed by Kempthorne (1957) had been widely used in estimating the combining ability effects of the parents in sorghum by numerous workers.

Kambel and Webster (1965) worked on the data collected over two years from a set of 190 F1 crosses of grain sorghum obtained by crossing 10 male-sterile lines and 19 restores. They concluded that both general and specific combining ability were important in determining the characters studied, but general combining ability effects were considerably more important and more stable over years.

A detailed survey of literature on combining ability and gene action for relevant characters is presented in the following.

Plant height: Preponderance of GCA effects for plant height was reported by Whitehead (1962), Niehaus and Pickett (1966), Liang (1967), Kirby and Atkins (1968), Rao et al. (1969), Rao (1970), Shankaregowda et al. (1972b), Borikar and Phadnis (1973), Subba Rao et al. (1976b and 1978), and Singhania (1980). A similar trend for plant height in forage sorghum was also observed by Grewal and Paroda (1974), Bittinger et al. (1981), Boora and Lodhi (1981), Sharma et al. (1981), Thanky et al. (1981), and Monpora and Sanghi (1982).

In contrast, Goud (1971), Govil and Murty (1973a), Subba Rao et al. (1975 and 1976), and Kukadia et al. (1983) found that the nonadditive type of gene action to be more important for the trait.

Days to 50 per cent flowering: Estimates of GCA variance being greater than that of SCA were reported by Whitehead (1962), Niehaus and Pickett (1966), Rao et al. (1969), Rao (1970), Shankara Gowda et al. (1972b), Subba Rao et al. (1976 a & b and 1978), Bittinger et al. (1981), Singhania (1982), Boora and Lodhi (1981). Thanky et al. (1981) and Monpora and Sanghi (1982).

Contrary to the above studies, Goud (1971), Goud et al. (1973 a & b), Govil and Murthy (1973a), Borikar and Phadnis (1973). Subba Rao et al. (1975) and Kukadia et al. (1983) reported greater magnitude of SCA effect compared to GCA

indicating the importance of non-additive gene action in determining the trait.

Panicle length: Predominance of GCA variance for panicle length was reported by Govil and Murthy (1973a), Borikar and Phadnis (1973), Chauhan and Singh (1974), Singhania (1980), Bittinger et al. (1981) and Shinde and Sudewad (1981). The reverse was found true by Goud (1971), Goud et al. (1973 a & b), and Thanky et al. (1981).

Panicle Weight: Chiang and Smith (1967b), Chauhan and Singh (1974) and Bittinger et al. (1981) reported the preponderance of additive gene action in the expression of this character. While Nagur and Murthy (1970), Nagur and Madhava Menon (1974b) and Subba Rao et al. (1975, 1976 a & b, and 1978) found greater SCA variance, suggesting preponderance of the nonadditive type of gene action.

Threshing per cent: Niehaus and Pickett (1966) reported the ratio of GCA/SCA variance to be 1.47 emphasizing the additive type of gene action for this character.

Grain yield: The importance of both GCA and SCA variances for grain yield was reported by Kambel and Webster (1965), Rao (1970), Govil and Murthy (1973a), Subba Rao et al. (1976 a & b) and Dobhalkar and Baghel (1980).

Liang et al. (1968), Kirby and Atkins (1968), Goud (1971),
Goud et al. (1973 a & b), Subba Rao et al. (1975 and 1978),
Singhania' (1980), Bittinger et al. (1981), Bhole and Borikar
(1982), Harer and Bogot (1982) and Patel and Thombre (1984) found
greater SCA variance of grain yield. Wilson et al. (1978). Liang
et al. (1968) and Indi and Goud (1981) reported over-dominance
operating for grain yield.

In contrast, Niehaus and Pickett (1966), Liang (1967), Beil
and Atkins (1967), Rao et al. (1969), Collins and Pickett
(1972b), Shankaregowda et al. (1972b), Laosuwan and Atkins
(1977), Baldha et al. (1979), Haripatidar and Dobholkar (1981)
Thanky et al. (1981) and Rao et al. (1982) observed GCA variance
to be more important than those of SCA. Beil and Atkins (1967)
reported GCA variance to be three times greater whereas Malm
(1968) found it to be 20 times greater than SCA.

Shankar Gowda et al. (1972b) and Chavan and Nerkar (1978)
observed differential estimates of additive and non-additive
components over locations and seasons respectively. GCA was more
important in Kharif and SCA in Rabi.

100 grain weight: Estimates of GCA variance was three times
greater (Beil and Atkins, 1967) and 64.1 times greater (Malm
1968) than SCA variance for size. Greater GCA variance was also
reported by Borikar and Phadnis (1973), Laosuwan and Atkins
(1977), Baldha et al. (1979), Singhania (1980), Srihari and Nagur
(1980), Dobhalkar and Baghel (1980), Bittinger et al. (1981),

Hari Patidar and Dobhalkar (1981), Thanky et al. (1981), Harer and Bogot (1982), Patil et al. (1982) and Rao et al. (1982).

Contrary to the above studies, Niehaus and Pickett (1966) reported SCA variance that was twice the GCA, suggesting predominance of non-additive type of gene action in their material. Similar trends were reported by Govil and Murthy (1973a), Chauhan and Singh (1974), Subba Rao et al. (1975, 1976a and 1978), Bhole and Borikar (1982) and Patel and Thombre (1984).

Grain number per panicle: High GCA:SCA ratio was reported by Beil and Atkins (1967) and Baldha et al. (1979). These workers as well as Niehaus and Pickett (1966), Chauhan and Singh (1974), Laosuwan and Atkins (1977), Singhania (1980) and Srihari and Nagur (1980) suggested predominance of additive gene action for this character. On the other hand, Shankaregowda et al. (1972b) found that the SCA variance was higher than the GCA variance.

Dominant gene effects were observed by Liang and Walter (1968) and over-dominance by Vasudeva Rao and Goud (1977) and Dobhalkar and Baghel (1980).

III. MATERIALS AND METHODS

3.1 EXPERIMENTAL MATERIAL

Random-mating sorghum populations have been developed at ICRISAT and recurrent selection procedures were used since 1974 to improve US/R and RS/R populations used in this study (ICRISAT 1974). Each cycle of selection was aimed at simultaneous improvement of various characters, namely, grain yield, grain quality, disease and insect resistance and overall agronomic desirability. No deliberate selection was made for yield components except that bold grains were preferred. Different populations are in different stages of improvement. The US/R and RS/R populations were chosen for this study after five cycles of recurrent selections.

The US/R population was constituted by random mating selected early generation lines from Nebraska and Purdue populations ($NP_1BR + NP_3R + NP_4BR + NP_5R + NP_8R + PP_1R + PP_3R + PP_5R$). Similarly the RS/R population was synthesized from restorer RS and PRS populations from Serere, Uganda. The first cycle of selection (first two cycles in the case of RS/R) were completed on the basis of S_1 family evaluation and subsequent cycles of selection were completed following S_2 family evaluation. Table 3.1 gives the details of various progenies evaluated, number of test environments used and number of lines recombined during each recurrent selection cycle. Some additional elite lines from other sources were recombined with the S_2 lines in the last three cycles of selection of both populations.

Table 3.1 Number of lines evaluated and recombined and number of
test environments for progeny evaluation in different
cycles of US/R and RS/R populations.

Population	Cycle	No.of progenies evaluated	No.of test environments	No.of lines recombined
US/R	1	S_1 - 1852	4	104
	2	Half sib - 825	-	
		S_1 - 433	-	
		S_2 - 194	4	38
	3	Half sib 1230	-	
		S_1 - 473	-	
		S_2 - 195	5	30 + 9 elite lines
	4	Half sib 1167	-	
		S_1 367	-	
		S_2 195	5	28 + 11 elite lines
	5	Half sib 796	-	
		S_1 379	-	
		S_2 196	4	41 + 17 elite lines
RS/R	1	S_1 98	1	98
	2	Half sib 978	-	
		S_1 484	1	28
	3	Half sib 971	-	
		S_1 395	-	
		S_2 195	3	26 + 11 elite lines
	4	Half sib 900	-	
		S_1 347	-	
		S_2 195	5	31 + 10 elite lines
	5	Half sib 4576	-	
		S_1 397	-	
		S_2 196	3	35 + 17 elite lines

The random-mating bulks of the five cycles of recurrent selection (C_1 to C_5) plus the original population (C_0) of each of the populations were used as pollinators and were crossed to four male-sterile lines, namely, MA6, D3A, 296A, and 623A. MA6 and D3A were developed by the Sorghum Improvement Program of ICRISAT, 296A by the All India Coordinated Sorghum Improvement Project (AICSIP), and the 623A by Texas A & M University, U.S.A.

The forty-eight F1 hybrids constituted the experimental material for this investigation.

3.2 CROSSING PROGRAM

An A-line x cycle bulk crossing program was undertaken in summer 1984 (Feb-May) at Bhavanisagar, India, in irrigated nurseries, to obtain seeds for the 1984 Kharif plantings at ICRISAT Center. The parents were again crossed in Rabi 1984 (Oct 1984 - Jan 1985) at ICRISAT Center to obtain sufficient seed for the F_1 experiment in Summer 1985 at Bhavanisagar. In the second crossing, an additional A-line, 2077A, was included making F1 hybrids 60 instead of 48.

The panicles of the cycles (males) were covered with paper bags before anthesis, and the panicles of the A-lines were bagged before the stigmas were visible. Hand pollination was made on to the female panicles using the pollen of each male parent. For each cross combination approximately 15-20 panicles were pollinated.

3.3 FIELD EXPERIMENT

The experiment was conducted in two locations, ICRISAT Center during the 1984 rainy season (Kharif) and Bhavanisagar, under irrigation, during the 1985 Summer season. The first trial consisting 48 Fl hybrids was designated to LT-1, and the second trial consisting 60 Fl hybrids was designated to LT-2.

The entries in both trials were planted in a randomized complete block design with three replications. The experimental unit consisted of six row plots 4 meters long with spacing between rows of 75 cm., and thinned after emergence to about 12 cm between plants giving a plant population of about 111,000 plants per hectare. In 1984, the experiment received two irrigations to avoid stress in the first and middle parts of the growing season.

3.4 DATA COLLECTION

Data were recorded on the following characters on 25 randomly chosen plants from the four middle rows.

1. Days to 50% flowering : Average number of days from sowing up to 50% anthesis in the panicles.

2. Plant height : Average height in centimeters from the ground to the top of the head.

3. Panicle length : Average length in centimeters from the botton to the top of the panicles.

4. Grain number per panicle : The grain number per panicle was estimated as follows :

$$\text{Grain number} = \frac{\text{Average grainweightperpaniclein grams} \times 100}{\text{hundred-grain weight in grams}}$$

The following characters were measured on whole plot basis:

5. Panicle weight : The total head weight in grams from each plot was recorded (including the 25 randomly selected plants) and multiplied by 0.83333 to covert to kg/ha.

6. Grain weight : The total grain weight in grams from each plot was recorded (including the 25 randomly selected plants) and multiplied by 0.83333 to convert to kg/ha.

7. 100-seed weight : The weight of 100 grains sampled from the plot was recorded in grams.

8. Threshing percentage : The threshing per cent was calculated as :

$$\text{Threshing \%} = \frac{\text{Plot grain weight} \times 100}{\text{Plot head weight}}$$

3.5 STATISTICAL ANALYSES

3.5.1 Analyses of Variance

The analyses of variance (ANOVA) were performed for each environment according to Steele and Torrie (1980) and then combined over environments as described by McIntosh (1983). One of the underlying assumptions of the analysis of variance is homogeneity of error variance. The combination of experiments into a single analysis is valid only when all experiments have error variances that are homogeneous. When this condition is met, the set of experiments may be considered as random samples drawn

from the same population, and all the pooled error terms for each character are applicable to all analyses involving that character., Thus, Bartlett's test for homogeneity of error variances was computed for each charater in the two environments before pooling them. The model considers combined data over the two environments of this study where both the treatments and environments were assumed to be fixed. For an individual environment analysis, the terms containing the environment attributes are dropped. The linear additive model assumed is as follows :

$$Y_{ijkl} = u + m_i + f_j + (mf)_{ij} + p_l + (mp)_{il} + (fp)_{jl} + (mfp)_{ijl} + (rp)_{kl} + e_{ijkl}$$

Where

Y_{ijkl} = the observed value of the ith cycle and j^{th} A-line in k^{th} replication of lth environment.

u = the general mean of all the entries

n_i = the fixed effect of the ith cycle, i=1 to 12

f_j = the fixed effect of the jth A-line; j=1 to 4

$(mf)_{ij}$ = the effect due to the interaction of ith cycle and j^{th} A-line.

p_l = the fixed effect of the lth environment, l=1 to 2

$(mp)_{il}$ = the effect of the interaction of the ith cycle and the lth environment.

$(fp)_{jl}$ = the effect of the interaction of the jth A-line and l^{th} environment.

$(mfp)_{ijl}$ = the effect due to the interaction of the ith cycle and j^{th} A-line in the lth environment.

$(rp)_{kl}$ = the effect of the kth replication in the lth environment, k = 1 to 3.

e_{ijkl} = the random error associated with the ith cycle and j^{th} A-lines in the kth replication of the lth environment.

The construction form of the analysis of variance is presented in Table 3.2.

The general form of the analysis of the variance for an orthogonal break up of cycles within populations for the crosses is given in Table 3.3 (Ostle, 1974).

3.5.2 Estimation of Combining Ability Effects

General combining ability (GCA) was calculated for the cycles and A-lines, and specific combining ability (SCA) was calculated for their crosses. Calculations of their effects were estimated as follows where i and j have already been defined (Singh and Chaudhary, 1977).

$$GCA \text{ (cycles)} = X_{i...} - X_{...}$$
$$GCA \text{ (lines)} = X_{.j..} - X_{....}$$
$$SCA \text{ (crosses)} = X_{ij..} - X_{i...} - X_{.j..} + X_{....}$$

GCA and SCA estimates were tested for significance (difference from zero) using the t-test (Singh and Chaudhury, 1977).

