Genetic Variability Studies in Minicore Collections of Chickpea (*Cicer arietinum* L.) under Different Environments

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The present investigation was carried out on chickpea germplasm lines representing minicore collection obtained from ICRISAT, Patancheru (AP) for assessing genetic variability under three environments. Considerably high variability was observed for most of the productivity related traits in E3 (irrigated 2005–06). This was evidenced by high range of mean performance for different traits in E3 compared to E1 (rainfed 2004–05) and E2 (rainfed 2005–06). Moderately high heritability and genetic advance (GA) was observed for many productivity related traits under E3. The higher PCV, although, heritability was reduced or remained same as that under E2. These findings revealed the importance of productivity related traits giving more response under E3 than E1 and E2 for better expression for crop improvement in chickpea. Over three environments, genotype ICC 6279 was found to be early flowering irrespective of the environmental effect while ICC 1882 was found to be early flowering in E1 and E2 whereas ICC 13124 and ICC 6279 were early in flowering in both E2 and E3 compared to early flowering check JGK-1. For seed yield/plant, 24, 22 and 17 genotypes showed significantly higher yield over check A-1 in E1, E2 and E3, respectively. Out of these, ICC 13124 (31.25 g, 32.85 g and 32.95 g) is the only top yielder in all the three environments. While genotypes ICC 6279 (28.9 and 27.85 g), ICC 13892 (30.05 g and 27.65 g) and ICC 13187 (27.45 g and 36.55 g) were top yielders in both E1 and E2 and ICC 12866 (27.65 and 40.15 g) and ICC 4533 (29.38 and 38.8) were identified as top yielders in E2 and E3, while ICC 12947 (27.9 g and 40.9 g) and ICC 6877 (18 g and 35.33 g) were top yielders in E1 and E3, respectively. On overall basis, the genotype ICC 13124 was found promising for earliness, large seed size and high yield/plant in all the environments suggesting that this accession is best suited for both rainfed and irrigated condition during the *rabi* season.

Key Words: Chickpea, Environments, Genetic advance, Genetic variability, Heritability, Minicore

Introduction

Chickpea (*Cicer arietinum* L.) is an important pulse crop of the semi-arid tropics, particularly in the rainfed ecology and resource poor farmers of the Indian subcontinent, the Mediterranean region, the west Asian and North American region, Eastern Africa and Latin America. In the recent past, this crop has experienced an export-driven expansion in new niches such as Australia and Canada. Globally, chickpea is cultivated on about 10.4 million hectare area adding 8.8 million tonnes of grains to the global food basket, with an average productivity of 826 kg/ha (FAO. 2007). It is cultivated in about 50 countries in the arid and semi arid regions. India grows chickpea on about 7.29 million hectare producing 5.77 million tonnes seed, which represents 30% and 38% of the national pulses acerage and production respectively with an average productivity of 792 kg/ha. In Karnataka, it is grown on an area of 0.33 million ha with a production of 0.18 million tonnes with an average productivity of only 578 kg/ha (Anonymous, 2007).

The variability for the characters of economic importance is the basic pre-requisite for improvement of any crop species. Lack of adequate variability has been implicated as one of the major limitation in improving the productivity of chickpea. There have been reports on genetic variability in chickpea but mostly based on limited number of germplasm lines (Arunkumar *et al.*, 1998; Sivakumar and Muthiah, 2001). Upadhyaya and Ortiz (2001) developed chickpea minicore of 211 accessions that represent the core collection of 1956 accessions (Upadhyaya *et al.*, 2002) and entire collection of about 17,000 accessions at ICRISAT. A set of minicore of chickpea (Upadhyaya and Ortiz, 2001) received from ICRISAT, Patancheru, which represents the whole range of variation of cultivated chickpea is an ideal material for assessing the exact nature of diversity, which helps in inferring about the extent of diversity in the entire collection and to determine how far it acts as limiting factors in improving productivity. Hence, the present investigation was carried out to gather information on

variability under three different environments in minicore collections of chickpea for eight quantitative characters of economic importance.

