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New early-maturing germplasm lines for utilization in chickpea improvement

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Abstract Early-maturity helps chickpea to avoid terminal heat and drought and increases its adaptation especially in the sub-tropics. Breeding for early-maturing, high-yielding and broad-based cultivars requires diverse sources of early-maturity. Twenty-eight early-maturing chickpea germplasm lines representing wide geographical diversity were identified using core collection approach and evaluated with four control cultivars in five environments for 7 qualitative and 16 quantitative traits at ICRISAT Center, Patancheru, India. Significant genotypic variance was observed for days to flowering and maturity in all the environments indicating scope for selection. Genotypes × environment interactions were significant for days to flowering and maturity and eight other agronomic traits. ICC 16641, ICC 16644, ICC 11040, ICC 11180, and ICC 12424 were very early-maturing, similar to or earlier than control cultivars Harigantars and ICCV 2. The early-maturing accessions produced on average 22.8% more seed yield than the mean of four control cultivars in the test environments. ICC 14648, ICC 16641 and ICC 16644 had higher 100-seed weight than control cultivars, Annigeri and ICCV 2. Cluster analysis delineated three clusters, which differed significantly for all the traits. First cluster comprised three controls, ICCV 96029, Harigantars, ICCV 2 and two germplasm lines, ICC 16644 and ICC 16641, second cluster comprised 13 germplasm lines and control cultivar Annigeri, and third cluster comprised 13 germplasm lines. Maturity was main basis of delineation of the first cluster from others. Plot yield and its associated traits were the main basis for delineation of the second cluster from the others. Identification of these diverse early-maturing lines would be useful in breeding broad-based, early-maturing and high-yielding cultivars.

Keywords Chickpea · Diversity · Early-maturity · Genetic resources · Quantitative trait · Utilization

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Introduction

Chickpea (*Cicer arietinum* L.) is an important food legume ranking third among the world's pulse crops. It is grown in 52 countries on an area of about 10.61 million ha annually producing about 8.69 million tons (FAO 2005). The Indian sub-continent (India, Pakistan, Myanmar, Bangladesh and Nepal)

contributes about 77.3% to the world's chickpea production. Chickpea is also cultivated in eastern Africa, Mediterranean and Near-East countries, Australia, Southern Europe, and North and South America. Being a legume, chickpea is a rich source of quality protein and starch to the predominantly vegetarian population in India, and other countries in South Asia and Near-East. In the developed countries chickpea is regarded as a health food. Chickpea is a valuable source of vegetable protein, as it is devoid of any anti-nutritional factors except oligosaccharides, which cause flatulence. However, cooking is known to overcome the problem of flatulence (Williams and Singh 1987).

In the last four decades area under chickpea has declined, replaced by crops like wheat, which produce higher and more stable yields under high input irrigated environments (Kelley and Parthasarathy 1994). As a result, chickpea has been relegated to poor and marginal lands with lower and unstable productivity. About 90% of chickpea production occurs on receding soil moisture under rainfed conditions (Sharma and Jodha 1984; Kumar and van Rheenen 2000), where terminal drought and heat stresses are major limitations to higher productivity (Johansen et al. 1997). Therefore, most breeding programs aim at developing early-maturing cultivars whose maturity period matches with the available crop duration. Phenology of the crop has an immense influence on productivity and stability. In pea Murfet and Reid (1985) have shown that flowering genes influence maturity and crop yield through their effects on the onset of reproduction, duration of the reproductive phase, number of branches, and number of flowers per node. Appropriate time to flowering is a major component of crop adaptation, particularly in the environments where the growing season of grain legumes including chickpea is restricted by terminal drought and high temperature (Subbarao et al. 1995). Early-flowering habit has been often associated with day length insensitivity in peas (Arumingtyas and Murfet 1994) and lentil (Erskine and Muehlbauer 1991).

The importance of increased use of genetic resources to enhance the genetic potential of the crop has been well recognized (Singh 1987; Upadhyaya et al. 2001). The chickpea germplasm collection at ICRISAT currently consists of 18,963 cultivated accessions of which about 2,000 have been added in 2005. However, a small fraction of this large collection has been used by the crop improvement programs, globally. For example, at ICRISAT in 27 years from 1978 to 2004 only 83 of the 17,123 germplasm accessions of cultivated chickpea and 5 out of 135 accessions of wild *Cicer* species available have been used compared to 480 breeding lines/cultivars in developing 3,430 breeding lines (Upadhyaya et al. 2006). Two Indian cultivars, L 550 (a kabuli type) and K 850 (a desi type) have been used, 847 and 808 times, respectively. Similarly, at the International Center for Agricultural Research in the Dry Areas (ICARDA) also a small number of available germplasm lines have been used in breeding programs. At ICARDA during the same period 250 germplasm lines were used in crosses, compared to 600 breeding lines in generating material from which 31 varieties were released (Upadhyaya et al. 2006). India, which is the largest chickpea producing country with a strong chickpea improvement program, has released 126 chickpea cultivar between 1967 and 2003. Pedigree analysis of 86 cultivars developed from hybridization has revealed that 95 progenitors were involved and only 10% of these contributed for 35% of the genetic base (Kumar et al. 2004). The exiguous use of germplasm in the breeding programs is due to lack of information on the traits of economic importance, which requires replicated multilocational evaluation. However, the large size of germplasm collections hinders multilocational evaluation for traits of economic importance. To overcome this, Upadhyaya et al. (2001), following Frankel's (1984) proposition of core collection to promote effective utilization of germplasm, developed a core collection of chickpea consisting of 1,956 entries using data on geographic origin and 13 quantitative traits. From this core collection and the reserve collection, 28 early-maturing germplasm lines were selected and evaluated extensively in three seasons, from 2001–2002 to 2004–2005, constituting five environments. The main objectives of this study were to assess the performance of these lines and discern patterns of diversity for traits related to maturity, agronomic values and morphology to promote their use in chickpea improvement programs in developing early-maturing high-yielding cultivars with a broad genetic base.