Table 3.2 Form of the analysis of variance used to analyze the data from 2 environments.

Source of variation	degrees of freedom		Mean Squares	F-test
Total	prmf-1	287		
Environment	p-1	1		
Rep./Environment	p(r-1)	4		
A-line	f-1	3	M7	M7/M1
Cycles	m-1	11	M6	M6/M1
A-line x Cycles	(f-1)(m-1)	33	M5	M5/M1
Environment x A-line	(f-1)(p-1)	3	M4	M4/M1
Environment x Cycles	(m-1)(p-1)	11	M3	M3/M1
Environment x (A-line x Cycle)	(f-1)(m-1)(p-1)	33	M2	M2/M1
Pooled error	p(r-1)(mf-1)	188	M1	

p = the number of environments
r = the number of replications with each environment.
f = the number of A-lines.
m = the number of cycles.
M(subscript) = the observed mean square value of the subscripted effect.

Table 3.3 General form of an orthogonal break up of the analysis of variance of testers within each population (Ostle 1974).

Source of * variation	degrees of * freedom	
Total	prmf-1	287
Environment	p-1	1
Rep./Environment	p(r-1)	4
A-lines	f-1	3
Cycles	m-1	11
Cycles between populns.	1	1
Cycles within populn.1	c-1	5
Cycles within populn.2	c-1	5
A-line x Cycles	(f-1)(m-1)	33
A-line x Cycles between populations	1(f-1)	3
A-line x Cycles within population 1	(f-1)(c-1)	15
A-line x Cycles within population 2	(f-1)(c-1)	15
Environment x A-lines	(p-1)(f-1)	3
Environment x Cycles	(p-1)(m-1)	11
Environment x Cycles between populations	1(p-1)	1
Environment x Cycles within population 1	(p-1)(c-1)	5
Environment x Cycles within population 2	(p-1)(c-1)	5
Environment x (A-line x Cycles)	(p-1)(f-1)(m-1)	33
Env. x (A-line x Cycles between populations)	1(p-1)(f-1)	3
Env. x (A-line x Cycles within population 1	(p-1)(f-1)(c-1)	15
Env. x (A-line x Cycles within population 2	(p-1)(f-1)(c-1)	15
Pooled error	p(r-1)(mf-1)	188

* Population 1, population 2 and c refer to US/R population, RS/R population and number of cycles in each popualtion, respecttively.

$$t = GCA/S.E._{gca} \quad \text{and} \quad t = SCA/S.E._{sca}$$

where

the standard error (S.E.) is $(Ml/rf)^{1/2}$, $(Ml/rm)^{1/2}$ or $(Ml/r)^{1/2}$ for cycles, lines, and their crosses, respectively, and where Ml is the error mean square from table 3.2.

3.5.3 Regression Analyses

In order to understand the trend of improvement of yield and its various components during the five cycles of recurrent selection, regression analysis was computed by using GENSTAT, a package of programs for data analysis, written on the VAX computer of ICRISAT. Mathematically, the simple regression coefficient (b) for different characters is calculated as (Steele and Torrie 1980):

$$b = \frac{Cov(x,y)}{Var(x)}$$

Where y is the dependent variable (in our case, characters such as yield and its components) and x is the independent variable (in our case five cycles of recurrent selection plus the base populations).

$$Cov (x.y) = \frac{(X_i - X)(Y_i - Y)}{(n-1)} \quad \text{and}$$

$$Var (x) = \frac{(X_i - X)^2}{(n-1)}$$

where Xi and Yi are the individual observations of X and Y

variables, and X and Y are their respective means, while n is the number of paired observations of x and y variables.

3.5.3.1 Regression Equations

The linear form of a regression equation is written as:

$$Y_i = y + b(X_i - X)$$
$$= (y - bX) + bX_i$$
$$= a + bX_i$$

where _a is the intercept and _b the slope of the linear equation.

3.5.3.2 ANOVA for the Regression Analysis

The variance of the dependent variable y can be partitioned into two components, namely variance due to regression on x and variance due to deviation from the regression on x. The construction form of the analysis of variance is as follows (Steele and Torrie):

Source	D.F.	S.S.	M.S.
Regression	1	RSS	RMS
Residual	n-2	ESS	EMS
Total	n-1	TSS	

The test of significance of the regression mean square is computed by using either a F-test or t-test (Steele and Torrie 1980). In the case of the F-test, the ratio of the regression mean square to error mean square, RMS/EMS, is compared with tabulated value of F for 1 and (n-2) degrees of freedom. While in

the case of the t-test, the value $t = b/SE_b$ is compared with the tabulated value of t at the desired level of significance and with error degrees of freedom, where b = regression coefficient; SE_b(standard error of regression coefficient) = $(EMS/Var(x))^{1/2}$.

IV.EXPERIMENTAL RESULTS

The results presented herein were determined from experiments conducted in the 1984 rainy season (Kharif) at ICRISAT Center and the 1985 Summer season in Bhavanisagar, India.

The Bartlett's test for homogeneity of error variances for each character in the two environments revealed that for the characters plant height, panicle length, panicle weight, and grain weight, the error variances were homogeneous. While for days to 50% flowering, 100-seed weight, number of grains per panicle, and threshing percent, the error variances were found to be heterogeneous. The combined analysis over environments for those traits that showed heterogeneity of error variances was performed following the procedure of partitioning the pooled error sum of squares into components corresponding to the set of orthogonal contrasts of treatment x environment sum of squares (Gomez and Gomez 1984). The mean squares of the various treatment and treatment x environment components were then tested against their appropriate pooled error mean squares for significance.

The results were presented in the following order: (1) Analysis of variance (2) General and specific combining ability effects and (3) Regression analyses of the GCA and SCA effects of various characters studied on the cycles of selection.

4.1 ANALYSIS OF VARIANCE

The analysis of variance for the hybrid experiment combined over environments is presented in table 4.1, while the individual

environments are presented in Appendices I and II.

The mean squares due to the A-lines and the cycles based on the pooled analysis (table 4.1) was highly significant (0.01) for all the characters studied except for threshing percent of both the A-lines and the cycles which were significant at 0.05 level of probability. The same thing was true for the individual analyses (Appendices I and II) except for number of grains per panicle in LT_1 which was nonsignificant for both the A-lines and the cycles. This indicated there was significant variations among the A-lines and among the cycles for the characters studied.

The A-line x cycle mean squares were generally smaller than the mean squares of the A-lines and the cycles, but were highly significant (0.01) for plant height and threshing percent, and significant (0.05) for days to 50% flowering. For individual environment, the A-line x cycle mean squares were found to be significant for all the characters in LT_1 except for number of grains per panicle and threshing percent, while only panicle length, panicle weight, grain weight, and number of grains per panicle were significant in LT_2.

The A-line x environment and the cycles by environment interactions were significant for all the characters except for days to 50% flowering of the A-lines and number of grains per panicle of the cycles. These significant mean squares of the interactions for the both A-lines and the cycles with environments indicated that the expression of these characters were not consistent over different environments.

Table 4.1 Mean squares pooled over environments for homogeneous traits.

Source	D.F.	Plant Height (cm)	Panicle Length (cm)	Panicle Weight per ha (kg)	Grain Weight per ha (kg)
Environment	1	22419.0	832.252	390751	2171531
Reps/Environment	4	6835.40	24.887	1657886	1842863
Hybrids	47	1438.54	8.926	7761026	4837706
A-Lines	3	4524.20**	58.616**	21251206**	6948555**
Cycles	11	3631.70**	11.999**	25601212**	17589639**
Cycles between populations	1	3341.50**	15.624*	7833262**	5519249**
Cycles within population 1	5	2645.60**	4.577	25037268**	17439624**
Cycles within population 2	5	4675.80**	18.696**	29718746**	20153732**
A-Line x Cycles	33	426.97**	3.384	587918	395166
A-line x Cycles between populations	3	816.20*	0.422	46109	224883
A-line x Cycles within population 1	15	229.00	3.048	789773*	425188
A-line x Cycles within population 2	15	547.10**	4.312	494424	399200
Environment x Hybrid	47	398.95	8.284	2102383	1353340
Environment x A-Line	3	1056.80**	26.456**	10813315**	9015200**
Environment x Cycle	11	594.89**	9.152**	2808043**	1271018**
Environment x Cycles between populations	1	362.30	4.273	7816791**	5309226**
Environ. x Cycles within population 1	5	676.80*	18.521**	2711228**	1339383**
Environ. x Cycles within population 2	5	559.50*	0.758	1903109**	395012
Environment x (A-Line x Cycle)	33	273.84	6.343**	1075260**	684248**
Env. x (A-line x Cycles betw. populns)	3	283.70	18.215**	2985365**	1978583**
Env. x (A-line x Cycle within popln.1)	15	387.70*	5.194*	998940*	595966*
Env. x (A-line x Cycle within popln.2)	15	158	5.118*	769559*	513662*
Pooled error	188	197.10	2.967	432159	251153
E.S.E.(A-Lines)		1.655	0.203	77.474	59.061
E.S.E.(Cycles)		2.866	0.352	134.189	102.297
E.S.E.(A-Line x Cycle)		5.732	0.703	268.378	204.594
C.V.%		8.3	6.6	12.5	12.7

Table 4.1 Contid. Mean squares pooled over environments for heterogeneous traits.

Source	D.F.	Days to 50% Flowering	100-Seed Weight (g)	Grain Number per Panicle	Threshing Percent
Environment	1	1093	2.8460	4683000	247.5
Reps/Environment	4	21.15	0.6348	1254000	106.9
Hybrids	47	44.46	0.1537	578890	62.38
A-Lines	3	113.40**	1.223**	5022000**	480.1*
Cycles	11	105.52**	0.1888**	514303**	79.97*
Cycles between populations	1	56	1.0190	96330	20.69
Cycles within population 1	5	150.10**	0.1229**	540200**	69.55**
Cycles within population 2	5	70.85**	0.0886*	572000	102.25**
A-Line x Cycles	33	17.83*	0.0448	196500	18.54**
A-line x Cycles between populations	3	53.62*	0.0184	198500	40.57
A-line x Cycles within population 1	15	11.48*	0.0522*	223900	10.43**
A-line x Cycles within population 2	15	17.03*	0.0427*	168700	22.24
Environment x Hybrid	47	14.42	0.0643	206795	31.04
Environment x A-Line	3	14.79	0.2421**	153300*	135.9**
Environment x Cycle	11	26.94**	0.0613*	248967	55.14**
Environment x Cycles between populations	1	9.03	0.0385	84640	51.00
Environ. x Cycles within population 1	5	37.80**	0.0799*	191200	36.54**
Environ. x Cycles within population 2	5	19.65	0.0472	339600	74.57**
Environment x (A-Line x Cycle)	33	10.22	0.4910	197600	13.48
Env. x (A-line x Cycles betw. populns)	3	12.65	0.0224	203100	31.14
Env. x (A-line x Cycle within popln.1)	15	9.17	0.0269	218000	0.81
Env. x (A-line x Cycle within popln.2)	15	10.77	0.0767	176100	22.62
Pooled error	188	—	—	—	—
Env. x A-Line pooled error	12	7.921	0.0328	40870	21.39
Env. x Cycle pooled error	44	4.842	0.0283	166506	5.72
Env. x Cycles betw. poplns. pooled error	4	4.361	0.0553	117100	0.42
Env. x Cycle within popln.1 pooled error	20	1.926	0.0290	246200	0.46
Env. x Cycle within popln.2 pooled error	20	7.854	0.0222	246200	12.03

– Contid –

Table 4.1 (continued)

Source	D.F.	Days to 50% Flowering	100—Seed Weight (g)	Grain Number per Panicle	Threshing percent
Env. x (A-Line x Cycle) pooled error	132	6.757	0.2198	195585	9.68
Env.x(A-Line x Cycle betw. poplns.)	12	10.370	0.1222	74930	26.12
Evn.x(A-Line x Cycle within popln.1)	60	5.819	0.2785	184000	0.89
Evn.x(A-Line x Cycle within popln.2)	60	6.973	0.1807	231300	15.17
E.S.E.(A-Lines)		0.332	0.021	23.825	0.545
E.S.E.(Cycles)		0.449	0.034	83.932	0.488
E.S.E.(Cycles between populations)		0.426	0.048	69.851	0.132
E.S.E.(Cycles within population 1)		0.283	0.035	101.283	0.138
E.S.E.(Cycles within population 2)		0.572	0.030	101.283	0.708
E.S.E.(A-Line x Cycle)		1.061	0.191	180.548	1.27
E.S.E.(A-Line x Cycles between poplns)		1.315	0.143	111.751	2.087
E.S.E.(A-Line x Cyclers within popln.1)		0.985	0.216	175.119	0.385
E.S.E.(A-Line x Cyclers within popln.2)		1.078	0.174	196.342	1.590

* significant at 5% level of probability
** significant at 1% level of probability
C.V.% coefficient of variation
E.S.E. effective standard error

The A-lines x cycles by environment interaction mean squares were found to be highly significant for panicle length, panicle weight, and grain weight which indicated that the interaction of the A-lines and the cycles for these characters differed in the different environments.

It was quite interesting to note the orthogonal break down of the cycles into cycles between populations and within populations, which was the main object of this study. Based on the pooled analysis, the mean squares of the cycles within populations were found to be highly significant for plant height, panicle weight, grain weight, days to 50% flowering, and threshing percent for both populations indicating high variability among the cycles within each population. In addition, the cycles within the US/R population showed highly significant differences for 100-seed weight, and number of grains per panicle, while the cycles within the RS/R population showed highly significant differences for panicle length, and significant differences for 100-seed weight.

