



Short Note

Metroglyph Analysis for Morphological Variation in Chickpea (*Cicer arietinum* L.)

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An experiment was conducted to study the pattern of morphological variation for nine characters in 25 elite chickpea lines and five check varieties by Metroglyph and Index score method. Seven progenies of a wide cross were represented by the open circle, 18 progenies of intervarietal crosses by closed circle and the five checks by semi closed circle. Two most variable characters, grain yield/ plant and primary branches/ plant were selected for X and Y axis, respectively. Scatter diagram revealed that maximum numbers of genotypes (9) were found in group III. Metroglyph and Index score analysis revealed maximum variability for different characters in third and sixth group which comprised nine and eight genotypes, respectively. The highest index score observed was 23 for genotypes Pusa 256 and PGO42.

Key words: Metroglyph, Index score, Intervarietal crosses

Chickpea is third most important pulse crop of the world after dry bean and dry pea and widely cultivated in west and south Asia and North African countries. India contributes 67% of the global chickpea production. Chickpea is cultivated on about 10.4 million hectares area adding 8.57million tonnes of grains to the global food basket, with productivity of 826 kg/ha (Ali and Kumar, 2005). The success of plant breeding for improving a trait of interest like yield, quality, disease resistance etc. depends on the availability of diverse germplasm, precise selection procedure and crossing programme. The experiment was conducted with an aim to evaluate the genetic potential of chickpea genotypes for yield and yield component characters by Metroglyph analysis and to develop a selection criterion. Information thus obtained could be used for the development of comprehensive breeding programme to evolve high yielding chickpea cultivars. This method was used to assess genetic diversity by Chandra (1976) in *Linum* species, Dewan et al. (1992) in Indian mustard, Rashid et al. (2007) in basmati rice mutants, Chandra et al. (1997) in turmeric, Laiju et al. (2002) in *Hordeum* species, Ghafoor and Ahmad (2005) in blackgram, Khan et al. (2007) in cotton and Bhargava et al. (2009) in *Chenopodium* species.

Materials and Methods

The present investigation was carried out during *rabi* 2005-06 with 25 genotypes derived from wide and intervarietal crosses and five check varieties of chickpea at Crop Research Centre, G. B. Pant

University of Agriculture and Technology, Pantnagar, Uttarakhand. The details of the experimental material of the present experiment were presented in Table 1. The genotypes were planted in a randomized block design with three replications. Row length was 4m and the spacing between two rows was 30cm. Ten plants were randomly selected from each genotype for recording observations. Data on nine characters *viz.*, growth habit, primary branches/plant, plant height, plant width, days to 50% flowering, days to maturity, pods/plant, seeds/ pod, 100 seed weight and grain yield/plant. The analysis of variance for all characters of genotypes was carried out following RBD design. Metroglyph and index score method advocated by Anderson (1957) were used for analysis of morphological characters in different crop species. Seven progenies of a wide cross *viz.*, PG057, PG058, PG059, PG060, PG061, PG062 and PG063 were represented by the open circle, 18 progenies of intervarietal crosses *viz.*, PG039, PG040, PG041, PG042, PG043, PG044, PG045, PG046, PG047, PG048, PG049, PGO50, PG051, PG052, PG053, PG054, PG055 and PG056 were represented by closed circle and the five checks (PBG 1, Pusa 256, PantG-186, Avrodhi and Pusa 1053) were represented by semi closed circle. X co-ordinate for each circle being the grain yield/ plant and Y co-ordinate for each circle being primary branches/ plant. Remaining seven characters have been represented by rays of different positions on the glyph and the range by length of rays *i.e.*, a line having low value with no ray, medium value with short ray and high value with long ray. The index values were divided into three classes *i.e.*, 1- no ray,

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2 -short ray and 3-long ray. The total index values were taken by adding up the index scores of all the nine characters studied.

