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

Tapan Kumar1, C. Bharadwaj1*, Afroz Alam2, Puja Singh1, Tripti Singhal, S. K. Chauhan1, Sabhya Bhatia3 and Ashutosh Sarkar4

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 (Cicerarietinum 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 (Upadhya 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 desibold type with 100 seed
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 pant 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

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

Table 2

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

Figure 1: Phenotyping of the RILs for plant height

Figure 2: Phenotyping of the RILs for 100 seed weight
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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.

ACKNOWLEDGEMENTS

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REFERENCES


