



## Research Article

# Impact of F<sub>2</sub> bi-parental on quantitative traits inter-relationships and frequency of transgressive segregants in Dolichos bean (*Lablab purpureus* L.)

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### Abstract

Beneficial effects of F<sub>2</sub> bi-parental (BIP) mating have been amply demonstrated in several self-pollinated crops. To explore such beneficial effects in Dolichos bean, a highly popular grain legume vegetable and self-pollinated crop in southern Karnataka, an investigation was carried out to assess the impact of *inter se* mating in F<sub>2</sub> population derived from HA 4 (a high yielding photoperiod in-sensitive determinate type released variety) × GL 37 (a photoperiod sensitive in-determinate type germplasm accession) on nine quantitative traits inter-relationship and frequency of transgressive segregants. Significant shift in correlation coefficient of fresh pod yield plant<sup>-1</sup> with racemes plant<sup>-1</sup> from -0.33 (in F<sub>3</sub> progenies) to 0.19 (in BIP F<sub>3</sub> progenies) suggested the possibility of increasing the number of racemes plant<sup>-1</sup> without penalty in fresh pod yield plant<sup>-1</sup> through selection. The frequency of individuals that surpassed higher scoring parent for days to flowering, racemes plant<sup>-1</sup>, fresh pods node<sup>-1</sup>, fresh pod yield plant<sup>-1</sup> and 100-fresh seed weight was higher from BIP F<sub>3</sub> than those from F<sub>3</sub> progenies. The results suggested better prospects of deriving superior pure-lines with desired traits/combination of traits from inter-mated population.

### Keywords

Bi-parental mating, dolichos bean, correlation, transgressive segregants

### Introduction

Dolichos bean (*Lablab purpureus* L.) var. Lignosus is a bushy semi-erect herb and belongs to family Fabaceae (Magoon *et al.* 1974) with 2n=22 chromosomes (Goldblatt, 1981). It is commonly known as Field bean, Hyacinth bean, Indian bean, Egyptian bean, Bonavist bean, Sem, etc (Shivashankar and Kulkarni, 1989). It is predominantly self pollinated crop (Shivashankar and Kulkarni, 1989). It is believed that Dolichos bean has originated in India, as it is documented by archaeo-botanical finds in India from 2000 to 1700 BC at Hallur, the earliest Iron-Age site in Karnataka to 1200 to 300 BC at Veerapuram excavation site in Andhra Pradesh (Fuller, 2003). Dolichos bean var. lignosus grown for fresh beans used as a vegetable and to a limited extent as split dhal. It is intercropped with finger millet, maize, and sorghum in southern India under rainfed conditions. In pure crop stands, the productivity of dry seed yield is 1.5 t ha<sup>-1</sup> while it is 0.4 to 0.5 t ha<sup>-1</sup> in inter-cropping system (Shivashankar and Kulkarni, 1989). In Karnataka, Dolichos bean (*Lablab purpureus* var. lignosus) is grown in an area of 85,000 hectares with a production of 18,000 t and contributes to nearly 90 per cent of both area and production in India. Efforts at University of Agricultural Sciences (UAS), Bangalore has resulted in the development and

release of high yielding, short duration, photoperiod in-sensitive and determinate growth type cultivars such as HA 3 (Shivashankar and Kulkarni, 1989) and HA 4 (Girish and Byregowda, 2009).

As is true in any other self-pollinated crop, pedigree breeding is the most commonly used method for developing improved cultivars in Dolichos bean. Owing to rapid approach of homozygosity, pedigree method of breeding limits opportunities for recombination leading to retention of linkage of genes controlling desirable and undesirable traits (Hanson, 1959; Pederson, 1974; Bos, 1977; Stam, 1977). One or a few cycles of inter-mating in F<sub>2</sub> generation results in break-up of linkage blocks and help create populations with high frequency of desired recombinants which otherwise cannot be realized in later generations (Hanson, 1959; Bos, 1977; Stam, 1977; Yunus and Paroda, 1983). The disruption of linkage of genes controlling traits could be evidenced by changes in direction and magnitude of correlation between traits controlled by linked genes. Miller and Rawlings (1967) reported a decrease in the magnitude of r<sub>g</sub> in populations showing coupling linkages and an increase in r<sub>g</sub> in those showing repulsion phase linkages subsequently it was confirmed by isolating homozygous lines equal to or superior to the original F<sub>1</sub> (El-Adl and Miller 1971). Bains (1971) also

found a change in the direction of correlations from negative to positive and vice-versa for various traits in cotton. Under these premises, the present investigation was carried out to assess impact of  $F_2$  *inter se* [Bi-parental (BIP)] mating on quantitative traits inter-relationships and frequency of transgressive segregants.

