Genetic Variability and Heritability in Recombinant Inbreed Lines Developed for Seed Traits in Chickpea (*Cicer Arietinum* L.)

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Abstract: Success of any plant breeding programme largely depends upon the knowledge of genetic variability present in the given crop species for the trait under improvement. Presence of variability in the RIL population of the cross SBD 377 and BGD 112 indicates that the developed RILs can be used for mapping seed yield traits. The study indicated that Seed yield per plant being a dependent trait cannot be selected per se *and selection need to be exercised through 100 seed weight and total number of seeds. Contrary to the general perception lines having greater seed number than the best parent with more seed weight could be obtained indicating when diverse crosses are mad. This indicates the negative linkage between these two traits can be broken without causing any yield penalty up to a level where the source does not become limiting. However, this requires extensive wide crossing and careful evaluation of the segregants.*

Keywords: Chickpea, Variability, heritability, Recombinant Inbred lines, Yield.

INTRODUCTION

Chickpea (*Cicerarietinum* L.; Family: Fabaceae) is a self-pollinated, diploid ($2n = 16$), cool season legume crop with a genome size of ~738Mb and an estimated 28,269 genes (Varshney *et. al.*, 2013)[16]. It is widely grown in more than 50 countries representing all the continents (Upad-hyay *et. al.*, 2011)[14]. Chickpea ranks third among world food legumes contributing almost 15% of the total pulse production of world. The worldwide chickpea area was about 13.5 million ha, with 13.1 million metric tons of production with the yield of 968 kg ha-1 (FAOSTAT, 2013).

India is the world's biggest producer, with an annual production of around 6.54 Mt, representing 66% of total world chickpea production covering an area of 9.6 mha (FAOSTAT, 2013). Yield being a complex trait, it is very difficult for *per se* selection by the breeders. The success in breeding program depends on the amount of variability present for different characters in population and its efficient management and utilization. Progress in varietal improvement in crops has been slow due to lack of imagination vision and efficiency in utilizing to assess the components of genetic variation for various quantitative traits, which is likely to provide genetic basis for choosing parents for the breeding program. One of the objectives of this study was to find out the variability occurring in RILs of the cross SBD377 and BGD 112 and to estimate heritability and quantitative characters so that the characters to be used as selection criterion can be identified.

MATERIALS AND METHODS

Mapping population having one hundred and seventy-seven F_{11} recombinant inbred lines (RILs) derived of the cross SBD 377 (Desi Bold Type with 100 seed weight 48g and seed number per plant of

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34 per plant) and BGD 112 (Desi small seeded with 100 seed weight of 12-15g and seed number per plant of 90) was raised in randomized block design with three replications and a spacing of 30cm to10cm at Division of Genetics, IARI, Delhi, during rabi 2009-2010, 2010-2011,and 2011-2012. Standard agronomic practices for fertilization, tillage, weed and insect control were followed to ensure adequate plant growth and development.

Observations on the basis of five randomly taken competitive plants were recorded on nine quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, total branch per plant, pods per plant, total number of seeds per plant, 100-seed weight (g) and seed yield per plant (g). Heritability (broad sense) estimates were categorized into high, moderate and low by Robinson *et. al.* (1966)[9].

RESULT

Significant variability among the RILs with respect to nine agronomic traits were observed. Data on mean and range indicates that considerable variability exists within the mapping population for quantitative traits (Table 1). Days to flowering (DTF) ranged from 69.66 days to 96 days with a mean of 87.28 days. The genotypic and phenotypic coefficients of variations were recorded 7.0 and 9.27 respectively, indicating the high environmental influence. Heritability for this trait was high with value of 56.94. Days to maturity (DTM) ranged from 106 days to 158 days with the mean of 147 days. Phenotypic coefficient of variation (4.37) was higher than genotypic coefficient of variation (2.90). High heritability (44.13) for this trait is recorded. Plant height (PH) ranged from 37 cm to 66cm with an average of 52 cm. PCV(14.33) was recorded higher than GCV(8.5).