Materials and Methods

The experimental material for the present study comprised of 203 chickpea germplasm lines from the minicore collection (Upadhyaya and Ortiz, 2001) obtained from ICRISAT. These lines were evaluated for assessing genetic variability under three environments (E_1, E_2 and E_3) for agronomic traits. Three experiments were conducted during *rabi* 2004–05 and 2005–06 under rainfed and irrigated situation at Genetics and Plant Breeding Garden, College of Agriculture, Dharwad, in medium black soils in randomized complete block design with two replications. Each genotype was grown in a single row of 4 m length with 30 cm spacing between rows and 10 cm within the row. Recommended agronomic practices were followed during the period of crop growth in both the situation. The crop was maintained free from weeds, diseases and pests by adopting appropriate plant protection measures. In irrigated situation, two irrigations were provided one at flowering and other at pod formation stage. The observations were recorded on eight quantitative characters *viz*., Days to 50% flowering (DFF), Plant height (PLHT), Number of primary branches/plant (PB), Number of secondary branches/plant (SB), Number of tertiary branches/plant (TB), Number of pods/plant (PPP), 100-seed weight (SDWT) (g) and seed yield/plant (YPP) (g). The data collected were subjected for statistical analysis. The analysis of variance for different characters was carried out using the mean data in order to partition variability due to different sources by following Panse and Sukhatme (1961). In order to assess and quantify the genetic variability among the genotypes for the characters under study, estimated the genetic parameters such as genotypic coefficient of variability (GCV%), phenotypic coefficient of variability (PCV%), heritability (h^2), genetic advance (GA) and genetic advance as % mean (GAM). Heritability in the broad sense was derived based on the formula given by Hansan *et al*. (1956). GA was obtained by the formula prescribed by Johnson *et al*. (1955). The method adopted by Burton and Devane (1953) was used to calculate phenotypic and genotypic coefficient of variation.

Results and Discussion

Mean, range and environmental index for different quantitative traits in minicore collection of chickpea were depicted in Table 1. The results of the present investigation indicated the prevalence of significant differences among 203 genotypes studied during the three environments for all the eight characters (Table 2). A narrow difference was observed between PCV and GCV for days to 50% flowering. These results are in conformity with the reports of many researchers (Chavan *et al*., 1994; Vijay Laxmi *et al*., 2000; Jeena and Arora, 2001). The present findings suggest negligible influence of extraneous factors on this trait.

For the character plant height, narrow difference between PCV and GCV were recorded in all the three environments. Similar observations were made by Lawrence and Kabbar (2004) and Jeena and Arora (2000). Narrow difference observed in the present investigation between PCV and GCV indicate negligible influence of environmental factors on plant height. For the characters number of primary branches, secondary branches and tertiary branches/plant, large difference between PCV and GCV were observed in E1 whereas difference in E2 and E3 were low to moderate. These observations are in accordance with the results of Chavan *et al*. 1994) and Patil (1996). This finding suggest that environmental factors have a role to play in influencing this trait.

Table 1. Mean, range and environmental index for different quantitative traits in minicore collection of chickpea

Characters	Mean			Range			Environmental index		
	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
DFF	60.26	56.9	56.13	38 to 78	38 to 77	36 to 76	1.27	0.80	0.80
PLHT (cm)	37.19	39.96	48.34	28 to 64	26 to 66	30 to 69	2.23	1.51	1.65
PB	2.55	3.71	3.91	2 to 4	2 to 6	2 to 8	0.22	0.32	0.38
SB	14.17	8.81	10.07	8 to 18	5 to 17	5 to 19	0.75	0.80	0.60
TB	18.87	17.08	20.23	11 to 28	6 to 40	9 to 34	0.95	1.30	1.38
PPP	91.05	114.35	126.78	21 to 162	25 to 182	27 to 200	4.06	9.54	7.65
SDWT (g)	16.28	17.40	18.58	9 to 38	11 to 36	13 to 39.9	0.53	0.45	0.69
YPP (g)	17.71	18.16	20.85	7 to 31	8 to 33	10 to 49	1.07	0.67	1.53

E_1-04–05 rainfed   **E_2-05–06 rainfed**   **E_3-05–06 irrigated**

Table 2. **Genetic variability, heritability and genetic advance for seed yield and its component traits evaluated under rainfed conditions of 2004–05(E1) and 2005–06(E2) and irrigated condition of 2005–06(E3)**