### Materials and Methods

The basic material for present investigation consisted of  $F_2$  population derived from HA 4  $\times$  GL 37. While HA 4 is a high yielding photoperiod insensitive determinate type released variety, GL 37 is a photoperiod sensitive in-determinate type local collection being maintained at All India Coordinated Research Project (AICRP) on Pigeonpea, ZARS, UAS, GKVK, Bangalore.

**Development of experimental material:** To raise  $F_2$  population, 150 seeds harvested from  $F_1$  (HA 4  $\times$  GL 37) plants were sown with inter-row spacing of 0.6 m and of 0.3 m between plants within a row at the experimental plots of AICRP on Pigeonpea, ZARS, UAS, GKVK, Bangalore during 2012-13 *rabi*-summer season. Due to non-germination of a few seeds and mortality of a few seedlings, the  $F_2$  population consisted of 132 plants at flowering. Randomly selected twenty pairs of  $F_2$  plants with flowering synchrony were *inter se* mated. Seeds from 20 paired crosses (here after designated as BIP $F_3$  progenies) and selfed seed ( $F_3$ ) from their 40 parents were collected, cleaned, dried and preserved. Twenty BIP  $F_3$  and 40  $F_3$  progenies constituted the experimental material for the study.

**Evaluation of experimental material:** Seeds of 20 BIP  $F_3$  and 40  $F_3$  progenies along with the two parents and three checks (HA 3, HA 4 and Kadle avare) were sown in Augmented Design (Federer, 1961) in five compact blocks at the experimental plots of Department of Genetics and Plant Breeding (GPB), UAS, GKVK, Bangalore during 2013 *Kharif* season. Each block consisted of 12 BIP  $F_3$  and/or  $F_3$  progenies, three checks and two border entries. Each entry in each block was sown in a single row of four meters length with a row spacing of 0.45 m and 0.3 m between plants within a row. Each of BIP  $F_3$  and  $F_3$  progenies consisted of 12 to 15 plants. Recommended agronomic and plant protection practices were followed to raise a healthy crop.

**Data collection:** The data on nine quantitative traits (QTs) namely, days to flowering, primary branches  $\text{plant}^{-1}$ , racemes  $\text{plant}^{-1}$ , nodes  $\text{raceme}^{-1}$ , fresh pods  $\text{node}^{-1}$ , fresh pods  $\text{plant}^{-1}$ , fresh pod yield  $\text{plant}^{-1}$ , fresh seed yield  $\text{plant}^{-1}$  and 100 fresh seed weight were recorded on the 10 plants (avoiding border plants) of BIP  $F_3$  and  $F_3$  progenies.

**Statistical analysis:** The nine QTs mean values computed based on data on 10 randomly labeled plants in each BIP  $F_3$  and  $F_3$  progenies and check

entries were used for statistical analysis. ANOVA was performed following Augmented Design (Federer, 1961) using WINDOSTAT 8.5 version. Adjusted trait value of each of the individuals in BIP  $F_3$  and  $F_3$  progenies were estimated by subtracting observed trait value of the individuals of BIP  $F_3$  and  $F_3$  progenies from the adjustment factor ' $a_j$ ' of  $j^{\text{th}}$  block; ' $a_j$ ' was estimated as ' $a_j = (x_j - x_{\dots})$ ',  $x_j$  = trait mean of checks in the  $j^{\text{th}}$  block and  $x_{\dots}$  = the overall trait mean of checks in the experiment (Federer, 1961). Adjusted means were used for estimating correlation of eight QTs, inter-relationships and frequency of transgressive segregants. Adjusted means were used for estimating simple correlation coefficients ( $r$ ) of eight QTs with fresh pod yield  $\text{plant}^{-1}$  (Weber and Moorthy, 1952) and direct effects of nine QTs on the fresh pod yield  $\text{plant}^{-1}$  as suggested by Wright (1921) and illustrated by Dewey and Lu (1957) and frequency of plants scoring lower than lower scoring parent and higher than higher scoring parents (designated as transgressive segregants) in both BIP  $F_3$  and  $F_3$  progenies.