Primary branch (PB) and total branches (TB) ranged from 2-6, and 16-84 with the mean of 3.95 and 34.78 respectively. PCV recorded for primary branch (31.19) was higher than GCV (16.38) indicating greater environmental influence. PCV and GCV recorded for total branch (TB) was 36.85 and 17.51 respectively. Moderate heritability was observed for both the traits (27.58) and (22.58). Pods per plants (PPP) showed the mean of 71.21 ranging

from 22.5 to 186.5. PCV (38.54) was higher than GCV (19.19). Heritability (24.80) was moderate for this trait. Total number of seed per plant (TNSPP) ranged from 17.83 to 232. PCV recorded 42.87 while GCV was 20.62 with a moderate heritability of 23%. Range for 100 seed weight was 14.48 g to 38.55 g with an average of 23.92 g. PCV value (25.32) was little higher than GCV value (21.20) indicating environmental influence. Very high heritability (70%) was exhibited by this trait. Plant yield (PY) ranged from 6.34g to 55.86 gms with the mean of 20.51g. A high influence of environment was indicated by greater PCV (68.80) value than GCV (35.68). Range and mean for plant height and hundred seed weight were similar to the results observed by Gupta *et al* (2015)[7]. The relative degree at which a trait is transmitted from parent to offspring is indicated by heritability. Maximum heritability (broad sense) was observed for 100 seed weight followed by days to flowering and days to maturity indicating less environmental influence. Similar findings were reported by Vaghela *et. al.*, (2009)[15].

Success of any plant breeding programme largely depends upon the knowledge of genetic variability present in the given crop species for the trait under improvement. Presence of variability in the RIL population of the cross SBD 377 and BGD 112 indicates that the developed RILs can be used for mapping seed yield traits. Further, availability of superior yield traits in some of the RILs over and above the parental yield (RIL 62, RIL66) and seeds per plant (RIL 44, RIL173) indicate the usefulness of using theses RILs directly into varietal development programs. The genotypic coefficient of variation measures the range of variability available in a crop and also enables to compare the amount of variability present in different traits. The phenotypic coefficient of variation indicates the result of interaction between genotype and environment. In present study the value of phenotypic coefficient of variation(PCV) was observed higher than the genotypic coefficient of variation (GCV) indicating the greater environmental effects. Similar results have been reported by Farshadafar and Farshadafar (2008)[6]. The traits hundred seed weight, days to flowering, days to maturity, exhibited high heritability

suggesting that when subjected to selection, these traits would attain maximum genetic progress. Seed yield per plant being a dependent trait cannot be selected *per se* and selection need to be exercised through 100 seed weight and total number of seeds. With low heritability the trait total number of seeds, needs to be selected with caution. The low heritability indicates that this trait is more influenced by environment and larger genotype × environment effects are more preponderant to overcome this problem, the direct and indirect effects of this trait needs to be studied. Such a selection would accumulate more favorable yield components in the selected line for higher seed yield. It is largely inferred that yield can be improved either by improving 100 seed weight or total number of seeds per pod.

However, most of the workers have reported a negative correlation between these two. Contrary to that we could identify RIL62, RIL66 having more seed weight along with more seed number than the best parent SBD 377, which had a seed weight of 55g and seed number 232. Similar trans-aggressive segregants for number of seeds, exceeding BGD 112 (RIL62 with seed number 232 and RIL44 with seed number 222) could be identified along with greater seed weight in RIL62 (55g) and RIL66 (48 g). This indicates the negative linkage between these two traits can be broken without causing any yield penalty up to a level where the source does not become limiting.

However, this requires extensive wide crossing and careful evaluation of the segregants. Selections can only be done in such population if there exists greater variability in such population. The above study concludes the same.

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Table 1
Estimates of Mean, Range (lower-higher), GCV, PCV, *h²b*, for 177 RILs of cross SBD 377 × BGD 112 for nine traits.

| Traits | Mean | Range | | GCV | PCV | Heritability |
		Minimum	Maximum			
DTF	87.28492	69.66(RIL1)	96(RIL162)	7.00018	9.276653	56.94239666
DTM	147.31	106(RIL106)	158(RIL175)	2.90715	4.375758	44.13959085
PH	52.30168	37(RIL134)	66.33(RIL100)	8.55208	14.33564	35.58849689
PB	3.954376	2(RIL100)	6(RIL76)	16.38228	31.19477	27.57940854
TB	34.78399	16.66(RIL2)	84.83(RIL64)	17.51637	36.85615	22.5875147
PPP	71.21601	22.5(RIL157)	186.5(RIL136)	19.19494	38.54385	24.80065546
TNS	89.66667	17.83(RIL38)	232(RIL62)	20.62443	42.8781	23.13624679
100SW	23.92662	14.63(RIL53)	38.55(RIL37)	21.20837	25.32965	70.10618023
SY	20.51704	6.342(RIL38)	55.86(RIL62)	35.68153	68.80594	26.89273815