Characters	E1				E2				E3			
	GCV %	PCV %	h² (%)	GAM (%)	GCV %	PCV %	h² (%)	GAM (%)	GCV %	PCV %	h² (%)	GAM (%)
DFF	16.29	16.30	99.87	33.54	18.02	19.42	86.10	34.44	17.39	17.48	98.68	35.65
PLHT (cm)	23.07	27.56	70.07	39.80	15.06	18.29	67.83	25.55	14.99	15.95	88.24	29.00
PB	12.69	24.04	27.87	13.73	21.29	25.37	70.46	36.82	24.70	34.17	52.26	36.79
SB	19.05	49.91	14.57	14.98	25.75	26.78	99.80	55.06	30.17	58.34	26.74	32.13
TB	15.92	25.62	38.61	20.37	33.34	54.37	37.62	42.13	23.10	24.08	92.4	45.66
PPP	18.90	29.47	41.13	24.97	33.17	41.43	64.08	54.70	38.68	51.33	56.78	60.03
SDWT (g)	34.65	35.35	96.07	69.97	26.94	27.70	94.59	53.99	29.58	38.87	57.90	46.35
YPP (g)	27.85	29.79	87.36	53.63	32.30	32.34	89.75	66.46	31.51	35.17	80.29	58.18

The phenotypic and genotypic coefficient of variations were high for number of pods/plant in all the three environments. Similar results were reported by Yaman *et al*. 1997) and Jeena and Arora, 2001). The present finding suggests the role of environmental factors in influencing this trait. For the character 100 seed weight, the genotypes recorded a wide range of variation in E3 whereas low variations were observed in E1 and E2. These results are in accordance with the results of several workers (Salimath and Bahl, 1985; Salimath and Patil, 1990; Upadhyaya *et al*., 2002). For seed yield/plant, high values of PCV and GCV were recorded in all the three environments. Similar results were reported in chickpea by Wanjari *et al*., 1996; Yaman *et al*., 1997).

The coefficient of variation indicates only the extent of variability present for different characters and do not indicates the heritable portion. To obtain the heritable portion of variability, it is essential to compute the heritability estimates for different characters. The heritability estimate separate the environmental influence from the total variability and indicate the accuracy with which a genotype can be identified by its phenotypic performance, thus, making the selection more effective. As such the heritability in a broader perspective is the proportion of genotypic variability to the total variability. Its importance has been emphasized by Lush (1949) in animals and Johnson *et al*. (1955) in plants. Heritability estimates in the broad sense alone is not a true indicator of effectiveness of selection for the trait since their scope is restricted by their interactions with the environment (Johnson *et al.,* 1955). Hence, heritability values considered along with predicted genetic gain increases the reliability of the parameter as a tool in selection programme.

High amount of heritability estimates were recorded for days to 50% flowering coupled with moderate genetic advance in all the three environments, respectively. Similar results were also reported by Agarwal (1985) and

Chavan *et al*. (1994). The results obtained in the present investigation suggest that high heritability with moderate GAM is the indication of presence of both additive and non-additive gene action operating for this character. Plant height showed high heritability coupled with low GAM in all the three environments. But Singh and Rao (1991) and Patil (1996) have reported high heritability coupled with high GAM for the trait. High heritability with low GAM recorded for the traits in the present investigation indicated that they are controlled to greater extent by non-additive gene action.

Low heritability coupled with low GAM was observed for primary branches/plant in E1 whereas in E2 and E3 high heritability with moderate GAM was noticed for this trait. Low GA reflects higher influence of environment on this trait. This is in contrast to the results of Patil (1996). Low heritability estimates coupled with low GAM were observed for secondary branches/plant in E1 and E3 whereas, high heritability estimate with moderate GAM was observed for this trait in E2, while many researchers (Jahagirdar *et al.,* 1994; Patil, 1996; Chauhan and Singh, 2000) reported higher estimate of heritability and GA. Moderate heritability estimates coupled with low GAM were recorded for tertiary branches in E1 and E2, while high heritability estimate along with high GAM were observed in E3 suggesting this trait could be improved through simple selection. These results are in accordance with the findings of Patil (1996). For the character number of pods/plant, it was observed that the heritability was moderate to high coupled with moderate to high GAM in all the three environments. But several workers (Singh and Rao, 1991; Chavan *et al*., 1994, Mishra, 1991; Patil, 1996) reported high heritability coupled with high GAM for number of pods/plant. Moderate heritability with high GAM is the indication of presence of both additive and non-additive gene action in the control of this character.