Materials and methods

The chickpea core collection consisting of 1,956 germplasm lines (Upadhyaya et al. 2001) was evaluated in 1999–2000 postrainy season at ICRISAT Center, Patancheru for yield and other agronomic traits. The postrainy season crop was planted in the last week of October and harvested in the second week of February of the following year. During this evaluation a set of 12 early-flowering/maturing lines were selected. The selected 12 early-maturing lines with four early-maturing control cultivars (ICCV 2, Harigantars, ICCV 96029, and Annigeri) were evaluated during 2000–2001 postrainy season in a Randomized Complete Block Design (RCBD) with three replications. ICCV 2 (ICC 12968; GP-46) is an ICRISAT bred early-maturing kabuli cultivar released in India (Kumar et al. 1985). ICCV 96029 (PI 612869; ICC 17258) was also developed and identified by ICRISAT as the earliest flowering desi chickpea germplasm (Kumar and Rao 2001). Annigeri (ICC 4918) is an early-maturing desi cultivar cultivated in large areas of peninsular India (Ali and Kumar 2003). Harigantars (ICC 5810) is an early-maturing breeding line from Maharashtra, India (Roberts et al. 1985). Similarly, another experiment with additional 72 early-maturing lines, selected from the reserve collection (remaining part of entire collection after selecting core collection), was planted using the same control cultivars in RCBD with two replications during 2000–2001 postrainy season. The four early maturing controls were used to classify selected 28 germplasm lines as early (similar to Annigeri), very early (similar to ICCV 2 and Harigantars) and super early (similar to ICGV 96029). Based on the data of these two experiments, we selected 28 accessions, 11 from the first experiment and 17 from the second experiment for further evaluations. These selected 28 early-maturing germplasm lines were evaluated in three postrainy seasons (2001–2002, 2002–2003, and 2004–2005) constituting five environments with the same set of four early-maturing control cultivars. In the 2001–2002 and 2004–2005 seasons the experiment was conducted under both irrigated and non-irrigated conditions, separately. Whereas in 2003–2004 postrainy season the experiment was conducted only under irrigated conditions. The details of these experiments, conducted from 2001–2002 to 2004–2005 are given in Table 1.

Sowing was done manually in the last week of October in all the seasons. Care was taken to sow the seeds at uniform depth. Crop was protected from insect pests. Experiments were kept weed free. In all the experiments, five representative plants from each plot were randomly selected to record observations on plant height (cm), plant width (canopy spread, cm), number of basal primary branches, apical primary branches, basal secondary branches, apical secondary branches, tertiary branches, and pods and yield per plant (g). Ten mature pods from each of the five selected plants were used to determine number of seeds per pod. Days to 50% flowering (days from sowing to the stage when 50% plants have begun flowering), days to maturity (from sowing to the stage when 90% pods have matured and turned yellow), flowering duration (days between 50% flowering and end of flowering in 50% plants), plot yield (kg ha^{-1}), and 100-seed weight (g) were recorded on plot basis. The yields of five sampled plants were added to the plot yield to obtain total plot yield. Per day productivity (kg ha^{-1} d^{-1}) was calculated by dividing total plot yield with days to maturity on plot basis. Data on seven qualitative traits (growth habit, plant

Table 1 Experimental details of evaluation of early-maturing germplasm lines, 2001–2002 to 2004–2005, ICRISAT Center, Patancheru, India

Season	Number of entries	Number of replications	Spacing (cm)	Plot size (m^2)	Fertilizer applied (kg ha^{-1})	Number of irrigations
2001–2002	28 test + 4 controls	3	30 × 10	6.0	18N:46P_2O_5	2
2001–2002	28 test + 4 controls	3	30 × 10	6.0	18N:46P_2O_5	0
2003–2004	28 test + 4 controls	3	60 × 10	4.8	18N:46P_2O_5	2
2004–2005	28 test + 4 controls	2	60 × 10	4.8	18N:46P_2O_5	2
2004–2005	28 test + 4 controls	2	60 × 10	4.8	18N:46P_2O_5	0

pigmentation, flower color, seed color, seed shape, dots on seed testa, and seed texture) were recorded following morphological descriptors (IBPGR, ICRISAT & ICARDA 1993).

Data on all quantitative traits were analyzed following Residual Maximum Likelihood (REML) method for all seasons separately as well as combined on Genstat 8.1. Environments and irrigations regimes were considered as fixed and genotypes and blocks as random. Variance components due to genotype ($\delta^2 g$), genotype (g) × environment (e) ($\delta^2 ge$), and error ($\delta^2 e$) and their standard errors were estimated.

Broad sense heritability (h^2) was estimated using the following model;

$$\text{Heritability}\,(\%) = \frac{\delta^2 g}{\delta^2 p} \times 100;$$

$\delta'^2 p$ was estimated as follows

$$\delta^2 p = \delta^2 g + \frac{\delta^2 ge}{ne} + \frac{\delta^2 e}{ne * r}$$

Where ne = no. of environments

r = no. of replications

Best Linear Unbiased Predictors (BLUPs) were calculated for all quantitative traits. In the subsequent analyses, environment-wise mean values were considered for those traits, which showed significant g × e interaction while for other traits pooled mean over environments was considered. The correlation coefficients among all characters were estimated for each environment separately as well as on the basis of pooled mean values.