Results and Discussion

The scatter diagram revealed that eight groups could be distinguished on the basis of

morphological variation (Fig.1). The Index scores and signs used for nine characters for Metroglyph analysis were presented in Table 2. The group I was represented by five genotypes with low grain yield/ plant and medium primary branches/ plant. This group comprised four progenies of wide cross (PG0 59, PG0 60, PG0 61, and PG0 63) and one

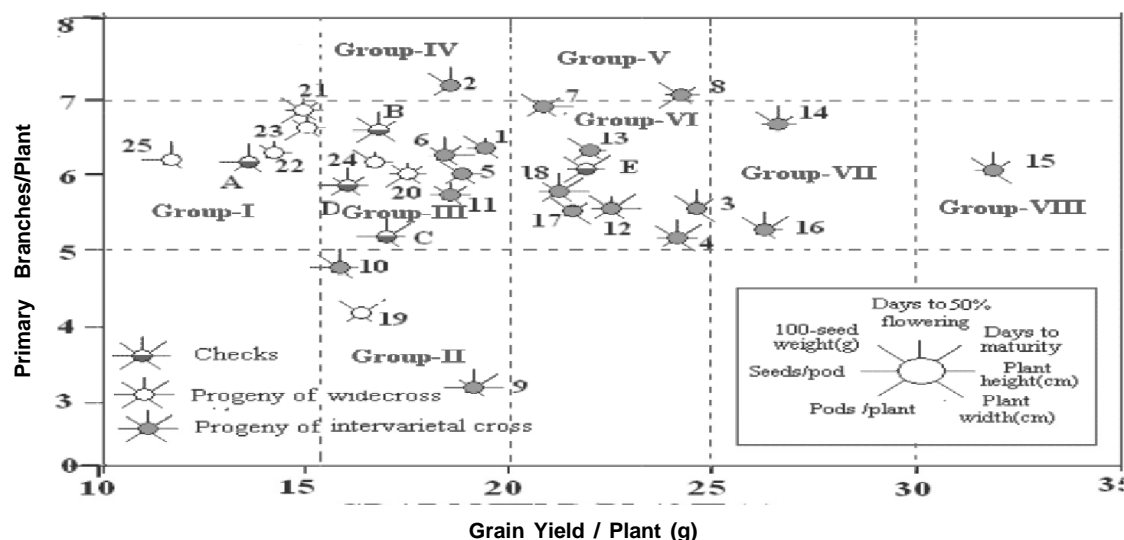


Fig:1 Scatter diagram of Metroglyph analysis of 25 progenies of intervarietal and wide crosses of chickpea and five checks

check, PBG1. This group showed high pods/ plant and or high seeds/ pod and early days to 50% flowering. The group II was characterized by three genotypes with medium grain yield/ plant and low primary branches/ plant. Two intervarietal cross progenies (PG 048 and PG 047) and one wide cross progeny, PG 057 were included in this group. Two characters viz., 100 seed weight and seeds/ pod were high in this group. Bhargava *et al.* (2009) reported high 100 seed weight in *Chenopodium* species. The group III consisted of nine genotypes including two wide cross progenies; PG058, PG062 and three checks cultivars; Pusa256, PantG186, Avrodhi and four progenies from intervarietal crosses; PG039, PG049, PG043 and PG044. All genotypes showed medium grain yield/ plant and medium primary branches/ plant. In this group the characters, days to 50% flowering and pods/ plant varied between early to late and low to high, respectively. Among the genotypes seeds/ pod were low to high, plant height was also low to high and days to maturity were also early to late. Group IV comprised of one genotype (PG 040) showing medium grain yield/ plant, high primary branches/ plant, late in days to 50% flowering, high 100 seed weight and average pods/ plant. Group V consisted of one genotype, PG 046 and it showed medium grain yield/ plant, high primary branches/ plant, 100 seed weight and pods/ plant. For other characters, PG 046 showed medium or low values. Group VI consisted of eight genotypes, of these; seven genotypes (PG041, PG 042, PG 045, PG 050, PG 051, PG 055, and PG 056) are from intervarietal crosses and one check (Pusa1053). All genotypes