High estimates of heritability along with high GAM were noticed for 100-seed weight and seed yield/plant in all the environments and this is in line with the findings of earlier workers including Singh and Rao (1991) and Jahagirdar *et al.* (1994) for test weight and seed yield/plant. High heritability coupled with high GAM values for characters studied suggest the importance of additive gene action for these traits (Sidramappa, 2003). These traits could be improved through simple selection

Mean performance of minicore germplasm

In order to identify the elite lines the mean performance of the test entries for different traits with checks has been compared. Annigeri-1 and KAK-2 were used as check varieties. The genotype performing significantly higher than their checks in all the environments for various characters are presented in Table 3. Since chickpea is mainly grown as a *rabi* crop, the terminal water stress is going to affect the yield potentiality of the crop. So one has to identify the genotypes which are early in flowering and maturity and hence, they can escape the terminal drought condition. The lines which are early in flowering and maturity have been identified in three different environments (E1, E2 and E3). In E1, out of 203 genotypes, 10 genotypes showed significantly lower value for days to 50% flowering. ICC 6279, ICC 1882, ICC 14699 were significantly early in flowering (38 days) as compared to other genotypes. In E2, among 203 genotypes only six genotypes showed significantly lower value for

days to 50% flowering. ICC 6279, ICC 13124, ICC 1882 and ICC 14669 were significantly early in flowering (less than 38 days). In E3, out of 203 genotypes, nine showed significantly lower value for days to 50% flowering. ICC 6279 and ICC 13124 were significantly early in flowering (39 days). These results are in conformity with the report of Upadhyaya *et al.* (2007).

Out of 203 genotypes 21, 19 and 17 genotypes expressed significantly higher pods/plant over check Annigeri-1 in E1, E2 and E3, respectively. ICC 14831 was found to be promising for pods/plant in both rainfed and irrigated condition suggesting that the genotype is fairly tolerant to drought. With regard 100 seed weight, out of 203 genotypes 22, 21 and 18 genotypes had significantly higher seed weight over check A-1 in E1, E2 and E3, respectively. ICC 8261, ICC 13357, ICC 16903, ICC 10341, ICC 13124, ICC 15406, ICC 2969, ICC 7315 and ICC 1915 are the top bold seeded genotypes ranging from 23 g to 40 g in all the 3 different environment suggesting that their characteristic feature of bold seededness. In general, *kabuli* types had higher seed weight in the study.

In respect of seed yield/plant 24, 22 and 17 genotypes showed significantly higher yield over check A-1 in E1, E2 and E3, respectively. Out of these, ICC 13124 (31.25 g, 32.85 g and 32.95 g) is the only top yielder in all the 3 environments. While genotypes ICC 6279 (28.9 and 27.85 g), ICC 13892 (30.05 g and 27.65 g) and ICC 13187 (27.45 g and 36.55 g) were top yielders in both E1 and E2 and ICC 12866 (27.65 and 40.15 g) and ICC

Table 3. Promising accessions in respect of seed yield and its component traits identified based on the evaluation of chickpea minicore in three different environments (E1, E2 and E3)

Trait	E1	E2	E3
DFF	**(< 40 days):** ICC 16903, 13357, **6279**, 13124, **1882, 14669**, 15888,1164, 8318, **JGK 1**	**(< 38 days):** ICC 8058, **6279, 13124,** 12824, **1882, 14669**	**(<39 days):** ICC **6279, 13124**, 506, 11879, 15888, 6874, 1164, 1356, JGK 1
PPP	**(>153 pods):** ICC 13523, 637, 10341, 1230, 6279, 12824, 3325, 4872, 13863, 15888, 14051, 1397, 3512, 7819, 12155, 3421, 6877, 6537, 3776, 2507, L 550	**(> 161 pods):** **ICC 14831**, 6816, 2969, 5434, 4918, 14402, 10945, 2277, 13764, 12726, 1205, 9402, A-1, ICC 708, 1164, KAK-2, ICC 12328, 6293, 10399	**(> 169 pods):** **ICC 14831**, 2969, 13124, 2065, 4182, 2720, 12866, 15264, 2580, 2263, 4463, 6571, 13816, 1710, 1052, 8318, 4567
Bold seed	**(Seed weight >24.0 g):** **ICC 8261, 13357, 10341, 15406, 2969,** 2242, **13124**, 1923, 15518, **7315, 1915,** 16261, 2919, 12947, 3512, 13219, 1164, KAK 2, 5879, 1356, 12492, JGK 1	**(seed weight >25.0 g):** **ICC 16903, 8261, 13357, 10341, 15406, 13124,** 1923, **7315, 1915,** 16261, 13892, 2072, 456, 12947, 11284, 3512, 11627, 2720, 7272, 6263, 7554	**(seed weight >26.4 g):** **ICC 16903, 8261, 13357, 10341, 15406, 2969, 13124, 7315, 1915,** 16261, 2072, 12947, 1397, 3512, 11627, 1164, 7272, JGK 1
High yield	**(>24.85 g/plant):** ICC 1230, **6279**, 5504, **13124**, 506, 7315, **13892**, 15333, 12947, 11284, 3512, **13187, 6877**, KAK 2, 12328, 6537, 15606, 2580, 5879, 5383, 1431, 1715, L 550, ICC 7554	**(>26.5 g/plant):** ICC 16903, 15406, **6279**, 2242, **13124**, 4841, 14402, 15610, 13892, 2072, 2919, 12947, 13077, **13187, 12866**, 2990, 9848, 67, 7867, 5135, 10399, **4533**	**(>30.4 g /plant):** ICC 637, 13124, 8195, 7308, 6816, 11879, 15888, 16796, **12947**, 1510, 13524, 13219, **12866, 6877**, 13816, 12928, **4533**