The mean observations for all traits for each season were standardized by subtracting from each observation the mean value of the character and subsequently dividing it by its respective standard deviation. These standardized values, with average 0 and standard deviation of 1, were used for Principal Component Analysis (PCA) on Genstat 8.1 to know the importance of different traits in explaining multivariate polymorphism. Cluster analysis was performed using the scores of first three PCs following Ward (1963). Mean, range, variance and Shannon–Weaver diversity index (H‘) (Shannon and Weaver 1949) were computed for each trait and cluster. Means of clusters were compared using Newman-Keuls (Newman 1939; Keuls 1952) procedure. The homogeneity of variances among the clusters was tested using Levene’s test (Levene 1960). A phenotypic distance matrix was created by calculating the differences between each pair of entries for each characteristic. The diversity index was calculated by averaging the differences in the phenotypic values for each trait divided by respective range (Johns et al. 1997). The mean, minimum and maximum diversity was calculated and the accessions showing minimum and maximum diversity were identified.

Results

The geographical origin and morphological descriptors of 28 early-maturing chickpea lines and four control cultivars used in the study are given in Table 2. All the test entries except ICC 12424 and ICC 16947 are landraces representing geographic diversity. Twenty one of these accessions originated from India (including ICRISAT) and of the remaining, three were from Iran, two from Pakistan and one each from Ethiopia and Mexico, indicating predominance of India and Iran in the ICRISAT chickpea collection (Upadhyaya et al. 2001). Twenty-six of these 28 accessions were desi types and the remaining two were kabuli types. Among the qualitative traits relatively high polymorphism was observed for seed color followed by seed surface.

The differences among environments were significant for all the traits, except apical secondary branches and tertiary branches (data not given). Similarly, the three seasons in which the experiment was conducted under irrigation, were significantly different for all traits except tertiary branches and seeds per pod. The two seasons in which the experiment was conducted under non-irrigated conditions, were significantly different for all traits except flowering duration, plant width and basal primary branches indicating that choice of environments both irrigated and non-irrigated were appropriate to exploit genotypic variability (data not given). REML analysis of data for individual environments revealed significant genotypic variance for days to 50% flowering and maturity in all the environments (Table 3). It indicated that even within this set of early-maturing lines, there is scope for selecting accessions with different maturity duration.

Table 2 Geographical origin and morphological descriptors of 28 early-maturing chickpea germplasm lines and control cultivars, ICRISAT Center, Patancheru, India

Germplasm accession	Identity	Biological status	Source country	Growth habit	Seed color	Seed surface
ICC1097	P 966; Karaj 153-3	Landrace	Iran	Semi-spreading	Yellow brown	Tuberculated
ICC1398	P 1244; 519	Landrace	India	Semi-erect	Yellow brown	Rough
ICC2023	P 1631; NP 10	Landrace	India	Semi-erect	Yellow	Rough
ICC2171	P 1751-1	Landrace	Mexico	Semi-spreading	Yellow brown	Rough
ICC2859	P 3166-2	Landrace	Iran	Semi-erect	Brown	Rough
ICC6919	NEC 1153; PI 360347; P 4203	Landrace	Iran	Semi-spreading	Yellow	Rough
ICC8378	Osmanabad 2-1	Landrace	India	Semi-spreading	Yellow brown	Tuberculated
ICC8618	WP 117 B	Landrace	Ethiopia	Semi-spreading	Yellow	Rough
ICC8931	JM 1975	Landrace	India	Semi-spreading	Yellow brown	Rough
ICC10232	H 1128	Landrace	India	Semi-spreading	Yellow brown	Rough
ICC10629	H 214	Landrace	India	Semi-erect	Yellow brown	Rough
ICC10822	140-6 T	Landrace	India	Semi-spreading	Yellow brown	Rough
ICC10926	2-16	Landrace	India	Semi-spreading	Yellow	Rough
ICC10976	RPSP 362	Landrace	India	Semi-spreading	Yellow	Rough
ICC10981	RPSP 372	Landrace	India	Semi-spreading	Yellow	Rough
ICC10996	RPSP 386	Landrace	India	Semi-spreading	Yellow	Rough
ICC11021	RPSP 410	Landrace	India	Semi-erect	Yellow brown	Tuberculated
ICC11039	RPSP 428	Landrace	India	Semi-erect	Yellow	Rough
ICC11040	RPSP 429	Landrace	India	Semi-spreading	Yellow	Rough
ICC11059	RPSP 444	Landrace	India	Semi-spreading	Yellow brown	Rough
ICC11160	C 28	Landrace	India	Semi-erect	Yellow brown	Tuberculated
ICC11180	C 16	Landrace	India	Semi-erect	Yellow brown	Tuberculated
ICC12424	ICCC 35; (NEC 249 × NEC 1639) × (Chafa × P 472)	Breeding material	ICRISAT	Semi-spreading	Light brown	Rough
ICC14595	RSW 1	Landrace	India	Semi-spreading	Yellow brown	Rough
ICC14648	RSW 43	Landrace	India	Semi-spreading	Light brown	Rough
ICC16641	BAM 2994 (1)	Landrace	Pakistan	Semi-spreading	Beige	Smooth
ICC16644	BAM 2995 (2)	Landrace	Pakistan	Semi-spreading	Beige	Smooth
ICC16947	GR 19; WR Pink dwarf	Breeding material	ICRISAT	Semi-spreading	Light brown	Rough
Control						
Annigeri	ICC 4918	Cultivar	India	Semi-spreading	Light brown	Rough
Harigantars	ICC 5810	Cultivar	India	Semi-spreading	Black	Rough
ICCV 2	ICC 12968	Cultivar	ICRISAT	Semi-erect	Beige	Smooth
ICCV 96029	ICC 17258	Cultivar	ICRISAT	Semi-erect	Yellow brown	Rough

The genotypic variance was also significant for flowering duration and 100-seed weight in all the environments. The significant variation for 100-seed weight may provide an opportunity to select for desired seed size as well as early-maturity. Genotypic variance was significant for plot yield in 2003–2004 irrigated and in 2004–2005 in both irrigated and non-irrigated environments (Table 3). Variance compo-