**Impact assessment of  $F_2$  BIP mating on QTs dynamics:** BIP  $F_3$  progenies were compared with those of  $F_3$  progenies with respect to correlation coefficients of eight QTs with fresh pod yield  $\text{plant}^{-1}$  and direct effects of nine QTs on the fresh pod yield  $\text{plant}^{-1}$  and frequency of transgressive segregants.

### Results and Discussion

**Analysis of variance:** Non-significance of mean squares due to blocks suggested poor evidence for detectable effect of edaphic factors and/or micro-environments associated with the blocks on the expression of BIP  $F_3$  and  $F_3$  progenies for all the traits except primary branches  $\text{plant}^{-1}$  and racemes  $\text{plant}^{-1}$  (Table 1). Experimental progenies (BIP  $F_3$  +  $F_3$  progenies) differed significantly for all the traits except primary branches  $\text{plant}^{-1}$ , nodes  $\text{raceme}^{-1}$  and fresh seed yield  $\text{plant}^{-1}$  (Table 1). The parents were selected based on phenotypic diversity for most traits and significant variability in  $F_2$  population derived from them confirms their diversity at genetic level as well. Significant variability between BIP  $F_3$  and  $F_3$  progenies adequately provided statistical and genetical validity for comparative assessment of BIP  $F_3$  and  $F_3$  progenies for inter-relationships among nine QTs frequency of transgressive segregants. Vinayan and Govindarasu (2010) in sesame, Selvam (2012) in bhendi, Koli *et al.* (2013) in aromatic rice, Shivakumar *et al.* (2013) in chickpea also compared BIP  $F_3$  and  $F_3$  progenies and reported significant differences between them. They further documented significant changes in direction and magnitude of correlation coefficients among QTs driven by  $F_2$  biparental mating and higher frequency of transgressive segregants in BIP  $F_3$  than that in  $F_3$  progenies.

***Impact of BIP mating on traits inter-relationships***

***Correlation coefficients:*** Decrease in correlation among QTs is attributed to breakage of coupling phase linkages while breakage of repulsion phase linkages increases the magnitude of correlation coefficient (ignoring signs) (Miller and Rawlings, 1967). Significant shift in magnitude and direction of correlation coefficient of fresh pod yield plant<sup>-1</sup> with racemes plant<sup>-1</sup> from -0.325\* (in F<sub>3</sub> progenies) to 0.192 (in BIP F<sub>3</sub> progenies) in the present study (Table 2) might be due to breakage of the coupling phase of linkages between the genes (presumably present far apart) controlling these traits in F<sub>1</sub>'s. It further suggested the possibility of increasing the number of racemes plant<sup>-1</sup> without penalty in fresh pod yield plant<sup>-1</sup>. Meredith and Bridge (1971) in cotton and Singh and Murty (1973) in pearl millet have also reported reduction in correlation coefficients of component traits with economic product yield following BIP mating. Miller and Rawlings (1967) documented a decrease in the magnitude of genotypic correlation in populations showing coupling linkages and an increase in genotypic correlation in those showing repulsion phase linkages in cotton. Subsequently, the findings of Miller and Rawlings (1967) were confirmed by isolating homozygous lines equal to or superior to the original F<sub>1</sub> (El-Adl and Miller, 1971).

