

GENETIC VARIABILITY AND CORRELATIONS IN FRENCH BEAN FOR YIELD IMPROVEMENT

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ABSTRACT

The field experiment was carried out to estimate the extent of genetic variability and correlation between yield related traits to be used in breeding. Forty genotypes were used for the traits: plant height at 30 days after sowing of FB-118, FB-119 (8.51cm), days to FB-121, FB-123, FB-124, FB-125 50% flowering, highest leaf length (9.6 cm), leaf width (8.49cm), pod length (12.94cm), pod width (10.04mm), number of marketable pods per plant (9.31), pod yield per plant (65.82g), number of pods per plant (9.31), pod weight (5.83g), days to 50% maturity (66.27), seed length (17.18mm), seed width (8.22mm), number of seed per pod (49.86), green pod yield (131.70 Mt-ha⁻¹), and 100 seed weight (49.86g) compared to Arka Komal, Arka Suvridha, Arka Anoop. Genetic analysis was used to estimate correlations of yield and related characters between French bean genotypes. Significant differences occurred for all characters studied. Green pod yield varied from 34.86 ('FB-125') to 133.26 Mt-ha⁻¹ ('FB-132'). Green pod yield exhibited a highly significant, positive, correlation with number of marketable pods per plant, pod yield per plant, and number of pods per plant, and was negatively correlated with days to 50% flowering. There was genetic variability for all traits among genotypes.

INTRODUCTION

French bean, (*Phaseolus vulgaris* L. 2n=2x=22) belongs to family Leguminosae is a nutritious vegetable, which contain high amounts of proteins and minerals consumed as tender pods, shelled beans and dry beans. During the process of domestication in cultivated *Phaseolus vulgaris* L. several morphological changes have been occurred from the wild spp. viz., *Phaseolus aborigineus* Burk, *Phaseolus coccineus*, *Phaseolus lunatus*, and *Phaseolus acutifolius*. Domestication of wild common beans occurred independently in Mesoamerica and Andean South America and gave rise to two major gene pools also within the cultivated forms ((Duke, 1981, Adams, 1985 and Mumtaj *et al.*, 2014 Angla *et al.*, 2010). The cultivated french bean is an erect growing plant with determinate branching, whereas, the wild type is indeterminate and profusely branched. The cultivated types have smaller number of nodes on main axis and internode length is relatively shorter than wild forms. The most important changes, which have been taken place in the genetic characteristics of *Phaseolus vulgaris* L. are in flower size, pod size and seed size. Variability in French bean is important for improvement of yield which is governed by a complex set of characters. Direct selection for yield is not very effective in French bean, but indirect selection for some characters are useful increasing the yield of French bean. A large amount of variability occurs in yield and related traits of French bean genotypes The magnitude of the variability present in a crop species is of utmost importance for the relative improvement

of the cultivars, suitable for a particular region. A great extent of variability has been observed in different agronomic characters of french bean with respect to plant height, days to flowering, pod length, seed shape and seed weight (Froussios, 1970). Evan (1973) suggested that a determinate/bush plant type with long internodes, long pods per node with higher number of seeds per pod would be a desirable combination. These characteristics along with round, fleshy and non stringy long pods will prove to be more important in case of vegetable type cultivars. The experimentation of interrelations among characters helps brought effective improvement to yield of French bean and is used to develop breeding strategies to identify elite genotypes through selection in advance generations. Correlations (at genotypic and phenotypic level) among yield associated traits are useful for yield improvement of French bean. (Kandpal 2008, Angadi *et al.*, and Kumar, 2014) evaluated that genotypic and phenotypic coefficients of variation were highest for plant height and lowest for days to maturity. Singh *et al.* (2007) recorded that high heritability, coupled with high genetic advance, occurred for plant height, days to 50% flowering and days to maturity. Devi *et al.* (2015) observed positive, significant, correlations of pod yield with days to flowering, average pod weight, branches/plant, pods/plant and plant height. In French bean it is necessary to evaluate relationships between yield component traits among genotypes to develop improved varieties which will deliver improved yield quantity and/or quality. Thus, there is a need to identify the lines having desirable horticultural traits, such as yield

and quality characters. To select better plants, the breeder requires a comprehensive knowledge of variability available in the germplasm. The subsequent worked of interrelations among different characters further helps in bringing effective improvement. In order to achieve these, the present investigation was, therefore, planned with forty germplasm of *Phaseolus vulgaris* L. with objective estimate the extent of genetic variability for various characters in French bean.

MATERIALS AND METHODS

Forty French bean genotypes were evaluated from January to June 2011 at the Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand), India, to estimate genetic variability and correlation between yield related traits. The sandy loam soil was prepared with 1 deep plowing followed by 3 diskings, clod breaking, hoeing and leveling. Flat beds were used to sow seed. The field was divided into plots of 15×5 m. Fertilizers were applied @120N:60P:40K kg·ha⁻¹. Half of the nitrogen, and all the phosphorus and potassium, were applied at soil preparation. The remaining nitrogen was top dressed in 2 split doses at 20 and 30 days after sowing. Nitrogen was applied as urea, phosphorus as ammonium phosphate, and potassium as muriate of potash. One irrigation occurred immediately after sowing. Weekly flood irrigation was used from sowing to harvest.