The mean squares of the cycles within populations by environment interaction was significant at the one percent probability level for panicle length, panicle weight, grain weight, days to 50% flowering, and threshing percent for US/R population, while plant height and 100-seed weight were significant at the five percent probability level. On the other hand, the cycles within the RS/R population by environment interaction was highly significant for panicle weight and

significant for plant height and threshing percent. This indicated that the cycles within RS/R population were more consistent over environments when compared to those of US/R population, for panicle length, grain weight, days to 50% flowering, and 100-seed weight.

The A-line x cycles within populations mean squares were found to be highly significant for threshing percent and significant for panicle weight, days to 50% flowering, and 100-seed for US/R population. While, on the other hand, A-line x cycles within RS/R population was highly significant for plant height and significant for days to flower, and 100-seed weight.

The interaction mean squares of A-line x cycles within population with the environment was found to be significant for panicle length, panicle weight, and grain weight for both populations and plant height for US/R population, indicating that the interactions of the A-lines x cycles within populations for these traits were subject to environmental influences.

The mean squares for the single degree-of-freedom contrast between the mean of all the cycles of US/R population and the mean of all the cycles of RS/R population was found to be highly significant for plant height, panicle weight, and grain weight and significant for panicle length. The test of significance for days to 50% flowering, 100-seed weight, number of grains per panicle, and threshing percent were not computed due to inadequate degrees of freedom of the (Reps within environment) x

cycles between populations, which was less than six and hence, invalidates the test (Gomez and Gomez, 1984).

4.2 GENERAL AND SPECIFIC COMBINING ABILITY EFFECTS

Estimates of GCA effects of the cycles within populations over environments are given in table 4.2 , and their corresponding mean values are presented in table 4.3.

An observation of the GCA effects indicated that cycles five of the two populations had the greatest positive GCA effects for grain yield and were highly significant at 0.01 probability level as were the GCA effects for cycles four. Cycle three of US/R population had a significant positive GCA effect at the 0.05 level of probability. Cycles zero, one, and two of the two populations had negative GCA yield effects, and all but cycle two of US/R population were significantly different from zero. This indicated that the GCA effect for grain yield has increased during the five cycles of recurrent selection.

Cycles five of US/R and RS/R populations were not only the highest in grain yielding, they were also the highest in panicle weight, threshing percent, and number of grains per panicle (table 4.3). All these characters were highly significant (0.01) for positive GCA effects except for number of grains per panicle of US/R population which was significant at the 0.05 level of probability. In addition to this, cycle five of US/R population was the latest in flowering (63 days) with GCA effect of 3.70

Table 4.2 Estimates of GCA effects for the cycles within populations for the characters studied.

Cycles	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-Seed Weight (g)	Grain No. per Head	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
			US/R Population					
0	-2.21**	13.67**	-0.77*	0.07	-233.88**	-0.88**	-1109.60**	-872.48**
1	-2.13**	-10.58**	-0.79*	0.09*	-137.21	-0.67**	-686.31**	-555.82**
2	-0.63*	-16.12**	0.11	0.16**	-31.63	-1.52**	-50.20	-136.60
3	1.16*	-7.83**	-0.17	0.09*	-38.10	-0.03	355.70**	254.37*
4	2.75**	-0.37	0.16	0.01	117.57	1.98**	753.62**	681.68**
5	3.70**	0.80	0.06	-0.05	213.50*	2.73**	1726.30**	1459.46**
			RS/R Population					
0	-1.25*	28.59**	-0.46	-0.10**	-225.46**	-2.90**	-1381.70**	-1163.90**
1	-1.92**	10.09**	0.37	-0.05	-57.88	-0.93	-1202.10**	-932.79**
2	-2.17**	-3.58	1.78**	0.04	85.50	-0.06	-731.22**	-566.35**
3	-0.63	-9.16**	0.54	-0.03	1.79	-1.88*	250.26	63.74
4	1.79**	-5.29	-0.17	-0.14**	72.49	1.69*	683.94**	568.14**
5	1.54*	-0.20	-0.67	-0.08*	233.30**	2.47**	1391.23**	1200.55**

* significant at 5% level of probability
** significant at 1% level of probability

Table 4.3 Grand means of individual cycles within population for the characters studied and their standard errors.

Cycle	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-seed Weight (g)	Grain No. Per Head	Threshi Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
				US/R Population				
0	56.67	181.88	25.28	2.3446	1563	74.03	4157	3078
1	56.75	157.63	25.26	2.3654	1660	74.24	4581	3395
2	58.25	152.08	26.16	2.4333	1766	73.39	5217	3814
3	60.04	160.38	25.88	2.3692	1759	74.89	5623	4205
4	60.04	167.83	26.21	2.2850	1915	76.89	6021	4632
5	62.58	169.00	26.11	2.2288	2011	77.65	6993	5410
Mean (US/R)	59.32	164.80	25.82	2.3400	1779	75.18	5432	4089
+ S.E.	0.283	2.866	0.352	0.035	101.283	0.138	134.189	102.297
				RS/R Population				
0	57.63	196.79	25.59	2.1800	1572	72.01	3885	2787
1	56.96	178.29	26.42	2.2321	1739	73.98	4065	3018
2	56.71	164.63	27.83	2.3158	1883	74.86	4536	3384
3	58.25	159.04	26.59	2.2487	1799	73.04	5517	4014
4	60.67	162.92	25.88	2.1425	1870	76.60	5951	4519
5	60.42	168.00	25.38	2.1933	2031	77.38	6658	5151
Mean (RS/R)	58.44	171.61	26.28	2.2200	1816	74.65	5102	3812
+ S.E.	0.572	2.866	0.352	0.030	101.283	0.708	134.189	102.297
Overall mean	58.88	168.2	26.05	2.2800	1797	74.91	5267	3950

which was highly significant, while cycle five of RS/R population was the second latest in flowering (60 days), after cycle four, and had GCA effect of 1.54 which was significant.

Cycles four of the two populations were the second highest in grain yield, panicle weight, threshing percent, and number of grains per panicle. All had positive GCA effects which were highly significant (0.01) except for number of grains per panicle which was nonsignificant for the two populations, and threshing percent of RS/R population which was significant at 0.05 level of probability. For days to 50% flowering, cycle four of US/R population was the second latest (62 days) in flowering with GCA effect of 2.75 which was highly significant.

Cycle zero of both populations were the lowest in grain yield, panicle weight, and number of grains per panicle, while for threshing percent, RS/R population was the lowest, and US/R population was the second lowest. All were highly significant for negative GCA effects. For days to 50% flowering, US/R population was the earliest to bloom and RS/R population was the third earliest with GCA effects of -2.21 and -1.25 that was significant at 0.01 and 0.05 level of probability for the two populations, respectively. In addition, cycles zero of the two populations were the tallest with GCA effects of 13.67 for US/R population and 28.59 for RS/R population which were highly significant.

GCA effects and means of the A-lines for the characters studied are presented in tables 4.4 and 4.5 , respectively. The A-line 2077A and its twelve crosses constitute the uncommon

Table 4.4 Estimates of GCA effects for A-lines for the characters studied.

A-line	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-Seed Weight (g)	Grain No. per Head	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A	0.25	9.27**	0.60**	0.07*	-104.10**	0.30	401.42**	323.01**
D3A	-1.70**	-5.02**	0.54**	-0.19**	100.31**	-2.02**	213.11**	56.49
296A	1.33**	3.73*	0.18	0.08**	5.08	-1.82**	187.76*	44.76
MA6	0.12	-7.97**	-1.32**	0.04	-1.29	3.53**	-802.29**	-424.26**

* Significant at 0.05 probability level
** Significant at 0.01 probability level

Table 4.5 Grand means of individual A-line for characters studied and their standard errors.

A-line	Days to 50% Flowering	Plant Height '(cm)	Panicle Length (cm)	100-Seed Weight (g)	Grain No. per Head	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A	59.13	177.47	26.65	2.3510	1693	75.21	5668	4273
D3A	57.18	163.18	26.59	2.0846	1898	72.89	5480	4007
296A	60.21	171.93	26.23	2.3596	1802	73.10	5455	3995
MA6	59.00	160.24	24.73	2.3178	1796	78.45	4465	3526
+ S.E.	0.332	1.655	0.203	0.0210	23.8	0.545	77.474	59.061

entries for the two environments and, hence, were not included in
the combined analysis. But this line showed highly significant
positive GCA effects for days to 50% flowering, plant height, and
panicle length (Appendix IV). While for the characters panicle
weight, grain weight, 100-seed weight, grain number per panicle,
and threshing percent, it showed highly significant negative GCA
effects. Its crosses with cycles 2 and 5 of US/R population
exhibited significant negative SCA effects for panicle length and
100-seed weight. But its crosses with cycle 3 of RS/R population
showed significant positive SCA effects for panicle length and
number of grains per panicle, while that with cycle zero of RS/S
population was significant for grain yield.

The grain weight for the A-lines ranged from 3526 to 4273
kg/ha. The A-line 623A was the highest yielding (4273 kg/ha) and
had a GCA effect of 323.01 that was significantly different from
zero at 0.01 level of probability. It was the only A-line with
significant positive GCA effect for grain weight. This line was
not only the highest yielding, it was also the highest in panicle
weight, panicle length, and plant height that were highly
significant for positive GCA effects

A-line MA6 was the lowest yielding among the female lines
with a mean yield of 3526 kg/ha and GCA effect of -424.26 which
was highly significant. This line had also the lowest GCA effects
of panicle weight, panicle length, and plant height; and they
were all significantly different from zero at 0.01 probability

which was highly significant, and which may be useful in breeding if it is highly heritable.

Estimates of SCA effects of the crosses are presented in table 4.6, and their mean values are given in table 4.7.

Two crosses out of 48 were found to be significantly different from zero with respect to their SCA effects for grain yield. These were 623A x US/R-C_4 and MA6 x US/R-C_4 with respective SCA effects of 706.39 and -480.6. The cross 623A x US/R-C_4 had also the highest SCA effect for panicle weight which was highly significant followed by D3A x US/R-C_5 that was also highly significant. For days to 50% flowering, significant positive SCA effects was found in 623A x cycles one of the two populations, 623A x RS/R-C_5, D3A x RS/R-C_4 and MA6 x US/R cycles four and five. While 623A x US/R-C_2, D3A x RS/R-C_5, and MA6 x RS/R-C_4 showed negative SCA effects that were significantly different from zero. For plant height, the crosses D3A x US/R-C_5 and MA6 x RS/R-C_3 were significantly different from zero for positive SCA effects, while 623A x RS/R-C_0, 296A x RS/R-C_3, and MA6 x US/R-C_4 were significant for negative SCA effects.

4.3 REGRESSION ANALYSIS

The linear regression analysis of the GCA means of the cycles and the SCA mean values of their crosses with the A-lines for the various characters on the cycles of selection was

Table 4.6 Estimates of SCA effects for the traits studied.

A-line x Cycle#	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	100-seed Weight (g)	Grain Number Per Head	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A x US/R-C0	-0.58	5.19	0.35	0.04	84.02	2.15	-195.4	-71.39
623A x US/R-C1	2.17*	-0.89	0.01	0.13	56.05	1.61	-184.4	-77.87
623A x US/R-C2	-2.33*	-5.35	-1.39*	0.02	-152.82	0.06	-226.07	-180.41
623A x US/R-C3	-0.95	3.36	0.35	-0.03	-32.63	0.58	8.3	43.43
623A x US/R-C4	-2.04	6.07	0.5	-0.06	240.97	1.67	747.42**	706.39**
623A x US/R-C5	-0.33	-6.93	0.31	0	-2.24	0.51	-47.02	37.87
D3A x US/R-C0	-0.8	-1.85	0.39	0.09	63.92	-0.93	27.63	-9.04
D3A x US/R-C1	-0.39	-3.43	0.77	0.06	-335.01	-1.15	-182.21	-176.63
D3A x US/R-C2	0.95	2.27	-0.2	-0.12	51.83	0.8	-91.93	-32.42
D3A x US/R-C3	0.82	-5.35	-0.17	0.04	19.49	1.14	-106.63	-31.72
D3A x US/R-C4	-0.09	-1.14	-0.12	-0.08	-29.25	0.95	-294.82	-172.92
D3A x US/R-C5	-1.39	14.52*	-0.23	-0.11	392.91*	-2.3	708.42**	327.07
296A x US/R-C0	0.34	1.73	0.11	-0.05	100.06	0.69	-81.28	7.78
296A x US/R-C1	-1.75	4.82	-0.9	-0.09	81.28	-0.76	234.81	155.47
296A x US/R-C2	0.75	7.69	1.45*	0.1	69.3	-1.45	75.55	-21.15
296A x US/R-C3	-0.37	0.4	0.12	-0.07	36.33	-0.66	127.98	54.08
296A x US/R-C4	-1.12	6.44	-0.67	0.06	-67.03	-0.52	12.47	-52.86
296A x US/R-C5	-0.41	-0.06	-0.05	0.1	-107.3	1.21	-306.97	-162.12
MA6 x US/R-C0	1.05	-5.07	-0.86	-0.08	-248.01	-1.91	249.04	72.64
MA6 x US/R-C1	-0.04	-0.49	0.12	-0.1	197.68	0.3	131.8	99.03
MA6 x US/R-C2	0.63	-4.61	0.14	0.01	31.69	0.59	242.45	233.98
MA6 x US/R-C3	0.5	1.59	-0.29	0.06	-23.19	-1.06	-29.66	-65.79
MA6 x US/R-C4	3.25*	-11.36*	0.29	0.09	-144.68	-2.1	-465.08	-480.6*
MA6 x US/R-C5	2.13*	-7.53	-0.03	0.01	-283.36	0.57	-354.43	-202.82

Table 4.6 Contd.

