



Studies on Association of Yield and Quality Contributing Parameters in Faba Bean (*Vicia faba* L.)

SK SINGH, SHAILESH CHAND GAUTAM*, CB YADAV AND RAM NIVAS

Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.) India

ABSTRACT

The present investigation was conducted in normal soil under irrigated condition. The experimental material constituted 25 germplasm lines with check variety Vikrant. A wide range of variation for different characters and comparison of means of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the germplasm collection. The superior lines identified for seed yield and other characters may be used as donor parents in hybridization programme for the characters to which they showed high mean performance. Seed yield per plant showed highly significant and positive correlation with plant height followed by days to maturity and showed non-significant correlation with other character. The characters identified above as important direct and indirect yield components merit due consideration in formulating selection strategy in faba bean for selection of high yielding varieties. The six clusters in divergence analysis contained genotypes of heterogeneous origin, thereby indicating no parallelism between genetic and geographic diversity.

Keywords: Phenotypic, genotypic, correlation, heritability, genetic diversity, path and cluster analysis

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INTRODUCTION

Faba bean (*Vicia faba* L.) is an important pulse crop of the world cultivated under both irrigated and rainfed conditions (Singh *et al.*, 2012b). It is crop which can be surviving under any adversity and can be grown under any climatic adversity. An excellent crop for climate change circumstance and a cheap source of vegetable protein (Singh *et al.*, 2013b). Faba bean is an annual legume botanically known as *Vicia faba* L is one of the oldest crops grown by man and is used as a source of protein in human diet, as fodder and forage crop for animals, and for available nitrogen in the biosphere (Singh and Bhatt, 2012b). Faba bean growth habit is mainly indeterminate; growth and flower induction continue while the lower part of the stem bears flowers and then pods (Singh *et al.*, 2012c). Reproductive nodes usually begin between nodes three and five, typically continuing to approximately node twenty to twenty nine (Singh *et al.*, 2013a). The flowers are borne on racemes which develop acropetally, the pedicel lengths vary considerably. The center of origin is believed

to be between the oriental Mediterranean countries and Afghanistan (De Candolle, 1882; Cubero, 1974; Ladizinsky, 1975; Zohary, 1977; Abdulla, 1979). Faba bean with its ~30% of seed protein content, constitutes a valuable source of protein for food in developing countries such as Asia, Central America and Africa where a large deficiency of animal protein has been recorded. In developed countries, faba bean is mainly used for animal feeding. Endowed with unique ability to trap atmospheric nitrogen in their root nodules in association with *rhizobium* bacterial and thrive well under harsh and fragile eco-system; pulses remained an integral component of subsistence farming system of dry land region since dawn of agriculture. Its rich source of protein, minerals, vitamins and crude fibre, pulses are considered as health food. Faba bean genotypes have a large genetic variability for starch, protein and fibre content (Singh *et al.*, 2013a). About 50% of water-insoluble cell walls are contained in seed coats. Their content is primarily determined by seed size and by the zero-tannin genes. Protein content usually has high heritability values and can be increased by breeding if needed. Faba bean storage proteins are rich in lysine and

* Corresponding author email: scgautamgb5@gmail.com

low in sulphur amino acids, Methionine and Cystine (Singh *et al.*, 2014). In the spontaneous genetic variability, the amino acid content is primarily determined by total protein content and any modification by breeding of individual amino acid content is no treaty available. The seeds of faba bean contain antinutritional compounds/factors that reduce their nutritional value. Faba bean contains small amounts of several anti-nutritional factors; however, their effects are less acute. The protease inhibitors remain in much lower (2%) concentrations is compare is to soybeans. Roasted seeds are eaten like peanuts in India.

MATERIALS AND METHODS

The present investigation entitled Studies on genetic variability, correlation & path and diversity analysis in Faba bean (*Vicia faba* L.) was carried out during Rabi 2012-13, at the Student's Instructional Farm of Narendra Dev University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.), India.

EXPERIMENTAL MATERIALS

The experimental materials for the present investigation consisted of 26 germplasm lines of faba bean and one check variety, namely, Vikrant. The material, comprising of indigenous as well as exotic germplasm lines, exhibiting wide spectrum of variation for various agronomic and morphological characters. This experiment was conducted in Augmented design (Federer, 1956). Each plot consisted of 4 rows 4 m length with the inter and intra row spacing of 45 cm and 15 cm. All recommended culture practices were adopted to raise a good crop.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) due to treatment showed high significant for majority of characters except 100- seed weight and protein content for which it was significant.