Details of observations

The observations were recorded on 16 quantitative and 14 qualitative characters. Five plants were tagged in each row and used for recording the data/observations and randomly selected.

Quantitative characters

Plant height at 30 days after sowing (cm), Days to 50 per cent flowering, Leaf length (cm), Leaf width (cm), Pod length (cm), Pod width (mm), Number of marketable pod at harvest, Pod yield per plant(g), Number of pods per plant, Pod weight (g), Days to 50 per cent maturity, Seed length (mm), Seed width (mm), Number of seeds per pod, Green pod yield per hectare(q/ha) and 100 seed weight (g)

Qualitative characters

Plant growth habit, Early plant vigour, Stem pigmentation, Flower colour, Leaf shape, Pod shape, Pod colour, Orientation of pods, Pod peak shape, Pod curvature, Parchment layer, Seed colour and Seed mottling. The characters, which showed significant differences among genotypes, were further subjected to analysis of the following parameters:

Variability

Heritability

Genetic advance

Genetic advance as percent of population mean

Correlation coefficient

Variability

Parameters of variability were estimated as per formulae given by Burton and De Vane (1953).

Phenotypic coefficient of variation (PCV)

$$PCV(\%) = \sqrt{\frac{\text{Phenotypic Variance } (V_p)}{\text{General mean of population } (G_m)}} \times 100$$

b. Genotypic coefficient of variation (GCV)

$$GCV(\%) = \sqrt{\frac{\text{Genotypic Variance } (V_g)}{\text{General mean of population } (G_m)}} \times 100$$

c. Environmental coefficient of variation (ECV)

$$ECV(\%) = \sqrt{\frac{\text{Environmental Variance } (V_e)}{\text{General mean of population } (G_m)}} \times 100$$

Where,

$$V_e = M_e$$

$$V_g = \frac{M_g - M_e}{r}$$

$$V_p = V_g + V_e$$

$$G_m = \frac{\text{Grand total}}{r \times g}$$

Estimation of Heritability

Heritability in broad sense was calculated for each character as described by Johnson et al. (1955) as follows.

$$h_{(b)}^2 = \frac{\sigma_{gi}}{\sigma_{pi}^2}$$

Where,

$h_{(b)}^2$ = Heritability in broad sense

σ_{gi}^2 = Genotypic Variance of character 'i'

σ_{pi}^2 = Phenotypic variance of character 'i'

The genotypic and phenotypic variance was obtained from the expectation of mean squares of analysis of variance of RBD.

Estimation of Genetic Advance

The expected genetic advance from (G.A.) straight selection was obtained by Allard (1960).

$$G.A. (s) = h_{(b)}^2 \times \sigma_{pi} \times K$$

Where,

GA (s) = expected genetic advance

$h_{(b)}^2$ = heritability in broad sense

σ_{pi} = phenotypic standard deviation of character 'i'

K = constant for which the value is given as 2.06 which is the expectation in the case of 5% selection intensity.

Genetic advance was expressed as per cent of population mean.

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic Advance} \times 100}{GM}$$

For categorizing the magnitude of different parameters the limits used as follows:

PCV and GCV

- > 20% High
- 10-20% Moderate
- < 10% Low

Heritability (h²)

- > 90% High
- 80-90% Moderate
- < 80% Low

Genetic advance as percent of population mean

- > 50% High
- 25-50% Moderate
- < 25% Low

Correlation coefficient

Analysis of variance and covariance

Source of variation	Degree of freedom	Mean squares		Mean sum of product	Variance
		X	Y		
Replication	r-1				
Genotype	g-1	Mgx	Mgy	Mgxy = MP1	MP1/MP2
Error	(r-1)(g-1)	Mex	MeY	Mexy = MP2	

Genotypic and phenotypic correlations were calculated by employing the technique to Statistical analysis in variance covariance matrix in which total variability had seen split into replications genotype and errors. All the components of variance were estimated from analysis of variance table (ANOVA) and those of covariance from the analysis of covariance table (ANOVA) as given below:

Genotypic, Phenotypic and environmental covariance between characters x and y were worked out as under:

Environmental covariance (Ve xy) = MP2
 Genotypic covariance (Vg xy) = MP1-MP2/r
 Phenotypic covariance (Vp xv) = Vg xy + Ve xy

Estimation of correlation

The correlations between all the characters under study were estimated at genotypic and phenotypic levels according to method given by Searle (1961) using the formula:

$$\text{Phenotypic correlation } \{r_{xy}(p)\} = \frac{\text{Cov}_{xy}(p)}{[\text{Var}_x(p) \cdot \text{Var}_y(p)]^{1/2}}$$

$$\text{Genotypic correlation } \{r_{xy}(g)\} = \frac{\text{Cov}_{xy}(g)}{[\text{Var}_x(g) \cdot \text{Var}_y(g)]^{1/2}}$$

Where,

Cov_{xy} (p) and Cov_{xy} (g) are the phenotypic and genotypic covariance between characters X and Y respectively.