A-line x Cycle#	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	100-seed Weight (g)	Grain Number Per Head	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A x RS/R-C0	0.96	-14.06*	0.27	0.05	91.84	-2.55*	-186.25	-248.43
623A x RS/R-C1	2.3*	5.77	0.01	-0.03	70.65	-4.26*	-126.07	-289.33
623A x RS/R-C2	-0.62	-4.89	0.79	-0.08	1.51	-0.89	56.34	6.28
623A x RS/R-C3	-1.16	3.02	-0.35	0.01	-164.1	0.23	-38.11	-32.61
623A x RS/R-C4	0.09	4.48	-0.34	-0.04	-82.84	1.59	-20.86	0.95
623A x RS/R-C5	2.5*	4.23	-0.51	0.01	-110.4	-0.7	212.12	105.12
D3A x RS/R-C0	-1.09	6.9	0.44	-0.04	197.11	-0.4	288.63	204.14
D3A x RS/R-C1	-0.93	-5.77	-0.66	0.02	-282.98	-0.53	-216.93	-142.26
D3A x RS/R-C2	1.32	0.9	-0.77	0.04	46.77	0.25	-420.63	-278.60
D3A x RS/R-C3	0.95	-0.52	-0.08	0.06	-74.33	-1.05	238.63	90.39
D3A x RS/R-C4	3.03*	0.44	-0.29	-0.01	-40.92	0.51	-243.2	-176.05
D3A x RS/R-C5	-2.39*	-6.98	0.9	0.06	-9.54	2.71*	293.03	398.02
296A x RS/R-C0	1.88	8.65	0.18	0.05	-32.24	2.03	-266.58	-79.96
296A x RS/R-C1	-0.95	-7.35	0.93	0.12	-7.82	3.24*	-27.69	124.57
296A x RS/R-C2	0.46	8.98	-0.2	-0.1	14.59	-0.71	170.46	100.26
296A x RS/R-C3	0.75	-19.93*	-1.23	-0.11	-8.68	-0.8	-162.88	-151.59
296A x RS/R-C4	0.34	-10.14	0.94	-0.01	71.01	-1.34	384.46	212.53
296A x RS/R-C5	0.09	-1.23	-0.67	0	-149.5	-0.93	-160.33	-187.01
MA6 x RS/R-C0	-1.75	-1.49	-0.89	-0.06	-256.71	0.92	164.21	124.24
MA6 x RS/R-C1	-0.41	7.34	-0.28	-0.11	220.16	1.56	370.69	307.01
MA6 x RS/R-C2	-1.16	-4.99	0.18	0.15	-62.87	1.36	193.84	172.06
MA6 x RS/R-C3	-0.54	17.43*	1.65*	0.05	247.1	1.63	-37.64	93.82
MA6 x RS/R-C4	-3.45*	5.22	-0.31	0.06	52.75	-0.76	-120.4	-37.43
MA6 x RS/R-C5	-0.2	3.97	0.28	-0.06	269.44	-1.08	-344.82	-316.13

* Significant at the 5% probability level.
** Significant at the 1% probability level.

Table 4.7 Grand means of the crosses for the characters studied and rank of yield within A-lines.

A-line	x Cycles	Yield Rank	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-Seed Weight (g)	Grain No. per Panicle	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A	x US/R-C0	6	56.33	196.33	26.24	2.4617	1543	76.48	4363	3330
623A	x US/R-C1	5	59.17	166.00	25.87	2.5633	1612	76.15	4798	3640
623A	x US/R-C2	4	56.17	156.00	25.38	2.5217	1509	73.75	5392	3956
623A	x US/R-C3	3	59.33	173.00	26.83	2.4117	1622	75.76	6032	4571
623A	x US/R-C4	2	59.83	183.17	27.31	2.2933	2052	78.85	7169	5662
623A	x US/R-C5	1	62.50	171.33	27.01	2.3050	1904	78.45	7348	5771
D3A	x US/R-C0	6	54.17	175.00	26.22	2.2367	1728	71.09	4398	3125
D3A	x US/R-C1	5	54.67	149.17	26.58	2.2333	1425	71.07	4612	3275
D3A	x US/R-C2	4	57.50	149.33	26.51	2.1167	1918	72.17	5338	3838
D3A	x US/R-C3	3	59.17	150.00	26.25	2.2150	1879	74.01	5729	4230
D3A	x US/R-C4	2	59.83	161.67	26.63	2.0100	1986	75.82	5939	4516
D3A	x US/R-C5	1	59.50	178.50	26.43	2.9250	2504	73.33	7915	5794
296A	x US/R-C0	6	58.33	187.33	25.58	2.3767	1669	72.90	4264	3131
296A	x US/R-C1	5	56.33	166.17	24.54	2.3567	1746	71.67	5003	3595
296A	x US/R-C2	4	60.33	163.50	27.79	2.6133	1840	70.13	5480	3838
296A	x US/R-C3	3	61.00	164.50	26.18	2.3800	1801	72.41	5938	4304
296A	x US/R-C4	2	61.83	178.00	25.72	2.4267	1853	74.56	6221	4624
296A	x US/R-C5	1	63.50	172.67	26.24	2.4083	1909	77.04	6874	5293
MA6	x US/R-C0	6	57.83	168.83	23.10	2.3033	1314	75.66	3604	2726
MA6	x US/R-C1	5	56.83	149.17	24.06	2.3083	1856	78.08	3910	3069
MA6	x US/R-C2	4	59.00	139.50	24.98	2.4817	1796	77.52	4657	3624
MA6	x US/R-C3	3	60.67	154.00	24.27	2.4700	1735	77.36	4791	3715
MA6	x US/R-C4	2	65.00	148.50	25.17	2.4100	1769	78.32	4753	3727
MA6	x US/R-C5	1	64.83	153.50	24.75	2.2767	1726	81.76	5837	4783
S.E.			0.985	5.732	0.703	0.216	175.119	0.385	268.378	204.594

Table 4.7 Contd.

A-line	x Cycles	Yield Rank	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-Seed Weight (g)	Grain No. per Panicle	Threshing Percent	Panicle Weight (kg/ha)	Grain Weight (kg/ha)
623A	x RS/R-C0	6	58.83	192.00	26.46	2.3017	1560	69.76	4100	2861
623A	x RS/R-C1	5	59.50	193.33	27.04	2.2700	1706	70.01	4340	3051
623A	x RS/R-C2	4	56.33	169.00	29.22	2.3050	1780	74.26	4994	3713
623A	x RS/R-C3	3	57.33	171.33	26.84	2.3283	1531	73.56	5881	4305
623A	x RS/R-C4	2	61.00	176.67	26.14	2.1750	1683	78.49	6331	4843
623A	x RS/R-C5	1	63.17	181.50	25.48	2.2750	1816	76.98	7272	5579
D3A	x RS/R-C0	5	54.83	198.67	26.57	1.9433	1869	69.59	4387	3047
D3A	x RS/R-C1	6	54.33	167.50	26.31	2.0633	1557	71.43	4061	2932
D3A	x RS/R-C2	4	56.33	160.50	27.61	2.1633	2030	73.08	4328	3162
D3A	x RS/R-C3	3	57.50	153.50	27.05	2.1150	1825	69.96	5969	4161
D3A	x RS/R-C4	2	62.00	158.33	26.13	1.9367	1929	75.09	5921	4399
D3A	x RS/R-C5	1	56.33	156.00	26.83	2.0567	2121	78.08	7164	5606
296A	x RS/R-C0	6	60.83	209.17	25.95	2.3150	1545	72.22	3806	2751
296A	x RS/R-C1	5	57.33	174.67	27.53	2.4350	1737	75.40	4225	3187
296A	x RS/R-C2	4	58.50	177.33	27.81	2.2933	1902	72.33	4894	3529
296A	x RS/R-C3	3	60.33	142.83	25.54	2.2183	1795	70.42	5542	3907
296A	x RS/R-C4	2	62.33	156.50	27.01	2.2183	1946	73.44	6523	4776
296A	x RS/R-C5	1	61.83	170.50	24.89	2.2733	1886	74.64	6687	5009
MA6	x RS/R-C0	6	56.00	187.33	23.38	2.1600	1314	76.47	3247	2487
MA6	x RS/R-C1	5	56.67	177.67	24.82	2.1600	1958	79.08	3633	2900
MA6	x RS/R-C2	4	55.67	151.67	26.68	2.5017	1819	79.75	3927	3132
MA6	x RS/R-C3	3	57.83	168.50	26.91	2.3333	2045	78.21	4677	3684
MA6	x RS/R-C4	2	57.33	160.17	24.25	2.2400	1921	79.39	5028	4057
MA6	x RS/R-C5	1	60.33	164.00	24.34	2.1683	2299	79.84	5511	4411
S.E.			1.078	5.732	0.703	0.174	196.342	1.590	268.378	204.594

computed to determine if there was a change in these effects during the cycles of recurrent selection.

The GCA means of the cycles over environments, lines, and replications for the traits that have established homogeneity of error variances in the two environments were regressed on the selection cycles. The ANOVA of the regression analysis and the regression coefficients for these traits is given in table 4.8.

An examination of table 4.8 showed that the regression mean squares for grain weight and panicle weight was highly significant (0.01) for both populations indicating linear improvement of the GCA means of the cycles within populations for these characters during the cycles of selection. There was also a good fit of the linear model assumed, as indicated by the coefficient of determination (R^2) in fig.1. The regression mean square for panicle length of US/R population, even though found to be significant at the five percent level of probability, the ANOVA (table 4.1.) showed no significant differences among the cycles of this population. Therefore, it can be concluded that this character remained unchanged during the cycles of selection.

For the characters in which homogeneity of error variances were not established by Bartlett's test, the GCA means of cycles over the A-lines and replications for each environment were regressed on the selection cycles. The ANOVA for the regression and the regression coefficients for these characters are presented in tables 4.9 and 4.10.

Table 4.8 Regression analysis of Cycle GCA means of Plant height, Panicle length, Panicle weight, and Grain weight on selection cycles pooled over environments.

Source	D.F.	Plant Height (1)	(2)	Panicle Length (1)	(2)	Panicle Weight (1)	(2)	Grain Weight (1)	(2)
Regression	1	10.40	548.80	0.64512*	0.21840	5106241**	6005915**	3549152**	4105775**
Residual	4	136.60	106.60	0.07885	0.93650	27483	46265	20894	23011
a		167.50	191.27	25.14500	26.6730	3541	3052	2513	2117
b		-0.77	-5.60	0.19200*	-0.1120	540.2**	585.8**	450.3**	484.4**
+ S.E (b)		2.79	2.47	0.06710	0.23100	39.6	51.4	34.6	36.3

* Significant at the 5% probability level.
** Significant at the 1% probability level.
a, b, S.E.(b), (1) and (2) are intercept, slope, standard error of the slope, US/R and RS/R populations, respectively.
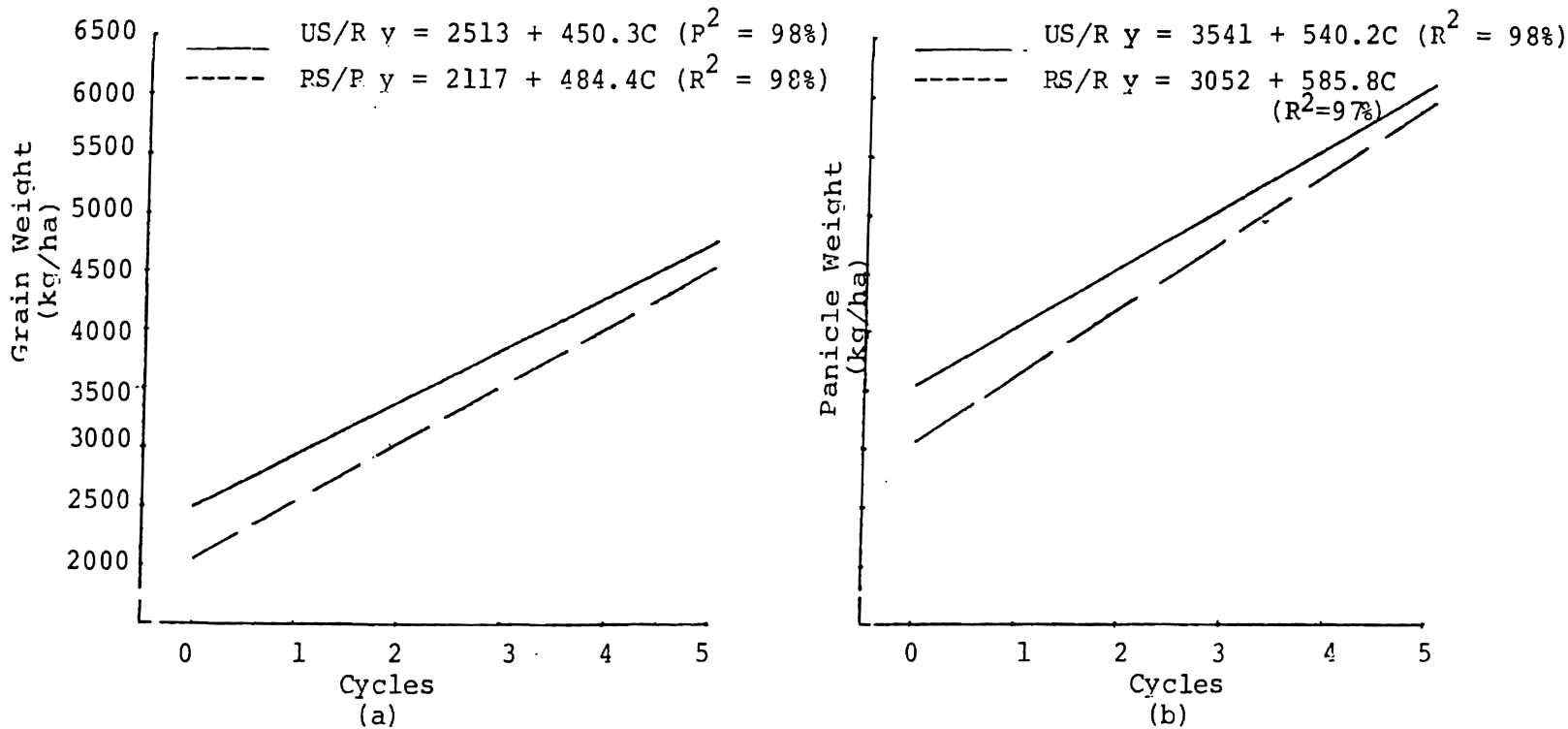
Figure 1: Regression of GCA means of cycles within populations on the selection cycles of
a) grain weight (b) panicle weight.

