

Development and Characterization of Recombinant Inbred Lines for Seed Related Traits in Chickpea

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ABSTRACT: Seed traits are very important factors in improving yield and productivity of chickpea. However being quantitative in nature, gains through direct selection for these traits particularly for bolder seed size with higher yield were never successful and thus the way forward is to identify QTLs linked to these traits. Such a study requires development of mapping populations segregating for traits of interest. Mapping population of the cross SBD 377 (Desi Bold Type with 100 seed weight 48g and seed number per plant of 34 per plant) and BGD 112 (Desi small seeded with 100 seed weight of 12-15g and seed number per plant of 90) was developed at Division of Genetics, IARI. The recombinant inbred line (RILs) has been extensively phenotyped. Contrasting variability exists among the RILs for quantitative characters studied. Plant height ranged from 20 to 70 cm with 1-4 primary branches, 0-23 secondary branches and 7-54 total branches per plant. Number of seeds ranged 5 to 250 seeds per plant and pod number 5- 180 per plant. The range of 100 seed weight was 13 - 50 g. Plant yield varied from 2- 69 g. Availability of such a RIL population shall serve as a good base for the QTL analysis.

Keywords: Chickpea, Recombinant Inbred Lines (RILs), yield traits.

INTRODUCTION

Chickpea (*Cicer arietinum* L.; Family: Fabaceae) is a self-pollinated, diploid (2n=16), cool season pulse crop with a genome size of ~738Mb and an estimated 28,269 genes (Varshney et al., 2013). It is widely grown in more than 50 countries representing all the continents (Upadhyay et al., 2011). Worldwide chickpea ranks third among legumes (Food and Agricultural Organization, 2006) contributing almost 15% of the total pulse production of world. In the duration of 2010, the worldwide chickpea area was about 12.0 million ha, with 10.9 million metric tons of production with the yield of 911 kg ha⁻¹ (FAOSTAT, 2012). Yield being a complex trait, it is very difficult for *per se* selection by the breeders. Indirect selection through selecting for component is the way out. However, most of these traits being quantitative, greater gains for yield through selection for these is very difficult. Seed traits particularly seed number per plant and seed size is very important factors in

improving yield and productivity of chickpea (Bicer, 2009 and Ambika et al., 2014). The narrow genetic base of chickpea is limiting the genetic improvement of chickpea through breeding efforts (Bharadwaj et al., 2011; Van Rheenen et al., 1993). The level of natural variation among cultivated chickpea and wild accessions at molecular level is essential to develop breeding strategies for chickpea improvement (Shubha et al., 2011). Different selection criteria have been proposed by researchers for yield improvement in chickpea (Singh et al., 1990; Dasgupta et al., 1993; Kumar et al., 1999; Toker and Cagirgan, 2004). The purpose of the current work is to evaluate for quantitative characters of mapping population SBD 377 x BGD 112.

MATERIALS AND METHODS

The parents for the mapping population were identified based on the molecular diversity studies (Bharadwaj et al., 2010) and their variability studies. The parent SBD 377 is a desi bold type with 100 seed

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weight of 48g and seed number per plant of 34 per plant. BGD 112 (Pusa Green 112) is also a desi type. It is small seeded with 100 seed weight of 12-15g and seed number per plant of 90.176 F₁₁ recombinant inbred lines (RILs) derived by single seed descent method from the cross between SBD377 and BGD112 were used (Table 1). The RILs and their parents were planted in the field at the experimental farm of Indian Agricultural Research Institute, New Delhi (28.0800° N, 77.1200° E) for *rabi* season in an augmented block design. Each experimental unit was a single 2 m row plot containing 20 plants. A spacing of 0.5 meter between rows and 10cm within a row was adopted. Standard agronomic practices were followed to ensure adequate plant growth and development. Observations were recorded for nine yield and yield related traits viz., Days to Flowering, Total Branches, Days to Maturity, Plant Height, Pods per Plant, Seeds per Pod, 100 Seed Weight, Seeds per plant, Yield per plant, such as plant height, pods per plant, 100-seed weight and total number of seeds per plant. (Table 1).