Table 3 Variance components due to genotype (δ^2_g), genotype × environment (δ^2_{gxe}), and their standard errors (SE) and broad sense habitability (h^2) of 16 quantitative traits in early-maturing chickpea lines and control cultivars evaluated in five environments at ICRISAT Center, Patancheru, India

Character	2001–2002 (Irrigated)		2001–2002 (Non-irrigated)		2003–2004 (Irrigated)		2004–2005 (Irrigated)		2004–2005 (Non-irrigated)		Combined analysis				
	δ^2_g	SE	δ^2_g	SE	δ^2_g	SE	δ^2_g	SE	δ^2_g	SE	δ^2_g	SE	δ^2_{gxe}	SE	h^2
Days to 50% flowering (number)	31.54	8.57	22.42	5.80	27.49	7.20	41.77	10.90	23.54	6.25	25.98	6.72	2.76	0.53	96.7
Flowering duration (number)	12.76	4.71	2.14	0.85	31.93	8.52	6.64	2.80	19.24	6.09	1.13	1.21	13.45	2.13	24.4
Plant height (cm)	4.96	2.02	3.52	1.11	9.31	2.67	3.92	1.61	4.33	1.84	4.14	1.20	1.22	0.41	85.4
Plant width (cm)	3.94	2.11	5.54	1.96	15.69	6.57	11.95	6.13	7.43	3.15	5.26	1.83	3.51	1.29	70.4
Basal primary branches (number)	0.00	–[a]	0.04	0.03	0.07	0.05	0.39	0.26	0.09	0.10	0.03	0.02	0.06	0.03	33.2
Apical primary branches (number)	0.00	–	0.18	0.12	0.05	0.14	0.13	0.23	0.95	0.34	0.003	0.03	0.17	0.08	2.3
Basal secondary branches (number)	0.13	0.19	0.10	0.12	0.92	0.48	1.68	0.59	0.82	0.38	0.34	0.14	0.25	0.12	62.0
Apical secondary branches (number)	0.70	0.30	1.02	0.33	1.51	0.57	0.68	0.38	1.65	0.76	1.08	0.30	0.01	0.09	87.3
Tertiary branches (number)	0.17	0.09	0.28	0.12	0.14	0.15	0.66	0.42	0.95	0.46	0.33	0.11	0.06	0.07	75.2
Days to maturity (number)	3.47	1.23	22.07	6.00	18.11	5.07	11.96	3.81	21.96	6.12	11.75	3.26	3.80	0.73	90.5
Pods per plant (number)	42.90	64.90	54.63	22.58	53.70	51.50	163.10	85.80	153.20	57.00	81.90	26.60	0.00	–	73.2
Seeds per pod (number)	0.01	0.003	0.02	0.01	0.01	0.005	0.01	0.01	0.00	–	0.01	0.003	0.002	0.002	71.5
Yield per plant (g)	0.09	1.57	0.40	0.29	1.43	1.45	1.43	1.97	3.83	1.54	1.14	0.46	0.00	–	56.9
Yield per plot (kg ha^{-1})	21,894	15,696	9,577	8,204	53,664	21,198	178,546	67,934	219,509	96,356	54,356	18,448	35,767	11,888	73.9
100-seed weight (g)	16.76	4.31	17.84	4.59	21.94	5.65	22.69	5.76	19.21	4.96	19.00	4.79	0.33	0.08	99.3
Productivity per day (kg ha^{-1} d^{-1})	1.67	1.32	0.95	0.81	3.90	1.69	12.65	5.81	21.17	10.15	3.88	1.45	3.80	1.23	66.1

[a] Estimates of variance very low

nents due to genotypes were significant for all the traits except flowering duration, basal primary and apical primary branches under three irrigated environments. However, in two non-irrigated environments variance was significant for nine traits (Days to 50% flowering, plant height and width, days to maturity, basal primary, apical secondary, and tertiary branches, 100-seed weight and seed yield per plant) (data not given). The pooled analysis also indicated significant genotypic variation for all the traits except flowering duration, basal primary branches, and apical primary branches (Table 3). The g × e interaction variance was significant for all the three traits related to early maturity (days to 50% flowering, flowering duration, days to maturity) and eight traits of agronomic importance (plant height, plant width, basal primary, apical primary, and basal secondary branches, and plot yield, 100-seed weight, and productivity per day) (Table 3), indicating a differential response of genotypes to environments. The estimates of broad sense heritability were highest for 100-seed weight (99.3%) (Table 3). Among the three maturity related traits, the heritability was high for days to 50% flowering (96.7%) and days to maturity (90.5%) whereas it was very low for flowering duration. Several agronomic traits such as plant height (85.4%), plant width (70.4%) seeds per pod (71.5%), apical secondary branches (87.3%), tertiary branches (75.2%), pods per plant (73.2%), and plot yield (73.9%) showed high estimates of heritability.

ICCV 96029, the super early-maturing control cultivar was consistent in all environments (data of individual environments not given). Despite significant g × e interactions for days to 50% flowering and maturity, ICCV 96029 displayed a narrow range of mean number of days to 50% flowering (24.7–32.4 days) and maturity (78.0–96.9 days) over environments. Harigantars and ICCV 2, the two very early-maturing control cultivars took on average from 29.8 to 32.6 days for 50% flowering and from 99.0 to 100.0 days for maturity; and the newly selected early germplasm accessions were similar to them. ICC 16641 and ICC 16644 were significantly earlier in flowering and maturity than Annigeri in all the environments. Based on pooled data over environments, ICC 16641, ICC 16644, ICC 11040, ICC 11180, and ICC 12424 were identified as very early-maturing, similar to ICCV 2 and Harigantars but earlier than Annigeri (Table 4).