Table 4.9 : Regression analysis of Cycle GCA means of Days to flower, 100-seed weight, Grain number per panicle, and Thresing percent on selection cycles in LT_1 (ICRISAT 1984).

Source	d.f	Days to 50% 'Flowering		100-seed Weight		Grain Number Per Panicle		Threshing Percent	
		(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)
Regression	1	8.0106*	2.1050	0.0023	0.0062	48885	31153	13.729	0.602
Residual	4	0.6696	1.5360	0.0052	0.0062	10613	32750	4.776	4.578
a		54.8250	55.4500	2.4633	2.3960	1484	1523	70.730	73.490
b		0.6770*	0.3470	-0.0140	-0.0189	53	42	0.886	0.185
+ S.E (b)		0.1960	0.2960	0.0172	0.0188	25	43	0.522	0.511

* Significant at the 5% probability level.
** Significant at the 1% probability level.
a, b, S.E.(b), (1) and (2) are intercept, slope, standard error of the slope, US/R and RS/R populations, respectively.

Table 4.10 Regression analysis of Cycle GCA means of Days to flower, 100-Seed weight, Grain number per panicle, and Threshing percent on selection cycles in LT_2 (Bhavanisagar 1985).

Source	D.F.	Days to 50% Flowering		100-seed Weight		Grain Number Per Panicle		Threshing Percent	
		(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)
Regression	1	66.7389**	24.0960*	0.0265	0.0001	244497**	198117**	8.235*	50.303**
Residual	4	0.2249	1.3280	0.0087	0.0065	2550	4866	0.792	1.136
a		54.6100	56.1000	2.3859	2.0989	1476	1588	74.127	69.216
b		1.9530**	1.1730*	-0.0389	0.0025	118**	106**	0.686*	1.695**
+ S.E (b)		0.1130	0.2760	0.0223	0.0193	12	17	0.213	0.255

* Significant at the 5% probability level.
** Significant at the 1% probability level.
a, b, S.E.(b), (1) and (2) are intercept, slope, standard error of the slope, US/R and RS/R populations, respectively.

The regression mean squares for days to 50% flowering on the selection cycles was significant (0.05) and highly significant (0.01) for the US/R population in LT_1 (table 4.9) and LT_2 (table 4.10) indicating that the days to flower has increased due to recurrent selection in this population even though the response to selection in the two environments was different as indicated by the test of homogeneity of the regression coefficients. While for RS/R population, on the other hand, the regression mean square was found to be significant only in LT_2, indicating differential response of the GCA means of the cycles to the two environments.

The regression mean squares for 100-seed weight on the selection cycles was found to be nonsignificant for the two populations in the two environments indicating that no linear improvement has been made in this trait during the cycles of recurrent selection for both populations.

The regression mean squares for grain number per panicle on the selection cycles was nonsignificant in LT_1 for the two populations, but was highly significant (0.01) for both populations in LT_2 which indicated a high environmental influence on the cycles within populations which responded differently in the two environments for this character.

The mean squares of the regression analysis for threshing percent on the cycles of selection was similar in trend to that of grain number per panicle and were nonsignificant in LT_1 for both populations, while it was significant (0.05) for the US/R

population and highly significant (0.01) for the RS/R population in LT_2 showing that the expression of this character was not consistent among the cycles within populations and that the environment has played an important role in its expression.

The SCA mean values over the environments and replications of cycle by A-line cross combinations were regressed on the cycles of selection for the characters that has established homogeneity of error variances in the two environments. The ANOVA of the regression analysis and the regression coefficients for these traits are given in table 4.11.

An examination of table 4.11 showed that no cross of either population with the A-lines was significant for plant height and panicle length, while all crosses of both populations with the A-lines were highly significant for panicle weight and grain weight except D3A x RS/R population which was significant at the five percent level of probability. This indicated that the response of A-lines due to the cycles of improvement was linear for these two characters and there was a good fit of the linear model assumed, as evidenced by the coefficients of determination (R^2) in figure 2.

The regression analysis of the SCA means of cycle x A-lines for the characters in which homogeneity of error variances were not established was carried out in each environment. The ANOVA of the regression analysis and regression coefficients are given in tables 4.12 and 4.13.

Table 4.11: Regression analysis of SCA means pooled over environments on the selection cycles for Plant height, Panicle length, Panicle weight, and Grain weight.

Character	Regression#	D.F	Residual#	D.F.	a	b	S.E.(b)
Plant Height:							
623A	46.7	1	232.20	4	180.00	−1.630	3.64
	144.23	1	97.69	4	190.63	−2.870	2.36
D3A	44.30	1	213.70	4	155.00	1.590	3.49
	877.60	1	134.20	4	190.5	−7.080	2.77
296A	19.40	1	103.60	4	175.71	−1.050	2.43
	1059.70	1	326.20	4	198.70	−7.780	4.32
MA6	58.80	1	101.70	4	158.67	−1.830	2.41
	330.10	1	119.80	4	183.40	−4.340	2.62
Panicle Length:							
623A	1.3221	1	0.35010	4	25.478	0.275	0.141
	1.4230	1	1.69100	4	27.860	−0.285	0.311
D3A	0.01262	1	0.03313	4	26.343	0.027	0.0435
	0.00060	1	0.36150	4	26.730	0.006	0.1440
296A	0.39100	1	1.32200	4	25.490	0.149	0.2750
	1.19100	1	1.41300	4	27.370	−0.261	0.2840
MA6	1.68800	1	0.29640	4	23.301	0.311	0.1300
	0.15700	1	2.48600	4	24.730	0.095	0.3770
Panicle Weight:							
623A	7347024**	1	49375	4	3583	647.90**	53.10
	7374263**	1	40490	4	3214	649.10**	48.10
D3A	6887284**	1	268709	4	3459	627.00**	124.00
	6363761*	1	314315	4	3194	603.00*	134.00
296A	4207632**	1	16408	4	3914	490.30**	30.60
	6877877**	1	36837	4	3085	626.90**	45.90
MA6	2731623**	1	82354	4	3209	395.10**	68.60
	3786263**	1	11958	4	2708	465.10**	26.10
Grain Weight:							
623A	5095443**	1	69726	4	2600	539.60**	63.10
	5464506**	1	23013	4	2103	558.80**	36.30
D3A	4355023**	1	99796	4	2384	498.90**	75.50
	4729401**	1	176498	4	2065	520.00**	100.00
296A	2947082**	1	12321	4	2695	410.40**	26.50
	3859643**	1	23880	4	2216	469.60**	36.90
MA6	2178893**	1	74010	4	2372	352.90**	65.00
	2659021**	1	4640	4	2081	389.80**	16.30

* Significant at 5% probability level.
** Significant at 1% probability level.
# For every A-line the upper number is for US/R population, while the lower number is for RS/R population.

Table 4.12: Regression analysis of SCA means on the cycles of selection for the heterogeneous traits in LT-1 (ICRISAT 1984).

Character	Regression#	D.F	Residual#	D.F.	a	b	S.E.(b)
Flower	,						
623A	0.5690	1	3.605	4	56.42	0.180	0.454
	11.4660	1	3.100	4	53.22	0.809	0.421
D3A	8.2286*	1	0.776	4	55.93	0.686*	0.211
	18.5350	1	6.264	4	53.73	1.029	0.598
296A	2.8000	1	12.010	4	56.04	0.400	0.828
	7.1300	1	13.860	4	53.1	0.638	0.890
MA6	0.0010	1	2.354	4	58.31	-0..009	-0.020
	2.2970	1	5.240	4	54.29	0.362	0.547
100-Seed weight							
623A	0.0239	1	0.006	4	2.63	-0.037	0.019
	0.0284	1	0.009	4	2.33	-0.040	0.023
D3A	0.0103	1	0.003	4	2.39	0.024	0.013
	0.0007	1	0.027	4	2.51	0.006	0.039
296A	0.0006	1	0.002	4	2.42	-0.006	0.012
	0.0171	1	0.001	4	2.26	-0.031	0.005
MA6	0.0085	1	0.012	4	2.39	-0.022	0.026
	0.0026	1	0.115	4	2.50	-0.012	0.081
Grain No/hd							
623A	11987	1	33045	4	1602	-26.200	43.500
	293933	1	52448	4	1295	129.600	54.700
D3A	1088	1	23683	4	1677	7.900	36.800
	176202	1	109117	4	1359	100.300	79.000
296A	72772	1	34440	4	1731	-64.500	44.400
	33136	1	144833	4	1606	43.500	91.000
MA6	14115	1	27965	4	1610	28.400	40.000
	457005	1	76094	4	1145	161.600	65.900
Threshing %							
623A	14.6290	1	7.343	4	71.80	0914	0.648
	14.6290	1	4.843	4	69.80	0.914	0.526
D3A	21.7290	1	5.776	4	67.93	1.114	0.575
	6.3000	1	2.800	4	73.40	0.600	0.400
296A	0.1290	1	5.146	4	75.13	-0.086	0.544
	3.6570	1	6.419	4	71.73	0.457	0.606
MA6	0.9140	1	7.105	4	71.87	0.229	0.637
	0.2290	1	5.276	4	75.27	0.114	0.549

* Significant at 5% probability level.
** Significant at 1% probability level.
# For every A-line the upper number is for US/R population, while the lower number is for RS/R population.

Table 4.13 Regression analysis of SCA means on cycles of selection for
the heterogeneous traits in LT_2 (Bhavanisagar 1985).

	Regression#	D.F	Residual#	D.F	a	b	S.E(b)
Flowering							
623A	61.6080*	1	3.404	4	54.150	1.876*	0.441
	23.2360	1	5.162	4	57.250	1.152	0.543
DA3	50.2187**	1	0.908	4	52.959	1.694**	0.228
	24.0260*	1	1.743	4	54.290	1.172*	0.316
296A	54.8790*	1	3.030	4	55.920	1.771*	0.416
	27.6950	1	4.449	4	57.710	1.258	0.504
MA6	106.4700**	1	5.004	4	55.420	2.467**	0.535
	21.7063**	1	0.423	4	55.159	1.114**	0.155
2077A	35.7286**	1	0.386	4	64.111	1.429**	0.148
	30.2680	1	8.591	4	65.290	0	0.701
100 Seed wt.							
623A	0.0648	1	0.017	4	2.561	-0.0609	0.031
	0.0046	1	0.015	4	2.205	-0.0163	0.029
DA3	0.1128*	1	0.011	4	2.339	-0.0803*	0.025
	0.0264	1	0.034	4	1.807	0.0389	0.044
296A	0.0043	1	0.034	4	2.433	-0.0157	0.044
	0.0170	1	0.002	4	2.381	-0.0311	0.011
MA6	0.0001	1	0.016	4	2.205	0.0023	0.030
	0.0062	1	0.003	4	2.001	0.0189	0.014
2077A	0.1440	1	0.038	4	2.299	-0	0.047
	0.0158	1	0.010	4	1.810	0	0.024
Grain No/hd							
623A	781134*	1	83315	4	1164.000	211.30*	69.000
	250551**	1	6487	4	1435.000	119.70**	19.300
DA3	605584*	1	49584	4	1413.000	186.00*	53.200
	114064	1	82403	4	1736.000	80.70	68.600
296A	103250*	1	10123	4	1632.600	76.80*	24.100
	171455	1	53977	4	1548.000	99.00	55.500
MA6	17	1	44110	4	1692.000	-1.00	50.200
	279683	1	36601	4	1632.000	126.40	45.700
2077A	209257	1	107346		1103.000	0	78.300
	2149	1	86426		1610.000	0	70.300
Threshing %							
623A	0.905	1	1.29	4	77.350	0.227	0.272
	218.702**	1	4.59	4	60.420	3.535**	0.513
DA3	7.303	1	8.95	4	70.570	0.646	0.715
	102.245	1	5.21	4	63.950	2.417*	0.546
296A	8.477	1	3.28	4	71.970	0.696	0.433
	0.005	1	7.74	4	73.420	0.018	0.665
MA6	24.214	1	8.47	4	76.620	1.176	0.696
	11.587	1	3.74	4	79.070	0.814	0.463
2077A	51.274*	1	5.25		60.190	1.712*	0.548
	55.880	1	25.51		59.830	0	1.210

* Significant at the 5% probability level.
** Significant at the 1% probability level.
# for every A-line the upper number is for US/R population,while the lower number
is for RS/R population.