RESULT AND DISCUSSION

Large variability was observed among the RILs for targeted traits. The leaf type ranged from simple to compound leaves. Data on mean and range of the characters studied. Plant height ranged from 20 to 70 cm with 1-4 primary branches, 0-23 secondary branches per plant, 7-54 total branches. Number of seeds per plant ranged from 5 to 250 seeds per plant and pods per plant ranged from 5 to 180. The range of 100 seed weight was 13 - 50 g and yield per plant varies from 2 - 69g. In quantifying plant height which had a mean of 48.65 cm. The graph was parabolic for plant height, pods per plants, 100 seed weight and seeds per plant indicating the polynomial distribution of these traits in the RIL population (Fig. 1-3). A perfect polynomic distribution was observed for 100 seed weight too with the maximum lines (71) in the range of 20.0 g to 24.9 g (Fig. 2). Transgressive segregants were recovered in the RILs for all the characters under study and about 20-30 per cent RILs clustered around the mean which indicated that the mapping population develop is suitable for identification of QTLs for these traits. There were 6 RILs having less number of seed per plant than that of the lowest parent (SBD 377 - 34) while there were 143 RILs having seeds per plant of more than 90 as found in the higher parent (BGD 112) (Fig. 3). A greater number of transgressive segregants for seeds per plant appear to have occurred at the cost of yield

Table 1
Phenotypic ranges for the traits under study in the RILs of the cross SBD377 x BGD 112.

Character	Min	Max
Days to Flowering	50 DAS	101 DAS
Total Branches	7	54
Days to Maturity	147 DAS	155 DAS
Plant Height	20 cm	80 cm
Pods per Plant	5	180
Seeds per Pod	1	2.4
100 Seed Weight	13.04g	48.04g
Seeds per plant	5	250
Yield per plant	2.03g	68.72 g

Table 2
Variability for yield parameters in the RILs of SBD377xBGD112

Character	Mean	SD	CV	Min	Max
plant Height (cm)	48.65263	5.921505	12.17099	20.0cm	80.0 cm
Pods per Plant	66.8956	34.82301	52.05575	5	180
100 seed weight (g)	25.04253	5.895564	23.5422	13.04g	48.04g
Total number of seeds per plant	79.68947	41.45352	52.01882	5	250
Yield per plant	17.58205	10.10124	57.45201	2.03g	68.72 g