1. Days to Flowering, 2. Days to Maturity, 3. Plant height(cm), 4. Primary branch, 5. Total branch, 6. Pods per plant, 7. Total number of seed per plant, 8. 100 seed weight(g), 9. Seed yield(g).
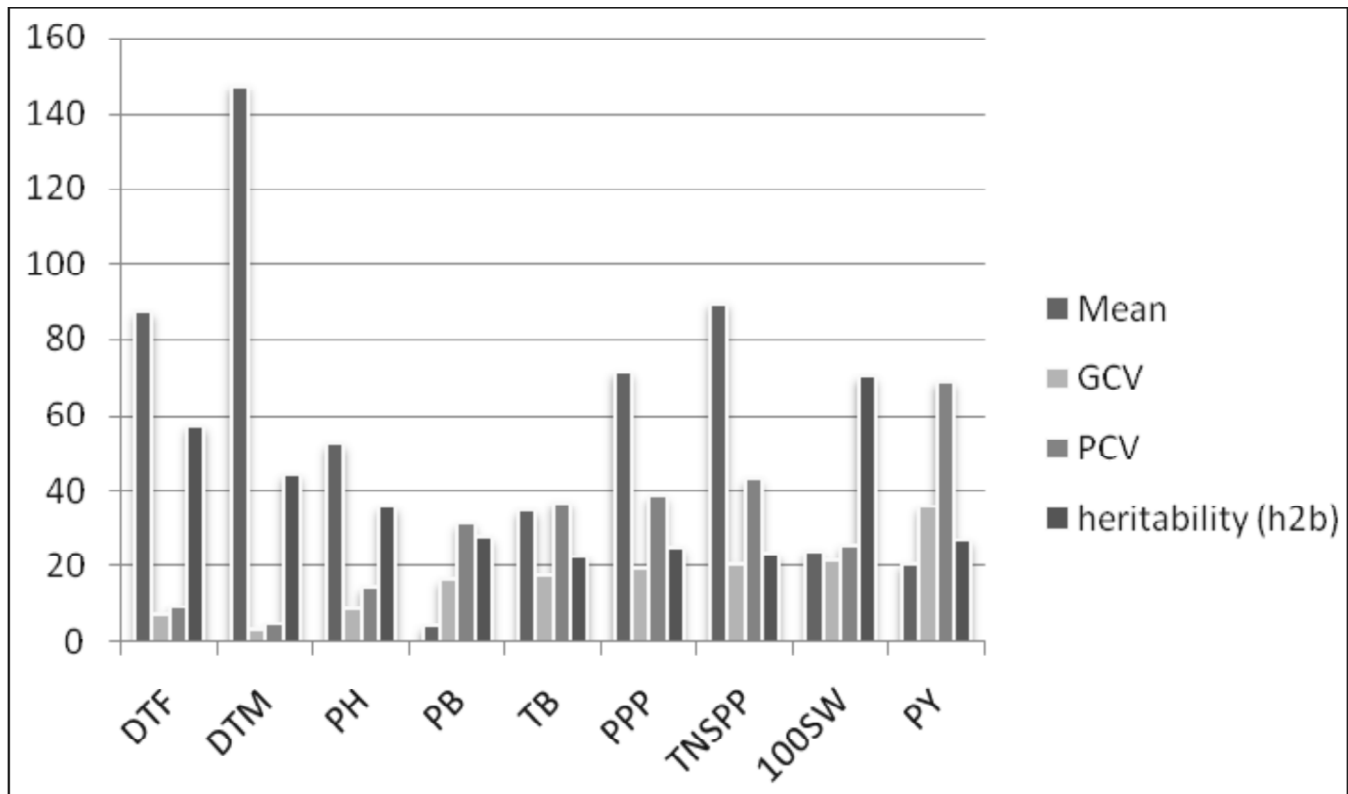
Figure 1: Graph representation of 177 RILs of cross SBD377 × BGD112 for nine traits.

DTF (Days to Flowering), DTM (days to maturity), PH (plant height), PB (primary branch), TB (Total Branch), PPP (Pods per plant), TNSPP (Total number of seed), 100SW (Seed weight), SY(Seed Yield).

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