1) $2600 + 539.6C$ $(R^2_2 = 95\%)$
2) $2384 + 498.9C$ $(R^2_2 = 92\%)$
3) $2695 + 410.4C$ $(R^2_2 = 98\%)$
4) $2372 + 352.9C$ $(P^2 = 88\%)$

1) $2103 + 558.8C$ $(R^2_2 = 98\%)$
2) $2065 + 520.0C$ $(P^2_2 = 87\%)$
3) $2216 + 469.6C$ $(R^2_2 = 98\%)$
4) $2081 + 389.8C$ $(R^2 = 99\%)$

Grain Weight (kg/ha)
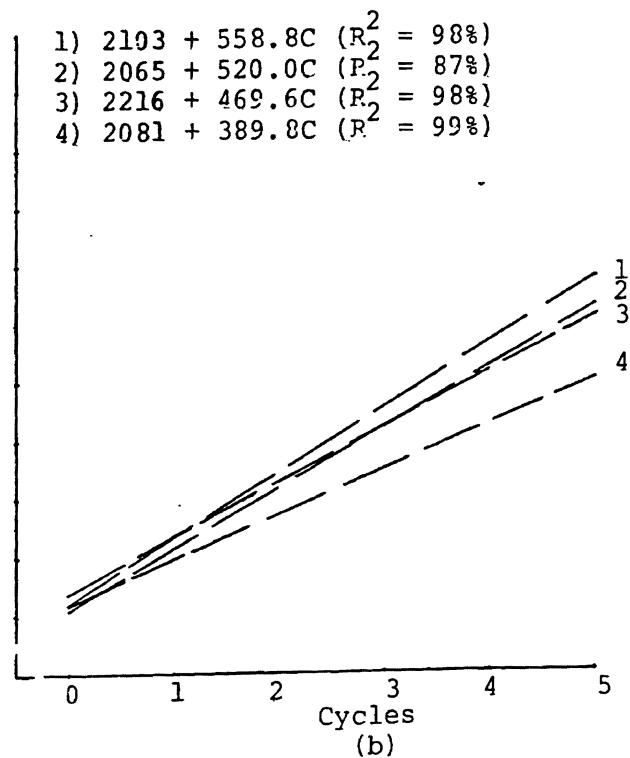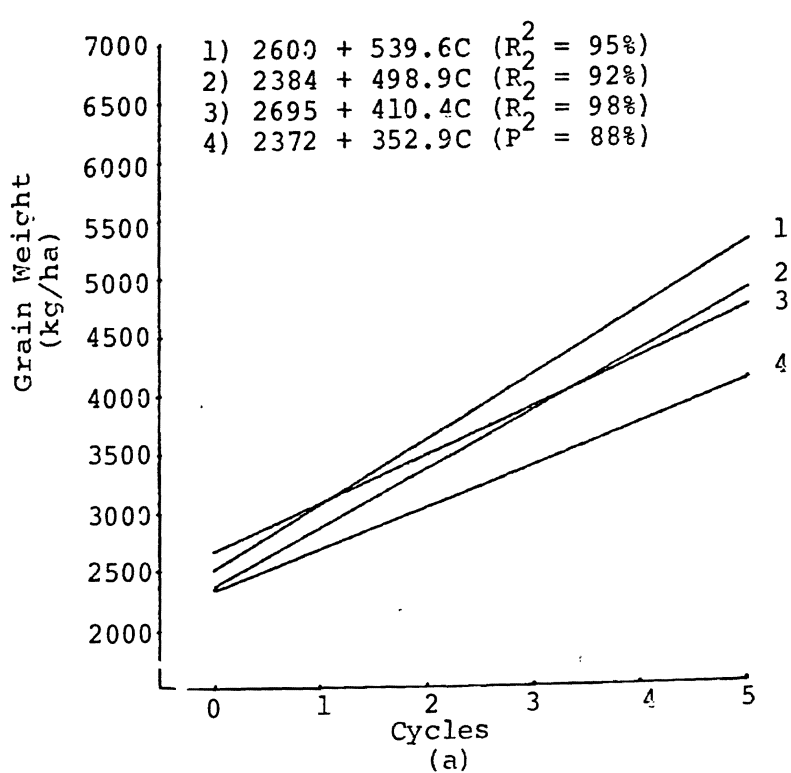
Cycles
(a)

Cycles
(b)

Figure 2: Regression of SCA means of A-line x cycles within populations on the selection cycles. a) US/R population; b) RS/R population.

1 = 623A ; 2 = D3A ; 3 = 296A ; 4 = MA6

An observation of table 4.12 showed that all the crosses were nonsignificant for all characters except the cross D3A x US/R population for days to 50% flowering which was significant at the five percent level of probability. The same thing was true in LT_2 (table 4.13) for 100-seed weight except D3A x US/R population, and for threshing percent except 623A x RS/R population. While for days to 50% flowering all crosses were either significant (0.05) or highly significant (0.01) except 623A x RS/R population, and 296A x RS/R population. For number of grains per panicle, the crosses, 623A x US/R, 623A x RS/R, D3A x US/R and 296A x US/R populations were found to be significant. The results from tables 4.12 and 4.13 suggest that the response of the A-lines due to the cycles of improvement for these characters was not consistent and the environment was greatly influencing them.

V. DISCUSSIONS AND CONCLUSIONS

Sorghum bicolor (L.) Moench is a highly self-fertilized
species with only a small percentage of cross pollination (Quinby
et al. 1958). The breeding methods that may be employed in a
particular crop are determined by its mechanism of reproduction.
Thus, most sorghum breeding programs relied almost exclusively on
pedigree-type methods. Significant progress has been made in
developing improved varieties, inbreds and hybrids by this
method. However, concern for diminishing variability and crop
vulnerability has prompted several sorghum workers to generate
broad-based random-mating populations using male sterility for
recombination (Doggett and Eberhart, 1968; Ross et al. 1971 and
Webster, O.J. 1976).

Following these developments, a substantial program on
improvement of sorghum populations was undertaken at ICRISAT.
Presently, several populations are available which are being
subjected to cycles of selection and recombination. To understand
the nature of changes that have occurred and progress made due to
recurrent selection, two of these populations, US/R and RS/R were
chosen for this investigation after five cycles of recurrent
selection.

Hallauer and Miranda (1981) stressed the importance of the
decision made about the parents included in the experiment rather
than how the experiment was conducted and analyzed. Because this
has great implications in the interpretations made from the
analysis of the data. In this study, it was assumed that the

parents are the reference genotypes and inference can only be made to those genotypes included in the experiment. The environments under which the experiment was conducted were also assumed to be fixed.

The results from the analysis of variance (ANOVA) of the hybrid experiment grown in two environments (Table 4.1) revealed that significant differences existed among the cycles within each of the two populations for all the characters studied except for panicle length within the US/R population and for number of grains per panicle within the RS/R population. However, these differences were subject to environmental influences as indicated by the significant cycles within populations x environment interactions. This was true, for all the characters within the US/R population except for number of grains per panicle, while the interactions within the RS/R population were significant only for plant height, panicle weight, and threshing percent. This indicated that the cycles within the RS/R population were more consistent than those within the US/R population for grain weight, panicle length, days to flower, and 100-seed weight.

The single-degree-of-freedom contrast between the means of the populations was significant for grain weight, panicle weight, panicle length, and plant height. However, the difference was not consistent over environments, particularly for grain weight, and panicle weight. The yield of the two populations was the same in 1984, at ICRISAT (Appendix I), but was signicantly different from each other in 1985, at Bhavanisagar (Appendix II).

There were significant differences for all the characters of
the A-lines and all the A-line x environment interactions except
for days to 50% flowering which indicated the existence of
variability among the A-lines for all the characters studied. But
these variabilities were subject to environmental influences
since their expressions were not consistent and varied with the
environments.

A-line x cycles within population interaction which reflects
the specific combining ability was found to be nonsignificant for
yield, the character of primary importance, but its interaction
with the environment was found to be significant indicating that
the specific combining ability of the A-line and cycles within
populations was different in the two environments. Similar
results were observed for panicle length of the two populations,
plant height of US/R population, and panicle weight of RS/R
population. For number of grains per panicle, the specific
combining ability of the A-lines and cycles within the
populations and its interaction with the environment was found to
be nonsignificant.

The concept of combining ability - a land mark in the
development of breeding procedures - is of great value to
breeders in designing breeding strategies.

The estimates of the general combining ability effects (GCA)
of the cycles within populations (Table 4.2) and their mean
values (Table 4.3) revealed that cycles five and four of both
populations had desirable GCA effects for grain yield as did

cycle three of the US/R population, while the remaining cycles had negative GCA effects which were significantly different from zero except cycle two of the US/R population.

Cycles five and four had not only good GCA effects for grain yield, but they also had desirable GCA effects for panicle weight, and threshing percent. For both populations only cycle five had a desirable GCA effect for the number of grains per panicle. In all instances, the average performance of cycle five of the two populations was greater than the average performance of any other cycle for the traits mentioned above, and they were always followed by cycle four. The average performance of the first three cycles were always poor. This suggested that recurrent selection has been effective in improving the GCA effects of the populations for these traits.

The GCA effects for days to 50% flowering has increased and was maximum at cycle five for US/R population which indicated that recurrent selection resulted in delay in flowering for this population, while the GCA effects of RS/R population was fluctuating as it was reduced for the first two cycles of selection, then increased the following two cycles, and slightly dropped in the last cycle of selection. It appears that the change in maturity was due to associated effect of increased yield for US/R population, while that of RS/R population appears to be a function of the direction of selection.

For plant height, the GCA effects were significantly reduced for the first two cycles of selection (first three cycles in the

case of RS/R population) and then increased later on. This
character might also be changing in response to the direction of
selection.

An observation of the GCA effects for yield components
indicated that while the GCA effects of panicle length and
hundred-seed weight for the two populations remained unchanged,
the GCA effects for threshing percent of both populations has
improved in the last two cycles of selection, and there was a
marginal increase for grain number per panicle. It was realized
that there was no deliberate selection for these yield components
during selection except that bold grains were generally
preferred.

Estimates of the GCA effects of the A-lines and their mean
values (Table 4.4 and 4.5) identified A-line 623A as a good
general combiner for grain yield. It was the only A-line with
significant positive GCA effect for yield. This line had also
desirable GCA effects for panicle weight, panicle length and 100-
seed weight. For plant height, it was the tallest with GCA
effect that was significantly different from zero which is
desirable in most cases except where the crop is harvested
mechanically for grain (Quinby and Schertz, 1970). A-line 623A
can be an excellent parent in hybrid combinations.

The A-line D3A was the next highest in mean grain yield
though its GCA effect was not significantly different from zero.
But this line had desirable GCA effects which were significantly
different from zero for panicle weight, panicle length, and

number of grains per panicle. It also had the lowest GCA effect which was significant for days to flower which is desirable in areas with short growing seasons.

Among the A-lines, MA6 had the lowest average performance for grain yield, panicle weight, panicle length, and plant height which were significantly different from zero. Its threshing percent which was the highest and significant, is of interest. If this trait is highly heritable, the line could be used in a breeding program.

SCA is useful in selecting or evaluating materials that combine well with each other but generally do not do well in other combinations. In this set of materials nonsignificant SCA effects were found for all the crosses for grain yield except two crosses. This may be explained by the fact that the SCA effects are of little importance in this material, and the two significant crosses could represent chance deviates from zero as the A-lines x cycles and A-line x cycles within populations were non-significant (Table 4.1).

Matzinger (1953), Rawlings and Thompson (1962) and Hallauer (1975) all defined a good tester as one that classifies correctly and discriminates efficiently among the genotypes under study. It was also mentioned that no one tester is ideal for all genotypes. In this study non-significant A-line x cycles within population effects for grain yield, the trait of major interest, indicates that the A-lines used as testers would rank the cycles within populations similarly . Table 4.7 lists the means of the

crosses for the characters studied and the rank of yield of the cycles within populations within each A-line.

All four A-lines ranked cycle five of each of the two populations as the top yielding cycle; cycle four as the second; cycle three as the third; cycle two as the fourth; cycle one as the fifth, except RS/R population in A-line 2 which was ranked sixth; and cycle zero as the sixth.

In general, the A-lines accurately evaluated the cycles within populations for grain yield and were consistant in their ranking.

The populations, on the other hand, appeared as competent testers of the A-lines (Table 4.7). They were able to discriminate efficiently among the A-lines and rank them accordingly.

Ultimately, it appears that the groups of genotypes used in this study are suitable testers for each other, particularly if specific combining ability is to be considered.

The results from the regression analysis of the GCA mean values of the cycles within populations on the selection cycles showed significant linear regression for grain yield, and panicle weight for both populations (table 4.8) and for days to 50% flowering for US/R population (tables 4.9 and 4.10) indicating that the response to selection for these traits was mainly due to linear component of the regression. The regression coefficient (b) expressed in percent of the original mean predicted by the

linear regression (ĝ) for grain yield, which is a good reference point (Hallauer and Miranda 1981), was found to be 17.9% and 22.9% for US/R and RS/R population, respectively. For days to 50% flowering of US/R populations, recurrent selection resulted in delay in flowering, but the response was different in the two environments, i.e. the delay in flowering per cycle of selection was 0.677 (1 day) in LT-1 (Table 4.9) and 1.955 (2 days) in LT-2 (Table 4.10).

Non significant linear regression analysis for the other traits means that the true relationship between the response and the cycles of improvement is not linear but does not imply that there is no response to selection. Deviations from the linear model involved different effects as can be seen from Table 4.2. For instance, deviations due to quadratic effect can be observed for height of the two populations, while cubic effect can be noticed for threshing percent of the two populations. It can be concluded that most traits have improved in the last cycle/cycles as compared to the original populations, and a much higher rate of selection advance can be realized for any one particular trait than was observed in this study if selection pressure is applied for only that trait, i.e. it has been observed as the number of traits selected for increases, the gain per cycle for each trait decreases compared to a situation where selection is only one of the traits.

The regression analysis of A-line x cycles within population mean grain yield and panicle weight on the selection cycles (Table 4.11) was significant for all the crosses indicating that

the response of A-lines was in linear direction to the improvement of the cycles. There was no interaction between the A-lines and the cycles within each population as revealed by figure 2 and by the tests of their slopes which were not significantly different from each other. This finding is in agreement with the results of the ANOVA (Table 4.1).

The regression analysis of A-lines x cycles within populations for the other traits (tables 4.12 and 4.13) indicated that the response of the A-lines to cycles of improvement was subject to environmental influences.

From the results obtained in this study, the following conclusions can be drawn:

1. Five cycles of recurrent selection have been effective in increasing the grain yield of the two populations, delayed the flowering of US/R population, and resulted ina simultaneous improvement of all other traits inthe desired directions, except panicle length and 100-seed weight which remained unchanged.

2. Selection for grain yield was effective primarily for general combining ability, which indicates that the improvement of this trait has involved largely additive effects. A per cycle selection gain in the GCA mean of about 17.9% and 22.9% was found for US/R and RS/R population, respectively.

3. Specific combining ability (SCA) appeared to be of little importance, particularly in grain yield, for these two populations.