Table 4. Mean, range and co efficient of variation for eight quantitative traits in minicore of chickpea

Trait	Mean		Range		Coefficient of variation (%)	
	Present study	Upadhyaya & Ortiz, 2001	Present study	Upadhyaya & Ortiz, 2001	Present study	Upadhyaya & Ortiz, 2001
DFF	60.3	62.2	38–78	33–82	16.30	14.21
PLHT (cm)	37.2	46.7	28–69	12.8–78.6	27.56	18.01
PB (no.)	2.55	2.89	2–4	0–6	24.04	82.96
SB (no.)	14.17	4.07	8–18	1.3–5.3	49.90	39.82
TB (no.)	18.87	2.28	11–28	0–7	25.62	80.69
PPP (no.)	91.1	83.3	21–162	13.3–247.3	29.47	45.34
SDWT (g)	16.28	17.21	9–38	8.3–57.2	35.35	44.54
YPP (g)	17.70	15.0	7–31	5.3–46.0	29.79	36.45

4533 (29.38 and 38.8) were identified as top yielders in E2 and E3, while ICC 12947 (27.9 g and 40.9 g) and ICC 6877 (18 g and 35.33 g) were top yielders in E1 and E3, respectively. The promising accessions identified for different traits from different environments are represented in Table 3. On overall basis, it was noticed from the present study that the genotype ICC 13124 is found promising for earliness, bold seed and yield/plant in all the environments suggesting that this entry is best suited for both rainfed and irrigated condition during rabi season.

Upadhyaya and Ortiz (2001) evaluated minicore consisting of 216 genotypes at ICRISAT. The same set of genotypes except 13 have been evaluated in this study during 2004–05 to 2005–06 at Dharwad. It thus, provides an opportunity to compare the performance of minicore at Dharwad and Hyderabad with the average of different years and the place in which they are evaluated (Table 4). Of the eight quantitative traits, a good correspondence between the studies at Dharwad and Hyderabad for days to 50% flowering in respect of mean, range and coefficient of variation. Despite the influence of environment, days to 50% flowering is fairly stable trait. It is reported to be controlled by few oligogenes (Kumar and van Rheena, 2000) and hence, the effect of environment is less. Even for complex trait like yield/plant a reasonably high degree of correspondence was observed particularly in respect of mean and coefficient of variation and to some extent in respect of range also. Similarly, seed weight which is again reported to be additive gene controlled (Salimath and Bahl, 1985; Sarode *et al*., 2000) there was good correspondence in respect of mean performance. A good correspondence with respect to mean was observed in respect of number of pods/plant also However, the estimates of coefficient of variation are slightly higher in Hyderabad report. The range of expression was also at variance between the two reports

for both these traits. For the three traits concerning the number of branches some correspondence is observed in respect of mean performance for primary branches. However, the number of secondary and tertiary branches, the mean values in the present study are much higher than at Hyderabad. We believe that this might be due to the error in the way of recording observation on these traits. However, for an important trait like yield/plant, pods/plant, seed weight and days to 50% flowering, it may be inferred that the expression of these traits was not very different than at Hyderabad. Thus, it may be concluded that the minicore obtained from ICRISAT can be very well used as a source population for genetic and breeding investigation.

Acknowledgements

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