Twenty-eight early-maturing lines produced greater mean seed yield than the mean of control cultivars in all the environments. The mean yield increase in the selected entries over the mean of control cultivars ranged from 12.9% in the 2004–2005 non-irrigated to 29.4% in the 2003–2004 irrigated environment (data not given). On the basis of mean of all five environments, 28 test entries produced 1646 kg ha^{-1}, 22.8% more than mean of four control cultivars. Among control cultivars Annigeri was the highest yielding and ICCV 96029 was lowest yielding in all the environments. None of the 28 entries produced significantly higher ($P = 0.05$) plot yield than Annigeri in any of the five environments and overall. ICC 14648 produced significantly greater plot yield than the control ICCV 2 in all the environments and overall. ICC 14648 and three other accessions ICC 10232, ICC 11039, and ICC 11180 were greater in plot yield than the control Harigantars in all the environments and overall. Twenty six accessions in 2000–2001 irrigated, 9 in 2000–2001 non-irrigated, 27 in 2003–2004 irrigated and 2004–2005 irrigated, 25 in 2004–2005 non-irrigated and 25 in overall produced significantly greater plot yield than the control ICCV 96029 (Table 4). The selected early-maturing entries showed promise for 100-seed weight, an economically important trait for trade. Three accessions, a desi type ICC 14648 (31.3 g) and two kabuli types ICC 16641 (24.8 g) and ICC 16644 (25.2 g) had greater 100-seed weight than desi cultivar Annigeri (21.2 g) and kabuli cultivar ICCV 2 (22.2 g) (Table 4). ICC 14648 ranked first and produced overall highest seed yield followed by ICC 11180 and ICC 11040, and were better among desi types and ICC 16641 and ICC 16644, the two kabuli types were similar to ICCV 2 and Harigantars in yield. These six could be potential donors for early-maturity with good agronomic background.

Correlation coefficients were calculated in each environment separately and also based on combined analysis to understand the association pattern among various traits in early-maturing chickpea germplasm. Of the 120 correlations, 58 and 59 were significant in 2000–2001 irrigated and non-irrigated, respectively, 70 in 2003–2004 irrigated, 70 and 76 in 2004–2005 irrigated and non-irrigated, respectively, and 78

Table 4 Performance of 28 early-maturing chickpea germplasm lines and control cultivars, 2001–2002 to 2004–2005, ICRISAT, Patancheru, India

Germplasm line	Days to 50% flowering (number)	Flowering duration (number)	Days to maturity (number)	100-seed weight (g)	Yield per plot (kg ha^{-1})	Productivity per day (kg ha^{-1} d^{-1})
ICC1097	45.8	32.7	101.2	13.4	1,620	16.2
ICC1398	43.5	34.1	102.2	17.5	1,605	16.0
ICC2023	41.6	34.4	102.2	12.2	1,619	16.0
ICC2171	43.5	31.8	100.9	17.5	1,617	16.1
ICC2859	43.7	32.9	100.4	17.2	1,629	16.2
ICC6919	46.8	31.5	100.1	14.7	1,346	13.5
ICC8378	43.4	32.4	101.0	15.0	1,592	16.0
ICC8618	42.5	35.4	101.3	11.0	1,547	15.5
ICC8931	40.5	34.7	100.5	13.8	1,596	16.1
ICC10232	45.2	31.9	101.1	17.2	1,744	17.3
ICC10629	40.0	36.5	102.2	15.0	1,648	16.3
ICC10822	40.6	34.8	101.9	13.1	1,678	16.6
ICC10926	44.4	33.8	102.2	16.9	1,671	16.5
ICC10976	43.5	33.8	101.5	16.2	1,617	16.1
ICC10981	41.9	33.5	101.8	12.7	1,558	15.5
ICC10996	42.1	35.3	101.1	12.4	1,750	17.3
ICC11021	43.6	33.5	101.5	15.7	1,696	16.8
ICC11039	43.9	33.5	101.6	16.6	1,796	17.8
ICC11040	41.6	33.3	99.6	16.3	1,794	18.3
ICC11059	40.8	35.2	99.6	14.2	1,704	17.1
ICC11160	43.4	32.6	101.6	15.6	1,787	17.7
ICC11180	40.6	32.5	100.0	16.5	1,821	18.2
ICC12424	40.2	35.4	99.4	14.9	1,754	17.4
ICC14595	37.3	37.5	104.7	20.8	1,745	16.9
ICC14648	38.7	35.2	102.6	31.3	2,070	20.3
ICC16641	29.6	32.3	95.4	24.8	1,230	13.0
ICC16644	30.8	30.5	96.2	25.2	1,237	12.9
ICC16947	45.5	34.5	103.7	15.4	1,617	15.8
Controls						
Annigeri	42.1	34.0	104.0	21.2	1,743	16.8
Harigantars	29.9	35.7	99.0	13.8	1,246	12.8
ICCV 2	32.6	28.7	100.0	22.3	1,417	13.9
ICCV 96029	26.8	32.1	85.5	12.7	953	10.9
Trial mean	40.77	33.62	100.5	16.78	1,608	16.22
SE±	1.51	0.94	1.56	0.71	155.3	1.40
CV (%)	4.48	8.50	2.23	5.32	22.86	23.20
LSD ($P = 0.05$)	4.21	2.61	4.34	1.99	431.8	3.90

correlation combinations were significant ($P = 0.05$) in combined analysis. Skinner et al. (1999) suggested only those correlation coefficients, which are greater than 0.707 or smaller than −0.707 as biologically meaningful so that 50% of the variation in one trait is predicted by the other. The character pairs showing such high correlation and their frequency over five environments are given in Table 5. In all, there were