Coefficient of Variation

The phenotypic and genotypic coefficient of variation for all the eleven characters showed (Table 2). In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters (Spark, 1973). The characters which exhibited moderate estimates 10 to 20% of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were seed yield per plant, number of pods per plant, biological yield per plant and number of

Table1: Analysis of variance for eleven characters in Faba bean

| Characters | Source of variation | | |
|------------------------------|---------------------|------------|-------|
| | Replication | Treatments | Error |
| Degree of freedom | 2 | 25 | 50 |
| Days to 50% flowering | 0.01 | 8.78** | 1.75 |
| Days to maturity | 0.81 | 15.52** | 1.15 |
| Plant height (cm) | 0.69 | 36.79** | 1.51 |
| No. of branches / plant | 0.07 | 0.83** | 0.26 |
| No. of seeds / pod | 0.03 | 0.12** | 0.02 |
| No. of pods / plant | 2.87 | 126.02** | 8.53 |
| 100-seed weight (g) | 0.09 | 0.83* | 0.46 |
| Biological yield / plant (g) | 16.19 | 367.44** | 42.69 |
| Harvest index (%) | 36.65* | 54.72** | 10.98 |
| Protein content (%) | 0.24 | 1.55* | 0.78 |
| Seed yield / plant (g) | 11.80 | 21.30** | 4.10 |

** indicate significant at 5% and 1% probability level,

branches per plant. The remaining characters *viz.*, days to 50% flowering, days to maturity, plant height, number of seeds per pod, 100 seed weight and protein content showed low estimates (< 10%) of PCV and GCV.

Heritability and Genetic Advance

Heritability and genetic advance in per cent of mean were showed (Table 2) High estimates of broad sense heritability (> 75%) were recorded for plant height (88.6%), number of pods per plant (82.1%) and days to maturity (80.6%). The moderate estimates of heritability (50-75%) were observed for biological yield per plant (71.7%), seed yield per plant (58.3%), days to 50% flowering (57.3%) and harvest index (57.0%) while the low estimates of broad sense heritability were shown by number of seeds per pod (49.3%), number of branches per plant (42.5%), protein content (24.8%) and 100 seed weight (21.0%). The high estimates of genetic advance in per cent of mean (>20%) were recorded for number of pods per plant (29.49%), harvest index (27.13%), biological yield per plant (24.59%) and seed yield per plant (23.62%). Number of branches per plant (13.64%) showed moderate estimate for genetic advance in per cent of mean, while the number of seeds per pod (7.91%), plant height (6.56%), days to 50% flowering (4.17%), days to maturity (3.19%), protein content (2.03%), and 100 seed weight (1.30) showed low estimate of > 75 high genetic advance in per cent of mean.

by no. of seeds/pod (-0.249) and protein content (-0.229) while among the other characters showed non-significant. Biological yield per plant had significant and positive correlation (0.263) with days to 50% flowering. The harvest index showed negative and highly significant correlation with biological yield per plant (-0.54), days to maturity (-0.339) and plant height (-0.337). The protein content showed significant and positive correlation with biological yield per plant (0.278) and significant and negative correlation with days to maturity (-0.229). The number of seeds per pod exhibited significant and negative correlation with number of branches per plant (-0.267) and days to maturity (-0.249). Number of pods per plant showed positive and significant correlations with days to maturity (0.267) and all the characters exhibited non-significant. The number of branches per plant recorded highly significant and positive correlation with plant height (0.291). Plant height showed highly positive significant association with days to 50 per cent flowering (0.336). 100-seed weight showed negative significant association with seeds per pod (-0.238).

Path coefficient analysis

The direct and indirect effects of different characters on seed yield per plant were estimated by path coefficient analysis Dewey and Lu (1959) using simple correlations in Table 4. The highest positive direct effect on seed yield per plant was exhibited by harvest index

(1.088) followed by biological yield per plant (0.745) and negative direct effect on seed yield / plant was exhibited by days to 50% flowering (-0.032) followed by plant height (-0.021) and 100 seed weight (-0.0210). The highest negative indirect effect on seed yield /plant was exerted by biological yield / plant (-0.587) followed by days to maturity (-0.369), plant height (-0.367) and 100 seed weight (-0.102) via harvest index. The highest positive indirect effect on seed yield / plant was exerted by protein content (0.207) followed by days to 50% flowering (0.175), days to maturity (0.165) and no. of seeds / pod (0.143) while the negative indirect effect was exerted by harvest index (-0.402) followed by no. of pods / plant (-0.049) and no. of branches / plant (-0.038), via biological yield / plant. The remaining estimates of the indirect effects in the present analysis were too low to be considered important. The residual effect observed was 0.3268 which indicates that some of the characters which might contribute to yield have not been included in the study.