VI. SUMMARY

Field experiments were conducted at the Center of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, during the rainy season (Kharif) of 1984, and at Bhavanisagar, under irrigation, during the Summer season of 1985 to examine the effect of recurrent selection on general and specific combining abilities of two random=mating sorghum populations. viz., US/R and RS/R populations.

The entries were planted in a randomized complete block design (RCBD) with three replications in both environments. The experimental unit consisted of six row plots 4 meters long with spacing between rows of 75 cm., and were thinned after emergence to about 12 cm. between plants. The data were recorded on: Days to 50% flowering, plant height, panicle length, 100-seed weight, grain number per panicle, threshing percent, panicle weight, and grain yield.

On the basis of the results obtained from this experiment, the following observations were made:

1) Five cycles ofrecurrentselectionsresultedin a linear improvement in grain yield for both populations.

2) Selection for grain yield was effective primarily for general combining ability which indicated that the improvement of this trait largely involved additive effects, and a per cycle

selection gain of about 17.9% and 22.9% was determined for US/R and RS/R populations respectively.

3) Specific combining ability does not appear to be important particularly for grain yield of the two populations.

4) Five cycles of recurrent selection have also been effective in reducing the plant height ,and increasing the maturity of both populations. While for yield components, significant improvement was realized for grain number per panicle, and threshing percent in the last cycle/cycles.

Based on the above observations, it was concluded that recurrent selection following progeny evaluation (S_1 and S_2) has been very successful in increasing the mean of the populations in the desired direction, and that there was a mean selection advance of 18% and 23% per cycle for grain yield of US/R and RS/R populations, respectively.

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Appendix I. Analysis of Variance for Hybrid Experiment in LT-1 (ICRISAT, 1984)

Source	D.F.	Days to 50% Flowering	Plant Height	Panicle Length	100-Seed Weight
Replication	2	9.174	12491.2	46.711	0.03295
Hybrids	47	18.850**	1072.2**	8.240**	0.1074**
A-Lines	3	44.269**	3677.6**	11.553*	0.75872*
Cycles	11	21.588**	2271.1**	14.350**	0.08878*٦
Cycles between populations	1	10.028	2952.1**	18.119*	0.33063*٦
Cycles within population 1	5	25.656**	1343.8**	16.442**	0.05658*
Cycles within population 2	5	19.833**	3062.2**	11.502*	0.07260*
A-Line x Cycle	33	15.627**	435.7*	5.900*	0.05439*
A-Line x Cycles between populations	3	7.935	239.8	7.378	0.02410
A-Line x Cycles between population 1	15	10.196*	405.9*	5.815	0.02930
A-Line x Cycles between population 2	15	22.596**	504.7*	5.690	0.08554٦
Error	94	4.372	206.7	3.509	0.01825
C.V.%		3.7	8.1	7.7	5.7
E.S.E. (A-Lines)		0.348	2.4	0.312	0.0225
E.S.E. (Cycles)		0.604	4.15	0.541	0.0390
E.S.E. (A-Line x Cycle)		1.207	8.30	1.082	0.0780

Appendix I. Continued

Source	D.F.	Panicle Wt. per ha	Grain weight per hectar	Grain No. per Panicle	Threshing Percent
Replication	2	1869482	833825	24239	3.861
Hybrids	47	6064227**	4119321**	223553	21.092**
A-Lines	3	6064227**	15616004**	435435	85.861**
Cycles	11	31056408**	8980944**	276553	56.755**
Cycles between populations	1	15128916**	1018	—	3.361
Cycles within population 1	5	4	8040367**	—	78.800**
Cycles within population 2	5	11847295**	11717506**	—	45.389**
A-Line x Cycle	33	770647*	456657*	186624	3.316
A-Line x Cycles between populations	3	1172635*	695867*	—	1.417
A-Line x Cycles between population 1	15	635084	400219*	—	1.800
A-Line x Cycles between population 2	15	825812*	465253*	—	5.211
Error	94	410760	224381	268379	3.202
C.V.%		12.3	12.3	31.0	2.4
E.S.E. (A-Lines)		106.8	78.9	86.3	0.298
E.S.E. (Cycles)		185.0	136.7	149.5	0.517
E.S.E. (A-Line x Cycle)		370.0	273.5	299.1	1.033

* significant at 5% level of probability
** significant at 1% level of probability
C.V.% coefficient of variation
E.S.E. effective standard error

Appendix II. Analysis of Variance for Hybrid Experiment in LT-2 (Bhavanisagar, 1985)

Source	D.F.	Days to 50% Flowering	Plant Height	Panicle Length	100-Seed Weight
Replication	2	35.44	2226.50	2.272	2.1395
Hybrids	59	73.88*	899.63**	10.277**	0.13272**
A-Lines	4	604.64**	3311.00**	88.078**	0.91435**
Cycles	11	127.10**	2538.5**	5.980*	0.16493**
Cycles between populations	1	31.25	653.6	2.222	0.73089**
Cycles within population 1	5	181.16**	2740.50**	5.413	0.18729*
Cycles within population 2	5	92.20**	2713.5**	7.298*	0.02939
A-Line x Cycle	44	12.33	270.7	4.278*	0.05361
A-Line x Cycles between populations	4	51.06*	670.9*	8.444*	0.02211
A-Line x Cycles between population 1	20	8.70	260.2	2.986	0.07131
A-Line x Cycles between population 2	20	8.20	201.1	4.737*	0.04221
Error	118	10.43	211.7	2.656	0.04385
C.V.%		5.2	8.9	5.6	9.8
E.S.E. (A-Lines)		0.538	2.43	0.272	0.0349
E.S.E. (Cycles)		0.834	3.76	0.421	0.0541
E.S.E. (A-Line x Cycle)		1.864	8.4	0.941	0.1209

Appendix II. Continued

Source	D.F.	Panicle Weight/ha	Grain Weight/ha	Grain Number per Panicle	Threshing Percent
Replication	2	3553134	4866718	4508887	269.16
Hybrids	59	5379754**	4255101**	350503*	117.19**
A-Lines	4	12650476**	13537391**	1085074**	1076.04**
Cycles	11	15082995**	11049478**	595128**	106.49**
Cycles between populations	1	13873459**	9414968*	358827	56.78
Cycles within population 1	5	18902412**	1503436**	802364**	53.28
Cycles within population 2	5	11505486**	12742690**	435151*	169.65**
A-Line x Cycle	44	825763*	552180**	222568**	32.69
A-Line x Cycles between populations	4	1881684*	1503436**	316179*	55.65
A-Line x Cycles between population 1	20	933045*	520378*	230982*	16.65
A-Line x Cycles between population 2	20	507297	393730	143433*	43.92
Error	118	464108	256447	99320	31.00
C.V.%		13.5	13.4	17	7.5
E.S.E. (A-Lines)		113.5	84.4	52.5	0.923
E.S.E. (Cycles)		175.9	130.8	81.4	1.438
E.S.E. (A-Line x Cycle)		393.3	292.4	182.0	3.214

* significant at 5% level of probability
** significant at 1% level of probability
C.V.% coefficient of variation
E.S.E. effective standard error

Appendix III: GCA effects of A-lines and cycles in LT_1 (ICRISAT 1984).

	Females				Males											
	623A	D3A	296A	MA6	US/R-C0	US/R-C1	US/R-C2	US/R-C3	US/R-C4	US/R-C5	RS/R-C0	RS/R-C1	RS/R-C2	RS/R-C3	RS/R-C4	RS/R-C5
FLWERING :	0.32	-1.21**	1.38*	-0.49	-0.35	-1.76**	-0.35	0.15	1.65*	2.24*	0.07	-0.76	-2.43*	-0.43	0.82	1.15
PLANT HEIGHT :	10.44**	-1.33	4.22	-13.33**	9.89*	-4.69	-15.69*	-17.78*	0.31	0.81	30.72	17.89	-1.53	-6.69	-6.11	-7.11
PANICLE LENGTH :	-0.22	0.61	0.28	-0.68*	-1.37*	-1.5**	-0.78	-0.67	0.90	1.28*	-0.58	0.33	2.06*	0.82	-0.09	-0.42
100 SEED WEIGHT :	0.07**	-0.21**	0.02	0.12**	0.05	0.02	0.07	0.15*	0.04	-0.06	-0.06	-0.04	0.10*	-0.08	-0.09*	-0.12**
THRESHING % :	0.96**	-0.82**	-1.74*	1.60**	0.01	-1.99**	-3.99*	0.01	2.01*	3.01*	-0.99	1.01	2.01*	-2.99*	-0.15	2.01**
GRND./PANICLE :	-161.84	84.02	37.1	40.72	-201.76	-11.17	83.91	-116.51	92.66	145.99	-262.26	-10.01	241.58	11.91	-118.42	144.08
PANICLE WEIGHT :	733.97**	377.03**	247.63*	-1358.62**	-1299.60**	-657.93**	72.63	301.1	-62.79	1647.63*	-1422.51	-1225.29	-891.26*	820.54*	1007.35*	1710.13**
GRAIN WEIGHT :	590.75**	245.60**	102.54	-938.89**	-958.80**	-575.47**	-162.97	226.62	66.2	1420.37*	-1091.41	-366.44	-566.44*	421.76*	679.40*	1407.17**

* Significant at the 5% probability level.
** Significant at the 1% probability level.

Appendix IV: GCA effects of the A-lines and the cycles in LT_2 (Bhavanisagar 1985).

	Females					Males											
	623A	D3A	296A	MA6	2077A	US/R-C0	US/R-C1	US/R-C2	US/R-C3	US/R-C4	US/R-C5	RS/R-C0	RS/R-C1	RS/R-C2	RS/R-C	RS/R-C4	RS/R-C5
Flowering	-1.56**	-3.92**	-0.45	-1.01	6.94**	-4.09**	-2.56**	-0.83	1.77*	3.57**	4.64**	-2.49**	-2.36**	-1.76*	-1.36	2.64**	2.84**
Plant Height	4.86*	-11.95**	-0.01	-5.84*	12.94**	15.12**	-18.95**	-17.55**	4.72	1.25	3.98	27.05**	2.78	-4.68	-10.6**	-6.40	3.30
Head Length	0.99**	0.04	-0.34	-2.4**	1.71**	-0.11	-0.04	0.49	0.42	-0.24	-1.18**	-0.38	0.02	1.09*	0.75	0.05	-0.78
100-seed Weight	0.12**	-0.13**	0.19*	0.01	-0.18**	0.11*	0.15**	0.19**	0.06	0.00	-0.12*	-0.11*	-0.06	-0.05	-0.01	-0.12*	-0.03
Grain No./Head	25.12	188.09**	44.55	28.2	-285.96**	-244.94**	-248.44**	-165.51*	-31.60	69.85	352.74**	-128.86	-84.61	-92.26	106.22	187.74*	279.65**
Threshing Perce	1.57	-1.28	0.04	7.43**	-7.77**	-2.03*	-0.16	0.92	-0.59	2.04*	3.18**	-4.21**	-2.73*	-3.41**	0.50	2.77*	3.71**
Panicle Weight	325.93*	306.25**	384.95*	11.11	-1028.24**	-906.94**	-675.46**	-285.65*	281.02*	1496.76*	1756.02**	-1201.39**	-1030.09**	-669.91**	-272.69*	496.76**	1011.57**
Grain Weight	326.85*	138.97	258.56*	361.96**	-1086.34**	-760.19**	-521.30**	-190.74*	153.70*	1219.44**	1471.3**	-1090.74**	-876.85**	-629.63**	-208.33*	475.93**	957.41**

* Significant at the 5% probability level.
** Significant at the 1% probability level.

Appendix V: SCA effects for the characters studied in LT_1 (ICRISAT 1984).

A-line	x Cycles	FLOWERING	PLANT HEIGHT	HEAD LENGTH	100 SEED WEIGHT	Gr.No. /Head	THRESHING Percent	HEAD WEIGHT	GRAIN WEIGHT
623A	x US/R-C0	-0.24	15.97	0.37	0.02	267.17	0.04	43.81	29.39
623A	x US/R-C1	3.51**	-9.44	-0.24	0.08	254.26	1.04	-220.08	-117.83
623A	x US/R-C2	-2.57*	-8.11	-1.60	0.04	-164.49	-0.96	-150.64	-174.77
623A	x US/R-C3	-1.40	0.97	0.53	-0.01	-124.74	0.04	12.56	35.64
623A	x US/R-C4	-0.57	5.89	-0.07	-0.06	-166.91	1.04	757.00*	682.17*
623A	x US/R-C5	-1.49	-3.94	0.61	-0.06	-41.58	0.04	-592.30	-388.66
D3A	x US/R-C0	-0.71	-9.25	0.51	0.10	59.98	-0.18	53.53	35.65
D3A	x US/R-C1	-1.63	0.67	2.35*	-0.04	-400.6	-0.18	56.31	24.54
D3A	x US/R-C2	1.63	-1.33	-0.18	-0.05	-57.69	-0.18	-110.36	-112.96
D3A	x US/R-C3	1.46	-7.25	-0.12	0.00	112.4	0.82	-241.61	-149.76
D3A	x US/R-C4	0.96	-9.67	0.07	-0.11	-147.1	-0.18	-1013.83*	-778.24**
D3A	x US/R-C5	-1.29	17.17*	-2.39*	-0.07	411.56	-0.18	250.75	159.26
296A	x US/R-C0	-0.96	-2.14	-0.44	0.00	88.23	-0.26	-650.40	-468.52
296A	x US/R-C1	-0.54	15.44	-2.05	-0.04	37.31	-1.26	-114.29	-140.74
296A	x US/R-C2	1.04	15.11	1.72	0.05	115.23	-0.26	-205.96	-169.90
296A	x US/R-C3	0.54	-10.81	-0.60	-0.12	-75.35	-0.26	-17.76	-48.38
296A	x US/R-C4	-0.96	8.11	-1.76	0.11	-17.85	-0.26	26.68	-15.74
296A	x US/R-C5	-0.54	-4.39	-0.10	0.20	-156.19	0.74	585.71	471.76
MA6	x US/R-C0	1.9	-4.58	-0.45	-0.12	-415.38	0.4	553.07	403.48
MA6	x US/R-C1	-1.35	-6.67	-0.07	-0.01	109.03	0.4	278.07	234.03
MA6	x US/R-C2	-0.10	-5.67	0.06	-0.03	106.95	1.4	466.96	457.64
MA6	x US/R-C3	-0.6	17.08*	0.20	0.13	87.7	-0.6	246.81	162.50
MA6	x US/R-C4	0.57	-4.33	1.77	0.07	331.87	-0.6	230.15	111.81
MA6	x US/R-C5	3.32**	-8.83	1.89	-0.08	-213.8	-0.6	-244.16	-242.36

Appendix V Contd.