Table 5 Pairs of characters showing more than 0.71 or less than −0.71 correlation coefficients and the frequency with which they occurred in five environments and overall, ICRISAT Center, Patancheru, India

Pair of characters	Correlation coefficients	
	Frequency	Value
Days to 50% flowering: Flowering duration	2	−0.72 to −0.73
Days to 50% flowering: Days to maturity	3	0.71 to 0.87
Days to 50% flowering: Basal primary branches	1	0.75
Days to 50% flowering: Apical secondary branches	6	0.73 to 0.85
Days to 50% flowering: Plot yield	1	0.73
Days to 50% flowering: Productivity per day	1	0.73
Plant height: Plant width	4	0.73 to 0.79
Days to maturity: Basal secondary branches	1	0.71
Days to maturity: Apical secondary branches	2	0.71 to 0.73
Days to maturity: Tertiary branches	3	0.71 to 0.74
Days to maturity: Plot yield	3	0.73 to 0.78
Days to maturity: Productivity per day	1	0.71
Basal primary branches: Apical secondary branches	1	0.76
Basal primary branches: Pods per plant	1	0.73
Basal secondary branches: Apical secondary branches	1	0.79
Basal secondary branches: Tertiary branches	6	0.71 to 0.91
Basal secondary branches: Pods per plant	6	0.71 to 0.76
Apical secondary branches: Tertiary branches	6	0.83 to 0.84
Apical secondary branches: Pods per plant	6	0.71 to 0.72
Plot yield: Productivity per day	6	0.97 to 0.99

20 pairs of characters, which showed correlation greater than 0.707 or smaller than −0.707. Nineteen of these were positive while one (days to 50% flowering and flowering duration) was negative (Table 5). Plot yield and per day productivity had correlation ranging from 0.97 to 0.99 in five environments and overall, while between days to 50% flowering and apical secondary branches it ranged from 0.73 to 0.85 in five environments and overall. Other notable meaningful correlations (>0.707 or <−0.707) in all environments separately and overall were between basal secondary branches and tertiary branches, apical secondary and tertiary branches, basal secondary branches and pods per plant, and between apical secondary and pods per plant (Table 5). Similarly, the negative correlations between days to 50% flowering and flowering duration (−0.72 to −0.73) and between number of pods and 100-seed weight (−0.64 to −0.66) were important. The nature and magnitude of association of days to 50% flowering and days to maturity with other traits were almost similar. They showed positive association with plant height, plant width, basal primary branches, apical primary branches, basal secondary branches, tertiary branches, and plot yield and per day productivity. Number of pods per plant and seeds per pod, the two most important components of yield were negatively associated with each other (data not given). It is interesting to note that the nature of association of number of pods per plant with plot yield, 100-seed weight, and days to 50% flowering observed in this set of early-maturing material corroborates the association pattern observed in the entire collection and core collection (Upadhyaya et al. 2001) from which these early-maturing accessions were selected. These associations may therefore be regarded as relatively stable.

A very large proportion of the total variation (74.3%) was explained by the first 3PCs (data not given). The first PC alone accounted for 49.4% of the variation followed by the second PC, which explained 14.7% of the variation. The third PC accounted for 10.2% of the variation. Based on loading for first three PCs, characters such as days to 50% flowering and maturity, flowering duration, and number of apical secondary, basal primary and

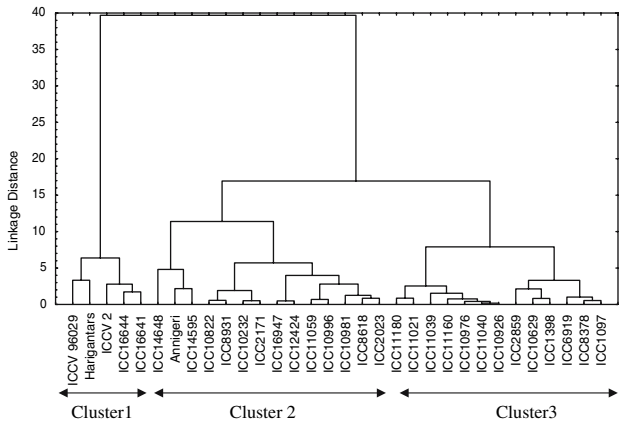

Fig. 1 Dendogram based on first three principal components of 16 quantitative traits of 28 early-maturing germplasm lines and four control cultivars capturing (74.3%) variation

secondary, and tertiary branches, yield per plant, plot yield, and 100-seed weight are important and adequate descriptors in this material.

Cluster analysis performed on scores of first three PCs resulted in to three clusters (Fig. 1). The first cluster comprised three control cultivars ICCV 96029, Harigantars, and ICCV 2 and two entries ICC 16644 and ICC 16641. The second cluster included ICC 14648, ICC 14595, ICC 10822, ICC 10996, ICC 8931, ICC 10232, ICC 2171, ICC 10981, ICC 16947, ICC 11059, ICC 2023, ICC 12424, ICC 8618, and Annigeri. The remaining 13 accessions were grouped into the third cluster. The range, means and variances for the three clusters are provided in Table 6. The delineation of the first cluster from the other two was mainly on maturity as evident by its significantly lower mean values than the two clusters for days to 50% flowering and maturity. Cluster 1 also appeared more divergent as it had significantly different mean values for 16 traits compared to either or both the clusters (Table 6). Clusters 2 and 3 differed for days to 50% flowering, plant height, yield per plant, number of pods per plant, number of seeds per pod, basal secondary and tertiary branches. A comparative view of mean of the three clusters for flowering duration vis-à-vis plot yield suggests that an optimum intermediate flowering duration as shown by cluster 2 may be ideal for getting higher yield in early-maturing chickpeas. The variances were homogeneous except for days to maturity and seeds per pods. Cluster 1 had high percentage of range of entire set for flowering duration, days to maturity, plant width, and plant yield, whereas cluster 2 had high percentage range for days to 50% flowering, plant height, basal and apical secondary and tertiary branches, pods per plant, seeds per pod, 100-seed weight, plot yield and productivity per day, and cluster 3 for basal and apical primary branches. Overall, cluster 2 represented 61.6% range of entire set compared to 48.8% by cluster 1 and 42.1% by cluster 3.