For most traits that had high genetic correlation in original population, genetic correlations were found to be lower in BIP F<sub>3</sub> progenies in cotton (Meredith and Bridge, 1971). Bains (1971) also found a change in the direction of correlations from negative to positive and *vice-versa* for among traits following BIP mating in bread wheat. Similarly, Yadav and Murty (1979) reported that a positive correlation of plant height with grain yield plant<sup>-1</sup> was broken down and weakened from  $r=0.62^{**}$  (in F<sub>2</sub> population to  $r=0.27^{**}$  (in BIP F<sub>3</sub> progenies) after one cycle of random mating in F<sub>2</sub> of 15 bread wheat crosses. Yunus and Paroda (1982) also reported several new correlations in BIP F<sub>3</sub> progenies as compounding F<sub>3</sub> self-progenies of two wheat crosses. Absence of changes/shifts in magnitude/direction of correlation coefficients of fresh pod yield plant<sup>-1</sup> with rest of the traits namely days to flowering, primary branches plant<sup>-1</sup>, racemes plant<sup>-1</sup>, nodes raceme<sup>-1</sup>, fresh pods node<sup>-1</sup>, 100-fresh seed weight, fresh pods plant<sup>-1</sup> and fresh seed yield plant<sup>-1</sup> in the present study could be attributed to LE of genes controlling these traits in F<sub>1</sub>'s or inadequacy of one cycle of F<sub>2</sub> inter-mating to break down tight linkages. Perhaps two or more cycles of inter-mating in F<sub>2</sub> population might result in breakages undesirable linkages between traits as suggested by Hanson (1959), Bos (1977) and Stam (1977).

***Path coefficients:*** There were shifts in direct effects of fresh seed yield plant<sup>-1</sup>, fresh pods plant<sup>-1</sup>, and fresh pods node<sup>-1</sup> (Table 3). These shifts in direct effects of component traits on fresh pod yield plant<sup>-1</sup>

could be attributed to breakage of linkages. However, direct effects of rest of the traits on fresh pod yield plant<sup>-1</sup> were comparable between BIP F<sub>3</sub> and F<sub>3</sub> progenies. Shifts in direct effects of component traits on dependent trait were also documented by Nematullah and Jha (1993), Balyan and Verma (1985) in bread wheat and Parameshwarappa *et al.* (2009) in safflower.

***Impact of BIP mating on frequency of transgressive***

***segregants:*** Probability of isolating genotypes with maximum number of 'plus' genes is remote considering most of the economically important traits are controlled by large number of genes. However, the genotypes with short of perfection are relatively common and will be useful (Palmer, 1953). Genotypes selected from segregating populations belong to this category. Crossing together genotypes which are short of perfection selected from same cross is expected to uncover relatively higher frequency of near perfection genotypes even from smaller F<sub>2</sub> populations which the breeders normally handle.

In the present study, frequency of individuals that surpassed higher scoring parent for days to flowering, racemes plant<sup>-1</sup>, fresh pods node<sup>-1</sup>, fresh pod yield plant<sup>-1</sup> and 100-fresh seed weight was higher from BIP F<sub>3</sub> than those from F<sub>3</sub> progenies (Table 4). For rest of the traits, frequency of individuals that surpassed higher scoring parents was higher from F<sub>3</sub> than those from BIP F<sub>3</sub> progenies. Frequency of individuals that surpassed lower scoring parents was higher from BIP F<sub>3</sub> than those from F<sub>3</sub> progenies for nodes raceme<sup>-1</sup>. For rest of the traits, frequency of individuals that surpassed lower scoring parents was higher from F<sub>3</sub> than those from BIP F<sub>3</sub> progenies. Genetic studies indicate that transgressive segregation mostly results from the combinations of alleles from both parents that have complementary gene effects dispersed between parents (Risenberg *et al.* 1999). That is, individuals that receives 'plus' alleles from both parents or 'minus' alleles from both parents are likely to have extreme phenotypes. BIP mating is likely to be useful for recovering such extreme rare recombinants especially when repulsion phase linkages are prevalent in the F<sub>1</sub>'s. The F<sub>2</sub> population used in the present study appears to have good potential to recover pure-lines with desired combination of traits in Dolichos bean.