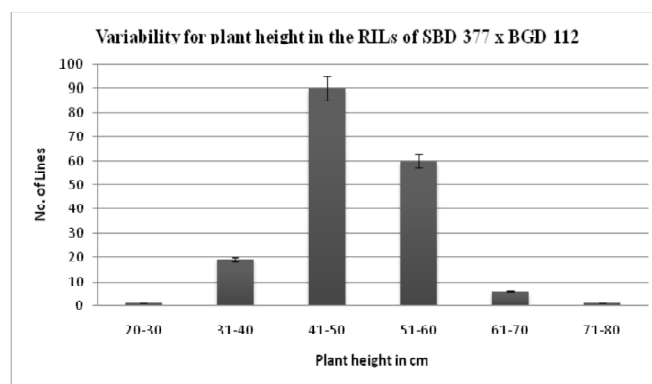


Figure 1: Phenotyping of the RILs for plant height

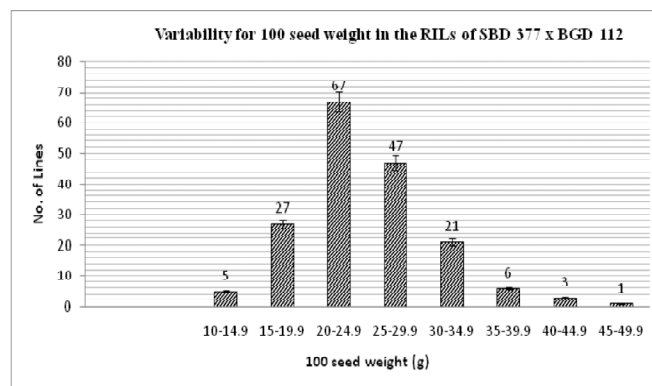


Figure 2: Phenotyping of the RILs for 100 seed weight

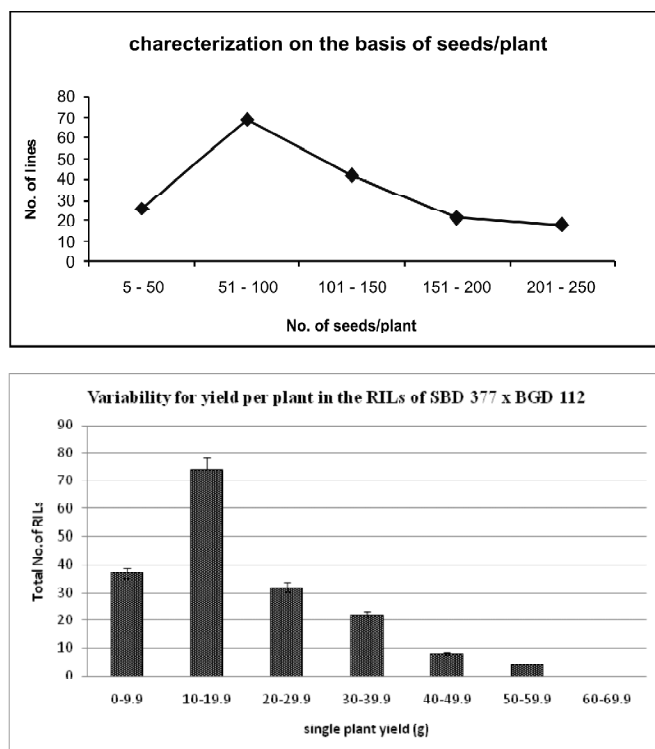


Figure 3: Variability for seeds per plant in the RILs of SBD 377 x BGD 112

compensation against the trait of 100 seed weight where in few segregants beyond the parental ranges could be recovered.

Plant grain yield and seed morphological traits are the two important factors used to evaluate genetic variation. The genetic diversity is essential for plant breeders seeking to improve existing germplasm by introducing novel genetic variation for certain traits into the breeding populations and introducing commercial varieties. Identification of QTLs requires a mapping population which is polynomial in distribution for the characters under study and non-biased in its construction. The knowledge and management of the genetic diversity can serve us to achieve long-term selection gain (Chowdhury *et al.*, 2002; Chaudhary *et al.*, 2010). High coefficient of variation indicates greater variability and also more influence of environment over these characters. Selection for such traits becomes difficult through conventional breeding. Efforts have been made by different scientists to track down QTLs controlling yield traits to boost the overall productivity in legumes (Ali *et al.*, 2013; Cobos *et al.*, 2009; Rehman *et al.*, 2010) these studies have been summarized by varshney *et al.*, 2013. A wide range of variations for such traits were also reported by Arshad *et al.*, 2003 and Ramanappa *et al.*, 2013. Tapping these variations

for crop improvement is essential. However presence of normal variation in a mapping population is essential for identification of QTLs. Further some of the RILs having high yield as well as high seed number can also be directly used in crop improvement programmes.

CONCLUSION

A biparental mapping population was established from the parents of SBD 377 and BGD 112. Seed traits particularly seed number per plant and seed size is very important factors in improving yield and productivity of chickpea. Identification of QTLs for yield contributing traits is required for bringing about greater gains in chickpea breeding. This requires development of effective mapping population which is polynomial in distribution with good variability for all the characters under consideration. The present mapping population provides such an opportunity to breeder's to identify yield related traits through molecular mapping and linkage analysis.

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