The Shannon–Weaver diversity index (H‘) was calculated to compare phenotypic diversity index among characters and clusters. The H‘ was estimated for each trait as well as for each cluster separately (Table 7). A low H‘ indicates an extremely unbalanced frequency class for the trait concerned and the lack of genetic diversity. The H‘ values for qualitative traits were low when compared to those for quantitative traits. The average diversity index for qualitative traits ranged from 0.115 ± 0.003 for growth habit to 0.310 ± 0.053 for seed color. The diversity for seed color was equally high in all the three clusters indicating an equal mix of accessions with different classes of seed color in all clusters. Cluster 1 showed high average H‘ (0.300 ± 0.023) for all the qualitative traits. For quantitative traits, the average H‘ values across traits ranged from 0.425 ± 0.025 for plot yield to 0.520 ± 0.031 apical primary branches and number of pods per plant (Table 7). Cluster 2 showed the highest average diversity index (H‘ = 0.501 ± 0.014) followed by

Table 6 Range, means, and variances for different traits in three clusters of early-maturing chickpea germplasm lines and control cultivars evaluated in five environments, ICRISAT Center, Patancheru, India

Character	Range			Mean			Variance				
	Cluster 1	Cluster 2	Cluster 3	Cluster 1	Cluster 2	Cluster 3	Cluster 1	Cluster 2	Cluster 3	*F* value	Prob > *F*
Days to 50% flowering (number)	26.81–32.60	37.32–45.51	40.03–46.80	29.94c	41.59b	43.86a	4.414	4.967	2.378	0.67	0.519
Flowering duration (number)	28.67–35.68	31.81–37.50	31.45–36.53	31.84b	34.56a	33.30ba	6.692	2.121	1.469	2.13	0.137
Plant height (cm)	22.11–25.40	24.55–30.23	26.94–29.73	24.34c	26.87b	28.68a	1.664	2.874	0.749	1.76	0.190
Plant width (cm)	36.69–45.49	39.94–47.30	41.11–45.66	40.90b	43.60a	44.03a	9.755	3.822	2.291	2.19	0.131
Basal primary branches (number)	2.37–2.52	2.64–2.93	2.52–2.87	2.45b	2.76a	2.73a	0.005	0.008	0.009	0.34	0.716
Apical primary branches (number)	1.54–1.79	1.70–1.97	1.63–1.97	1.70b	1.84a	1.84a	0.010	0.007	0.010	0.22	0.807
Basal secondary branches (number)	1.99–2.33	2.74–4.26	2.16–3.08	2.14c	3.28a	2.73b	0.017	0.196	0.067	2.14	0.135
Apical secondary branches (number)	1.53–2.85	3.96–5.83	3.48–5.25	2.29b	4.69a	4.46a	0.288	0.194	0.364	0.77	0.473
Tertiary branches (number)	0.39–0.56	1.13–2.39	0.94–1.74	0.47c	1.72a	1.25b	0.006	0.124	0.039	2.54	0.097
Days to maturity (number)	85.5–99.00	100.50–104.70	99.60–102.20	94.18b	101.99a	101.16a	26.132	1.732	0.781	5.81	0.008
Pods per plant (number)	33.48–44.20	40.84–68.04	43.02–57.18	39.61c	57.16a	50.94b	22.499	36.539	22.074	0.31	0.737
Seeds per pod (number)	1.10–1.39	1.06–1.38	1.13–1.24	1.26a	1.22ba	1.17b	0.012	0.008	0.001	3.25	0.053
100-seed weight (g)	12.71–25.16	11.01–31.31	13.44–17.48	19.74a	16.26b	15.90b	36.269	28.345	1.298	1.66	0.208
Yield per plant (g)	7.56–9.90	8.62–10.76	8.12–9.55	8.25b	9.47a	8.46b	1.094	0.402	0.186	2.77	0.080
Yield per plot (kg ha^{-1})	953–1,417	1,547–2,070	1,346–1,821	1,217b	1,696a	1,663a	27,776	17,163	15,882	0.10	0.903
Productivity per day (kg ha^{-1} d^{-1})	10.98–15.05	15.45–20.3	13.50–18.30	12.94b	16.91a	16.57a	2.081	1.802	1.594	0.02	0.980

Table 7 Shannon–Weaver diversity index for different traits and clusters of early-maturing chickpea germplasm accessions evaluated in five environments, ICRISAT Center, Patancheru, India