Genetic divergence

Then Mahalanobis D^2 analysis was employed to study genetic diversity was done followed by existing among 26 faba bean entries on the basis of 11 quantitative characters. The pseudo F-test revealed that six clusters arrangement was the most appropriate for grouping the 26 entries. Therefore, the 26 entries were grouped into

Table 4: Direct and indirect effect of different characters on seed yield per plant in faba bean

| Character | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of seeds/ pod | No. of pods/ plant | 100 seed weight (g) | Bio-logical yield/ plant (g) | Harvest index (%) | Protein content (%) | Correlation with seed yield |
|-----------------------------|-----------------------|------------------|-------------------|------------------------|-------------------|--------------------|---------------------|------------------------------|-------------------|---------------------|-----------------------------|
| Days to 50% flowering | -0.0324 | -0.0001 | -0.0072 | -0.0002 | 0.0007 | -0.0010 | 0.0016 | 0.1757 | -0.0271 | 0.0066 | 0.1168 |
| Days to maturity | 0.0019 | 0.0010 | -0.0018 | 0.0007 | -0.0010 | 0.0019 | 0.0001 | 0.1658 | -0.3692 | -0.0145 | -0.2151 |
| Plant height (cm) | -0.0109 | 0.0001 | -0.0213 | 0.0027 | 0.0000 | 0.0003 | -0.0015 | 0.0446 | -0.3677 | -0.0051 | -0.3588 |
| No. of branches/ plant | 0.0008 | 0.0001 | -0.0062 | 0.0092 | -0.0011 | -0.0008 | -0.0037 | -0.0388 | -0.0659 | -0.0012 | -0.1076 |
| No. of seeds/ pod | -0.0058 | -0.0002 | 0.0002 | -0.0025 | 0.0041 | -0.0015 | 0.0050 | 0.1436 | 0.0639 | 0.0104 | 0.2173 |
| No. of pods/ plant | 0.0045 | 0.0003 | -0.0009 | -0.0011 | -0.0009 | 0.0071 | 0.0013 | -0.0498 | -0.0175 | -0.0045 | -0.0614 |
| 100 seed weight (g) | 0.0024 | 0.0000 | -0.0015 | 0.0016 | -0.0010 | -0.0005 | -0.0210 | 0.0026 | -0.1027 | -0.0042 | -0.1242 |
| Biological yield/ plant (g) | -0.0076 | 0.0002 | -0.0013 | -0.0005 | 0.0008 | -0.0005 | -0.0001 | 0.7457 | -0.5875 | 0.0176 | 0.1670 |
| Harvest index (%) | 0.0008 | -0.0003 | 0.0072 | -0.0006 | 0.0002 | -0.0001 | 0.0020 | -0.4025 | 1.0884 | -0.0050 | 0.6902 |
| Protein content (%) | -0.0034 | -0.0002 | 0.0017 | -0.0002 | 0.0007 | -0.0005 | 0.0014 | 0.2078 | -0.0853 | 0.0633 | 0.1853 |

Residual effect = 0.3268, Bold figures indicate direct effects

six different non overlapping clusters. The distribution of 26 faba bean lines in six clusters is presented in Table 5. The highest number of genotypes appeared in cluster II which contained 13 genotypes followed by cluster I having 9 genotypes. Clusters III, cluster IV, cluster V and cluster VI were having 1 genotype respectively.

Table 5: Clustering pattern of 26 faba bean genotype & on the basis of Mahalanobis's D^2 statistic.

| Cluster Number | No. of genotypes | Genotypes |
|----------------|------------------|---|
| I | 9 | HB 187, HB 212, HB 186, HB65, HB 194, HB 193, HB 82, HB 48, HB 40 |
| II | 13 | NDFB 8, RFB 7, RFB 5, NDFB 11, DFB 101, IC 2011215, HB 195, IC 2011241, DFB 103, DFB 102, HB 39, RFB 6, VIKRANT |
| III | 1 | HB 122 |
| IV | 1 | HB184 |
| V | 1 | NDFB 12 |
| VI | 1 | HB214 |