Table 1. Chickpea genotypes used in the present study along with pedigree

Entries	Pedigree of genotypes	Generation
PG039	BG x KPG-59	F5
PG040	BG x KPG-59	F5
PG041	PG92-4 x Avrodhi	F5
PG042	PG92-4 x Avrodhi	F5
PG043	K850(LM) x Avrodhi	F5
PG044	K850(LM) x KPG-59	F5
PG045	K850(LM) x KPG-59	F5
PG046	K850(LM) x KPG-59	F5
PG047	K850(LM) x KPG-59	F5
PG048	BG362 x PG-186	F5
PG049	BG362 x PG-186	F5
PG050	BG362 x PG-186	F5
PG051	BG362 x PG-186	F5
PG052	BG329 x KPG-59	F5
PG053	BG329 x KPG-59	F5
PG054	BG329 x KPG-59	F5
PG055	BG362 x Avrodhi	F5
PG056	BG362 x Avrodhi	F5
PG057	PG92-97 x C.reticulatum	F7
PG058	PG92-97 x C.reticulatum	F7
PG059	PG92-97 x C.reticulatum	F7
PG060	PG92-97 x C.reticulatum	F7
PG061	PG92-97 x C.reticulatum	F7
PG062	PG92-97 x C.reticulatum	F7
PG063	PG92-97 x C.reticulatum	F7
PBG1 (check)	GG578 x NEC206	
Pusa256 (check)	(JG62x850-3/27) (L550x208)	
PantG186 (check)	ILC613 x PantG114	
Avrodhi (check)	T3 x K315	
Pusa1053 (check)	ICCV3 x FLIP88-120	

had high values of 100 seed weight and days to maturity showed low to high values. Plant height varied from low to high and plant width also showed medium to high value. This group showed medium grain yield/ plant and medium primary branches/ plant. Group VII consisted of two genotypes (PG 052 and PG 054) from an intervarietal cross and this group showed high grain yield/ plant and medium

Table 2. Index scores and signs used for characters for Metroglyph analysis of 30 genotypes of chickpea

Characters	Score 1		Score 2		Score 3	
	Values less than	Sign	Values between	Sign	Values more than	Sign
Days to 50% flowering	71	○	71-76	◇	76	◇
Days to maturity	130	○	130-135	○	135	○
Plant height	56	○	56-62	◇	62	◇
Primary branches/ plant	4.5	○	4.5-6.0	○	6	○
Plant width	27.5	○	27.5-29.5	○	29.5	○
Pods/ plant	91	○	91-98	○	98	○
Seeds/ pod	1.4	○	1.4-1.7	◇	1.7	◇
100-seed weight	15	○	15-24	○	24	○
Grain yield/plant	15	○	15-23		23	

primary branches/ plant. Both the genotypes were late for days to 50% flowering and had high 100 seed weight besides late maturity and medium plant height. Punitha *et al.* (2010) also showed in their findings of metroglyph analysis in sorghum that group VI having three genotypes with high yield and

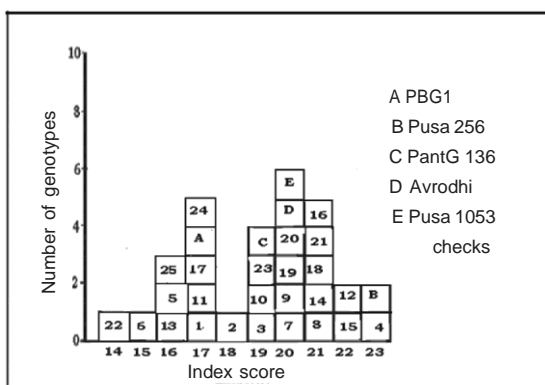


Fig. 2 Pattern of distribution of 30 genotypes of chickpea scored for 9 traits

moderate test weight. Similarly Bhargava *et al.* (2009) reported in *Chenopodium* species that group IV had three genotypes exhibiting high grain yield and medium to high primary branches/plant and plant height. Group VIII consisted of one genotype (PG 053) which showed very high grain yield/ plant and medium primary branches/ plant. The values for characters; days to 50% flowering, plant width and 100 seed weight were high in this group with medium values for seeds/ pod and days to maturity.

Majority of genotypes showed medium grain yield/ plant and medium primary branches/ plant. The frequency diagram showed the index score values for all characters (Fig. 2). The range of index score ranged from 14 to 23. Laiju *et al.* (2002) reported Index score ranging from 12 to 23 in *Hordeum* species. Maximum genotypes (6) had an index score of 20 and highest index score of 23 was observed for two genotypes, Pusa 256 and PG042; followed by (5) occurred around an index score of 17 and 21. Minimum frequency (1) occurred for index score of 14, 15 and 18. Laiju *et al.* (2002) reported that minimum frequency (1) occurred for index score of 13, 16, 18, 21 and 22 in *Hordeum* species.

Findings of the present study suggested that

genotypes in different groups can be used for crossing programme for harnessing maximum variability of good combinations of characters and also helped to ascertain the diversity for various characters among the 30 genotypes.

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