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**Table 1: Analysis of variance (Augmented design) for quantitative traits in Dolichos bean**

Source of variation	df	Mean sum of squares								
		Days to flowering	Primary branches plant <sup>-1</sup>	Racemes plant <sup>-1</sup>	Nodes raceme <sup>-1</sup>	Fresh pods node <sup>-1</sup>	Fresh pods plant <sup>-1</sup>	Fresh pod yield plant <sup>-1</sup> (g)	Fresh seed yield plant <sup>-1</sup> (g)	100 fresh seed weight (g)
Block (eliminating checks + F <sub>3</sub> + BIP F <sub>3</sub> progenies)	4	0.35	0.01	1.77*	0.24	0.01	3.02	107.98	14.03	13.85
Entries (checks + F <sub>3</sub> + BIP F <sub>3</sub> progenies) (ignoring blocks)	62	81.88**	0.31*	5.32**	0.50	0.04**	137.73**	1273.06**	175.83	66.63**
Checks F <sub>3</sub> + BIP F <sub>3</sub> progenies	2	1171.45**	3.03**	5.40**	0.02	0.13**	699.18**	3694.37**	612.40**	72.03**
Checks vs.(F <sub>3</sub> + BIP F <sub>3</sub> progenies)	59	38.84**	0.22	4.98**	0.52	0.03**	121.03**	1210.86**	161.70	66.29**
Non genetic (error)	1	442.33**	0.01	24.83**	0.19	0.37**	0.00	100.16	136.36	75.89**
	8	0.77	0.08	0.30	0.30	0.01	5.16	225.68	68.62	5.08

\*Significant @P=0.05;

\*\* Significant @ P=0.01

**Table 2: Estimates of correlation coefficients of different component traits with fresh pod yield plant<sup>-1</sup> in BIP F<sub>3</sub> and F<sub>3</sub> progenies of Dolichos bean.**

Traits	BIP F <sub>3</sub>	F <sub>3</sub>
Days to flowering	0.010	-0.121
Primary branches plant <sup>-1</sup>	-0.101	0.004
Racemes plant <sup>-1</sup>	0.192	-0.325*
Nodes raceme <sup>-1</sup>	0.327	-0.150
Fresh pods node <sup>-1</sup>	-0.370	-0.070
Fresh pods plant <sup>-1</sup>	0.789**	0.833**
Fresh seed yield plant <sup>-1</sup> (g)	0.891**	0.983**
100 fresh seed weight (g)	0.024	0.172

\*Significant @ P=0.05;

\*\*Significant @ P=0.01

**Table 3: Estimates of direct effects of different component traits on fresh pod yield plant<sup>-1</sup> in BIP F<sub>3</sub> and F<sub>3</sub> progenies of Dolichos bean.**

Traits	BIP F <sub>3</sub>	F <sub>3</sub>
Days to flowering	-0.041	0.024
Primary branches plant <sup>-1</sup>	-0.008	-0.014
Racemes plant <sup>-1</sup>	0.001	-0.020
Nodes raceme <sup>-1</sup>	-0.098	0.015
Fresh pods node <sup>-1</sup>	-0.132	-0.007
Fresh pods plant <sup>-1</sup>	0.105	0.021
Fresh seed yield plant <sup>-1</sup> (g)	0.780	0.974
100 fresh seed weight (g)	-0.044	0.027

Residual effects in BIP F<sub>3</sub> and F<sub>3</sub> progenies = 0.21 and 0.07, respectively.

**Table 4: Estimates of frequency (%) of transgressive segregants for quantitative traits in BIP F<sub>3</sub> and F<sub>3</sub> progenies of Dolichos bean.**

Traits	≥ P <sub>1</sub> (higher scoring parent)		≤ P <sub>2</sub> (lower scoring parent)	
	BIP F <sub>3</sub>	F <sub>3</sub>	BIP F <sub>3</sub>	F <sub>3</sub>
Days to flowering	5.0	2.5	0.0	0.0
Primary branches plant <sup>-1</sup>	0.0	0.0	0.0	5.0
Racemes plant <sup>-1</sup>	30.0	2.5	30.0	75.0
Nodes raceme <sup>-1</sup>	0.0	0.0	50.0	32.5
Fresh pods node <sup>-1</sup>	30.0	7.5	65.0	77.5
Fresh pods plant <sup>-1</sup>	60.0	60.0	0.0	10.0
Fresh pod yield plant <sup>-1</sup> (g)	55.0	47.5	10.0	12.5
Fresh seed yield plant <sup>-1</sup> (g)	60.0	60.0	5.0	15.0
100 fresh seed weight (g)	55.0	37.5	30.0	35.0