A-line	x Cycles	FLOWERING	PLANT HEIGHT	HEAD LENGTH	100 SEED WEIGHT	Gr.No. /Head	THRESHING Percent	HEAD WEIGHT	GRAIN WEIGHT
623A	RS/R-C0	1.68	−14.53	1.70	0.09	287.67	0.04	−72.16	−57.33
623A	RS/R-C1	1.51	3.31	0.94	−0.05	206.76	−0.96	−16.61	−54.64
623A	RS/R-C2	−1.15	−7.94	0.58	−0.17*	30.51	1.04	99.36	145.36
623A	RS/R-C3	−1.49	4.22	−1.95	−0.01	−232.49	0.04	−259.67	−165.05
623A	RS/R-C4	−2.07	8.64	−0.44	0.03	−82.83	1.54	103.53	32.86
623A	RS/R-C5	4.26**	4.97	−0.43	0.10	−233.33	−2.96*	295.20	32.86
D3A	RS/R-C0	−2.46*	12.25	0.10	0.09	81.81	−0.18	293.11	201.59
D3A	RS/R-C1	−1.63	−9.58	−1.35	0.09	−414.77	0.82	−65.22	−3.94
D3A	RS/R-C2	1.71	5.50	−0.14	−0.09	389.31	−2.18*	−568.69	−515.04
D3A	RS/R-C3	1.04	−1.00	−0.01	0.05	9.65	−0.18	713.95	457.87
D3A	RS/R-C4	5.46**	8.42	0.39	0.01	94.65	−0.01	143.81	139.12
D3A	RS/R-C5	−4.54**	−5.92	0.77	0.02	−139.19	1.82	488.25	541.9
296A	RS/R-C0	1.96	5.69	0.86	−0.02	20.73	−0.26	−349.71	−247.01
296A	RS/R-C1	−0.54	−5.14	2.10	0.13	156.48	0.74	72.51	103.01
296A	RS/R-C2	1.13	17.61*	−0.73	−0.17*	−219.77	0.74	−233.74	−133.10
296A	RS/R-C3	−0.54	−22.56*	0.29	−0.15	107.56	−0.26	12.79	−26.85
296A	RS/R-C4	−0.13	−14.81	1.14	−0.05	−21.44	−0.1	778.76*	582.18*
296A	RS/R-C5	−0.46	−2.14	−0.43	0.05	−34.94	0.74	95.43	93.29
MA6	RS/R-C0	−1.18	−3.42	−2.66*	−0.16	−390.22	0.4	128.76	102.75
MA6	RS/R-C1	0.65	11.42	−1.70	−0.17*	51.33	−0.6	9.32	−44.44
MA6	RS/R-C2	−1.68	−15.17	0.30	0.44*	−200.05	0.4	703.07	502.78
MA6	RS/R-C3	0.99	19.33*	1.67	0.11	115.28	0.4	−467.07	−265.97
MA6	RS/R-C4	−3.26**	−2.25	−1.09	0.01	9.62	−1.43	−1026.1**	−754.16**
MA6	RS/R-C5	0.74	3.08	0.09	−0.17*	407.45	0.4	−878.88*	−668.05*

* Significant at the 5% probability level.
** Significant at the 1% propbability level.

Appendix VI: SCA effects for the characters studied in LT_2 (Bhavanisagar 1985).

A-Line x Cycle	Days to 50% Flowering	Plant Height	Panicle Length	100-seed Weight	Grain No. Panicle	Threshing Percent	Panicle Weight	Grain Weight
623A x US/RC-0	-0.91	-3.26	0.28	0.03	-120.19	4.52	-447.22	-198.15
623A x US/RC-1	0.89	10.14	0.21	0.17	-156.97	2.99	-187.96	-52.78
623A x US/RC-2	-2.17	-1.59	-0.66	0.05	-122.81	1.10	-188.89	-105.56
623A x US/RC-3	-0.11	3.14	0.08	-0.09	131.41	1.64	133.33	179.63
623A x US/RC-4	-3.24	3.94	0.74	-0.09	721.48**	2.19	811.11*	808.33**
623A x US/RC-5	1.36	-13.12	0.01	0.14	-34.64	0.24	547.22	491.67
D3A x US/RC-0	-0.88	7.88	0.22	0.04	46.82	-1.42	-10.88	-79.71
D3A x US/RC-1	0.92	-5.05	-0.84	0.16	-284.22	-1.3	-459.95	-392.67
D3A x US/RC-2	0.19	6.88	0.29	-0.14	179.69	1.79	39.12	128.63
D3A x US/RC-3	0.59	-6.05	-0.31	0.05	-1.50	1.98	157.64	214.74
D3A x US/RC-4	-0.88	5.08	-0.64	-0.08	161.23	1.98	497.45	510.11
D3A x US/RC-5	-0.94	8.68	1.96*	-0.08	302.52	-5.15	1215.05**	522.14
296A x US/RC-0	1.65	7.94	0.61	-0.13	90.85	1.89	475.23	458.10
296A x US/RC-1	-2.88	-3.33	0.21	-0.14	110.44	0.56	544.68	436.81
296A x US/RC-2	0.38	1.27	1.68	0.20	41.72	-2.62	469.68	208.10
296A x US/RC-3	-0.88	9.01	0.74	-0.06	219.92	-0.54	403.01	284.95
296A x US/RC-4	-1.02	2.47	0.08	-0.01	-43.58	-0.87	71.53	-12.27
296A x US/RC-5	0.25	1.07	0.01	0.07	-130.15	0.96	-1150.69**	-768.75**
MA6 x US/RC-0	0.21	-3.23	-1.33	-0.07	-101.69	-3.98	-67.59	-284.18
MA6 x US/RC-1	1.34	8.17	0.27	-0.18	271.52	1.00	-53.70	-50.85
MA6 x US/RC-2	1.27	-2.56	0.73	0.10	-25.22	-0.21	130.56	90.82
MA6 x US/RC-3	2.01	-16.49	-0.87	-0.04	-62.17	-1.00	-176.85	-165.66
MA6 x US/RC-4	6.21**	-20.69*	-1.53	0.08	-548.6**	-3.72	-1087.04**	-995.29**
MA6 x US/RC-5	1.47	-9.43	-1.93*	0.17	-424.66*	1.01	-415.74	-136.03
2077A x US/RC-0	-0.07	-9.34	0.22	0.12	84.21	-1.01	50.46	103.94
2077A x US/RC-1	-0.27	-9.94	0.16	-0.02	59.23	-3.24	156.94	59.49
2077A x US/RC-2	0.33	-4.01	-2.04*	-0.21	-73.38	-0.06	-450.46	-321.99
2077A x US/RC-3	-1.61	10.39	0.36	0.13	-287.66	-2.09	-517.13	-513.66
2077A x US/RC-4	-1.07	9.19	1.36	0.11	-290.53	0.42	-293.06	-310.88
2077A x US/RC-5	-2.14	12.79	-0.04	-0.31*	286.93	2.93	-195.83	-109.03

A-Line x Cycle#	Days to 50% Flowering	Plant Height	Panicle Length	100-seed Weight	Grain No. Panicle	Threshing Percent	Panicle Weight	Grain Weight
623A x RS/RC-0	0.16	-14.19	-1.12	-0.01	-163.80	-5.75	-439.81	-585.19*
623A x RS/RC-1	2.36	7.74	-0.52	-0.02	-86.62	-7.73*	-384.26	-646.3*
623A x RS/RC-2	-0.24	-2.79	1.41	0.03	-5.80	-1.54	112.04	-69.44
623A x RS/RC-3	-0.31	0.81	0.74	0.06	-210.26	-0.85	136.11	13.89
623A x RS/RC-4	2.36	2.28	-0.46	-0.17	-7.19	2.41	-281.48	-50.00
623A x RS/RC-5	-0.17	6.88	-0.72	-0.11	55.39	0.78	189.81	213.89
D3A x RS/RC-0	0.19	0.95	0.82	-0.20	252.61	-1.22	144.68	61.03
D3A x RS/RC-1	-0.94	-2.45	0.42	-0.04	-172.36	-2.04	-517.36	-402.85
D3A x RS/RC-2	0.79	-4.65	-0.98	0.19	-274.08	3.95	-173.84	21.22
D3A x RS/RC-3	1.39	-1.05	-0.64	0.11	-272.85	-3.19	-284.03	-363.04
D3A x RS/RC-4	0.72	-5.58	-1.18	-0.09	-100.82	1.79	-766.44	-510.26
D3A x RS/RC-5	-1.14	-4.65	0.89	0.07	162.97	2.83	158.56	290.66
296A x RS/RC-0	1.72	11.01	-0.46	0.11	-145.02	3.71	-322.92	-58.56
296A x RS/RC-1	-2.08	-10.06	0.14	0.12	-193.28	5.59	-276.62	23.84
296A x RS/RC-2	-0.35	-0.59	0.74	-0.02	270.64	-0.87	673.38	396.99
296A x RS/RC-3	2.58	-18.33*	-3.26**	-0.04	-239.47	-2.6	-385.88	-362.27
296A x RS/RC-4	0.92	-3.53	0.54	-0.02	239.12	-1.83	-146.06	-176.16
296A x RS/RC-5	-0.28	3.07	-1.06	-0.08	-221.19	-3.38	-355.32	-430.79
MA6 x RS/RC-0	-2.39	-0.16	0.93	0.02	-183.01	0.82	60.19	0.08
MA6 x RS/RC-1	-2.19	2.77	1.53	-0.04	367.63*	3.56	583.33	536.19
MA6 x RS/RC-2	-0.79	4.24	0.47	-0.12	96.00	3.59	-216.67	-95.29
MA6 x RS/RC-3	-1.53	14.51	1.13	0.02	264.37	1.60	344.44	367.67
MA6 x RS/RC-4	-3.53	14.64	0.27	0.05	171.54	0.68	649.07	660.26*
MA6 x RS/RC-5	-2.06	8.24	0.33	0.02	174.30	-3.36	250	72.30
2077A x RS/RC-0	0.33	2.39	-0.18	0.08	239.21	2.45	557.87	582.64*
2077A x RS/RC-1	2.86	1.99	-1.58	-0.02	84.63	0.62	594.91	489.12
2077A x RS/RC-2	0.59	3.79	-1.64	-0.08	-86.75	-5.12	-394.91	-253.47
2077A x RS/RC-3	-2.14	4.06	2.02*	-0.14	458.21*	5.05	189.35	343.75
2077A x RS/RC-4	-0.47	-7.81	0.82	0.23	-302.65	-3.06	544.91	76.16
2077A x RS/RC-5	3.66	-13.54	0.56	0.10	-171.47	3.12	-243.06	-146.06

* Significant at the 5% probability level.
** Significant at the 1% probability level.

Appendix I. Analysis of Variance for Hybrid Experiment in LT-1 (ICRISAT, 1984)

| Source	D.F.	Days to 50% Flowering	Plant Height	Panicle Length	100-Seed Weight
Replication	2	9.174	12491.2	46.711	0.03295
Hybrids	47	18.850**	1072.2**	8.240**	0.1074**
A-Lines	3	44.269**	3677.6**	11.553*	0.75872*
Cycles	11	21.588**	2271.1**	14.350**	0.08878*
Cycles between populations	1	10.028	2952.1**	18.119*	0.33063*
Cycles within population 1	5	25.656**	1343.8**	16.442**	0.05658*
Cycles within population 2	5	19.833**	3062.2**	11.502*	0.07260*
A-Line x Cycle	33	15.627**	435.7*	5.900*	0.05439*
A-Line x Cycles between populations	3	7.935	239.8	7.378	0.02410
A-Line x Cycles between population 1	15	10.196*	405.9*	5.815	0.02930
A-Line x Cycles between population 2	15	22.596**	504.7*	5.690	0.08554*
Error	94	4.372	206.7	3.509	0.01825
C.V.%		3.7	8.1	7.7	5.7
E.S.E. (A-Lines)		0.348	2.4	0.312	0.0225
E.S.E. (Cycles)		0.604	4.15	0.541	0.0390
E.S.E. (A-Line x Cycle)		1.207	8.30	1.082	0.0780

Genetic Resources and Enhancement Program

Sorghum

Pearl millet
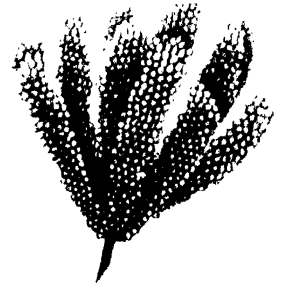
Finger millet

Archival Report for 1998 and 1999

Groundnut

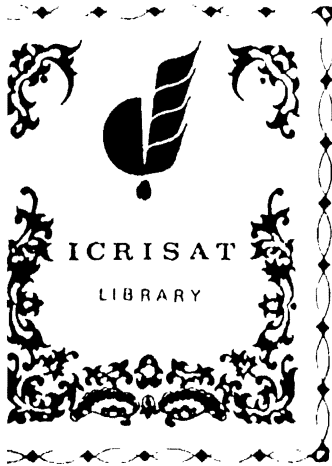Pigeonpea

Chickpea

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