Character	Cluster 1	Cluster 2	Cluster 3	Mean
Qualitative				
Plant pigmentation	0.292	0.000	0.000	0.292 ± 0.000
Flower color	0.292	0.000	0.000	0.292 ± 0.000
Growth habit	0.000	0.112	0.118	0.115 ± 0.003
Seed color	0.413	0.283	0.235	0.310 ± 0.053
Seed shape	0.292	0.000	0.000	0.292 ± 0.000
Seed surface	0.292	0.000	0.300	0.296 ± 0.004
Dots on seed coat	0.217	0.000	0.000	0.217 ± 0.000
Mean	0.300 ± 0.023	0.197 ± 0.061	0.217 ± 0.043	0.238 ± 0.031
Quantitative				
Days to 50% flowering (number)	0.413	0.561	0.345	0.439 ± 0.064
Flowering duration (number)	0.458	0.509	0.474	0.480 ± 0.015
Plant height (cm)	0.413	0.431	0.503	0.449 ± 0.027
Plant width (cm)	0.413	0.519	0.503	0.478 ± 0.033
Basal primary branches (number)	0.458	0.535	0.520	0.504 ± 0.024
Apical primary branches (number)	0.458	0.553	0.550	0.520 ± 0.031
Basal secondary branches (number)	0.413	0.520	0.550	0.494 ± 0.042
Apical secondary branches (number)	0.458	0.519	0.466	0.481 ± 0.019
Tertiary branches (number)	0.458	0.565	0.535	0.519 ± 0.032
Days to maturity (number)	0.458	0.485	0.427	0.457 ± 0.017
Pods per plant (number)	0.458	0.552	0.550	0.520 ± 0.031
Seeds per pod (number)	0.458	0.520	0.466	0.481 ± 0.020
100-seed weight (g)	0.458	0.361	0.550	0.456 ± 0.055
Yield per plant (g)	0.413	0.520	0.345	0.426 ± 0.051
Yield per plot (kg ha^{-1})	0.413	0.390	0.474	0.425 ± 0.025
Productivity per day (kg ha^{-1} d^{-1})	0.413	0.474	0.523	0.470 ± 0.032
Mean	0.438 ± 0.006	0.501 ± 0.014	0.486 ± 0.016	0.475 ± 0.019
Over all mean	0.383 ± 0.023	0.366 ± 0.052	0.367 ± 0.047	0.372 ± 0.006

cluster 3 (H‘ = 0.486 ± 0.016) and cluster 1 (0.438 ± 0.006) for quantitative traits. Overall cluster 1 had the highest average H‘ (0. 383). Maximum H‘ value of 0.565 was observed for number of tertiary branches in cluster 2 while minimum H‘ (0.345) was observed for days to 50% flowering and yield per plant in cluster 3 (Table 7).

The mean phenotypic diversity index was (0.2467) indicating high variability in the early-maturing accessions (data not given). This value is comparable to the mean phenotypic diversity index for the intermediate group of core set of chickpea accessions (Upadhyaya et al. 2002). The minimum phenotypic diversity index (0.0447) was observed between ICC 10926 and ICC 10976. These two are desi type landraces originating from India (Table 2). The maximum phenotypic diversity index (0.6767) was observed between ICC 14648 and control ICCV 96029. Comparison of the mean values of these two genotypes for different traits indicates that ICC 14648 represents the maximum mean value and ICCV 96029 represents the minimum mean value for plant height, 100-seed weight, per day productivity and plot yield and adequate diversity for other traits including maturity. The cross between these two accessions may result in useful variation for maturity, plant type, and other agronomic traits.

Discussion

Plant genetic resources will be the main contributing factor to much of the future progress in developing new cultivars. The size of germplasm collections in some species is large, which in turn increases the difficulty in using them in improvement programs through evaluations for traits of interest. Development of core collections, which make up about 10% of entire collection, has been proposed as a means to enhance efficiency of evaluation of germplasm collections to identify useful parents (Frankel 1984; Frankel and Brown 1984). Results of our study in identifying early-maturing parents using chickpea core collection has demonstrated the usefulness of core collection as a gateway for further exploitation of reserve collection. Early-maturity is advantageous in chickpea to avoid terminal drought and make adequate use of available soil moisture during growth. The reduced crop duration also helps in escaping severe effects of important biotic stresses (Nene and Reed 1994). In the present study additional very early-maturing genotypes such as ICC 16641, ICC 16644, ICC 11040, ICC 11180, ICC 12424, and ICC 14648 have been identified from the large chickpea collections available at ICRISAT.

Our results on correlation and heritability have implications for the chickpea breeders in their selection programs. Negative correlation between pods per plant and seeds per pod, the two most important yield component traits, would imply that breeder should select for higher number of pods per plant to enhance yield, which would also result in larger seeds (contained mostly in single seeded pods). The converse (selecting for more seeds per pod) may result in higher number of small-sized seeds packed in fewer pods on a plant. Seed size is an important quality attribute and fetches premium price particularly for kabuli types. Similarly, high estimates of broad sense heritability for two of the three maturity related traits (days to 50% flowering and days to maturity) and several agronomic traits (Table 3) indicated high reliability of selection for these traits in this material. Narrow variability and low heritability (24.4%) for flowering duration indicated that selection would not be effective for this trait and even if favorable conditions occur during the late stages of crop growth, the plant would not be able to utilize it to produce higher yield.

The multi-environment evaluation of the identified early-maturing chickpea germplasm lines revealed significant variations for different agronomic traits like seed yield and 100-seed weight. The possibility of combining early flowering with yield-promoting alleles has been demonstrated in desi chickpea (Siddique and Khan 1996). While selecting the exotic germplasm lines for inclusion in the breeding programs, it is important to consider the genetic background and agronomic performance of the lines, as it will be useful in predicting its behavior in hybrid combinations with the adapted genotypes. The less divergent the parental lines are, the more likely it will be that the additive gene effects will play a primary role in inheritance of quantitative traits (Isleib and Wynne 1983). As the diversity between parents increases, dominance effects and epistatic variations have significant roles in the inheritance of quantitative traits (Halward and Wynne 1991), which will have implications in choosing an appropriate selection strategy in a self-pollinated crop like chickpea. The early-maturing genotypes identified in the present study would serve as an ideal experimental material to study the allelic variation of the genes governing flowering/maturity in chickpea, to add to the scant information on genetic control of flowering in chickpea that is currently available. There are two reports, Or et al. (1999) and Kumar and van Rheenen (2000) that reported a major gene to explain the variation of flowering time between the early flowering and the late flowering genotypes. The variation in days to flowering in different seasons as observed in the present study could suggest the involvement of additional loci in determining the flowering phenotype. Studies involving some of these accessions are in progress at ICRISAT, Patancheru, India.

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