The estimates of average intra and inter cluster distance for the six cluster is presented in Table 6. The highest intra-cluster distance was recorded in cluster II (15.32) followed by cluster I (9.89), while the lowest value was recorded in case of cluster III, IV, V and VI (0.00). The maximum inter cluster distance was recorded between cluster IV and cluster VI (76.08) followed by cluster II and cluster IV (46.05). The minimum inter cluster distance was observed between cluster III and cluster V (10.20) followed by cluster I and cluster III (15.16). The mean performance of clusters, for eleven characters is

Table 7: Cluster means for different characters in Faba bean

| Cluster no. | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of branches/plant | No. of seeds/pod | No. of pods/plant | 100 -seed weight (g) | Biological yield/plant (g) | Harvest index (%) | Protein content (%) | Seed yield/plant (g) |
|-------------|-----------------------|------------------|-------------------|-----------------------|------------------|-------------------|----------------------|----------------------------|-------------------|---------------------|----------------------|
| I | 56.52 | 126.93 | 97.62 | 4.07 | 3.14 | 38.37 | 25.35 | 76.90** | 22.50 | 25.54 | 17.04 |
| II | 57.59 | 127.28** | 104.22** | 4.54** | 3.04 | 40.51 | 25.40** | 74.65 | 19.99* | 25.53 | 14.72 |
| III | 55.00 | 123.33 | 97.97 | 4.33 | 2.87* | 39.27 | 25.12 | 60.64 | 29.77** | 25.03* | 18.09 |
| IV | 55.33* | 127.00 | 96.02* | 3.50* | 2.93 | 51.30** | 24.57* | 60.39* | 28.25 | 25.87** | 18.86 |
| V | 56.00 | 121.00* | 102.56 | 4.33 | 3.10 | 40.87 | 25.12 | 63.68 | 22.36 | 25.37 | 13.99* |
| VI | 60.33** | 121.67 | 103.00 | 3.83 | 3.67** | 26.13* | 24.80 | 71.15 | 26.36 | 25.40 | 18.77** |

*, ** indicates lower & higher value

presented in Table 6.

Table 6: Estimates of average intra and inter-cluster distances for the six clusters in faba bean

| Clusters | I | II | III | IV | V | VI |
|----------|-------------|--------------|-------------|-------------|-------------|-------|
| I | 9.89 | 23.44 | 15.16 | 23.82 | 27.19 | 33.03 |
| II | | 15.32 | 28.49 | 46.05 | 23.20 | 31.65 |
| III | | | 0.00 | 18.67 | 10.20 | 34.21 |
| IV | | | | 0.00 | 41.84 | 76.08 |
| V | | | | | 0.00 | 24.08 |
| VI | | | | | | 0.00 |

Bold figures indicate intra-cluster D^2 value.

The cluster I showed high mean performance for biological yield / plant (76.90) while it exhibited average mean performance for remaining characters (Table 7). The cluster II had the genotypes having high mean performance for day to maturity (127.28), plant height (104.22), no. of branches / plant (4.54) and 100 seed weight (25.40), exhibiting and for the low mean performance harvest index (19.99) showed while other character showed average mean performance. The cluster III showed high mean performance for harvest index (29.77) and showed low mean performance for no. of seeds / pod (2.87) and protein content. The other characters showed average mean performance in cluster III. The cluster IV showed high mean performance for no. of pods / plant (51.39) and protein content (25.87) while it showed low mean performance for days to 50% flowering (55.33), plant height (96.02) no. of branches / plant (3.50) 100-seed weight (24.57) and biological yield / plant (60.39) and average performance for other characters. The cluster V showed low mean performance for days to maturity (121.00), seed yield

/ plant (13.99) while other characters showed average performance in cluster V. The cluster VI showed high mean performance for days to 50% flowering (60.33), no. of seeds / pod (3.67) and seed yield / plant (18.77) while low mean performance for no. of pods / plant (26.13). The remaining characters showed average mean performance in cluster VI (Dubey and Srivastava (2007), Lokere et al. (2007), Dwevedi and Lal (2009), Sial et al. (2010) and Yadav et al. (2010)).

Contribution of eleven traits of faba bean toward divergence

The contribution of eleven characters towards divergence in (Table 4) showed the highest contribution by plant height (36.62%) followed by no. of pods / plant (22.77%) Beale (1969) and Spark (1973). The seed yield / plant (0.31%) showed lowest contribution towards divergence.

CONCLUSION

This investigation confirms that wide ranges of variation for different characters are present in this gene pool consisting 26 germplasm lines. Since comparison of means of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the germplasm collection.

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