Var_x (g) and Var_x (p) are the genotypic and phenotypic variances, respectively for character x, while Var_y (p) and Var_y (g) are the phenotypic and genotypic variances, respectively for character y.

Testing of significance of correlation coefficient 'r' was done by using the formulae as given by Snedecor and Cochran (1967) as follows.

If 't'_{cal} > 't'_{tab}

Then 'r' is significant.

Where,

t_{cal} = calculated value of 't'

t_{tab} = table value of 't'

$$t'_{cal} = r \sqrt{\frac{n-2}{1-r^2}}$$

Where, r = S_{xy} / √(S_{xx} × S_{yy})

Here,

- Sxy = Measure of joint variability between X and Y.
- Sxx = Measure of variability between X.
- Syy = Measure of variability between Y.
- N = number of genotype

Table 1: Mean, range, general mean (GM), standard error mean (SEM), phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), environmental coefficient of variation (ECV %), heritability, genetic advance and genetic advance as percent of mean

Trait	Range	GM	SEM	Coefficient of variation (%)			Heritability h ² (%)	Genetic advance	Genetic advance as percent of mean (%)
				PCV (%)	GCV (%)	ECV (%)			
Plant height at 30 days after sowing (cm)	5.13-8.85	6.74	.122	14.00	13.64	3.13	94.98	1.84	27.29
Days to 50% flowering	45.00-60.00	47.55	0.370	9.17	9.07	1.34	97.83	8.78	18.46
Leaf length (cm)	5.68-10.29	7.54	0.217	12.54	11.50	4.99	84.16	1.64	21.75
Leaf width (cm)	4.62-9.14	6.16	0.233	15.48	14.02	6.56	82.00	1.61	26.13
Pod length (cm)	4.78-13.50	8.55	0.198	21.19	20.80	4.02	96.39	3.59	41.98
Pod width (mm)	5.20-10.73	9.20	0.243	14.34	13.59	4.58	89.76	2.44	26.52
Number of marketable pods/plant	2.80-10.00	6.26	0.242	28.65	27.86	6.70	94.52	3.49	55.75
Pod yield/plant (g)	17.43-66.63	44.38	0.286	27.57	27.55	1.11	99.83	25.16	56.69
Number of pods/plant	3.06-14.00	8.12	0.212	28.87	28.51	4.52	97.54	4.71	58.00
Weight of marketable pods/plant (g)	4.05-6.30	5.45	0.169	11.36	10.01	5.37	77.63	.992	18.20
Days to 50% maturity	46.93-68.66	56.91	0.543	7.62	7.43	1.65	95.29	8.51	14.95
Seed length (mm)	8.97-16.63	13.44	0.100	15.44	15.38	1.29	99.30	4.24	31.54
Seed width (mm)	5.51-8.44	6.80	8.09	11.62	11.43	2.06	96.85	1.57	23.08
Number of seed/pod	2.33-7.00	4.80	0.214	22.55	21.18	7.72	88.26	1.96	40.83
Green pod yield (Mt·ha ⁻¹)	3.49-13.33	8.87	0.556	27.55	27.53	1.08	99.84	50.31	56.67
100 seed weight	13.80-50.60	34.98	0.227	24.17	24.15	1.12	99.78	17.38	49.68

$$S_{xy} = \frac{1}{n-1} \left[\sum xy^2 - \left(\frac{\sum xy}{n} \right)^2 \right]$$

$$S_{xx} = \frac{1}{n-1} \left[\sum x^2 - \left(\frac{\sum x}{n} \right)^2 \right]$$

$$S_{yy} = \frac{1}{n-1} \left[\sum y^2 - \left(\frac{\sum y}{n} \right)^2 \right]$$

Data were recorded from 5 randomly selected plants in each plot for: plant height at 30 days after sowing, days to 50% flowering, leaf length, leaf width, pod length, pod width, number of marketable pods per plant, pod yield per plant, number of pods per plant, pod weight, days to 50% maturity, seed length, seed width, number of seed per pod, green pod yield and 100 seed weight. The experiment was arranged in a randomized complete block design with 3 replications. Mean values of each genotype in each replication for all traits were subjected to statistical analysis as per Johnson *et al.* (1955) and broad sense heritability computed for each trait. Genotypic and phenotypic correlations were calculated with a variance covariance matrix in which total variability was split into replications, genotype and errors.

RESULTS AND DISCUSSION

Analysis of variance indicated variability occurred for all traits (Table 1). Number of pods per plant, pod yield per plant, green pod yield per plant and 100 seed weight were highly variable indicating selection for these characters can be effective to improve yield.

Genotype affected all traits (Table 2). There was a close relationship between GCV and PCV for all characters, indicating very little influence of environment on their expression. The estimate of heritability was high (>80%) in most characters except marketable pod weight per plant indicating a greater possibility of selection on the basis of phenotypic measures for better yield using these traits (Table 1). The high heritability may be due to additive gene effects and these traits are likely to respond to direct selection. Number of pods per plant, number of marketable pods per plant, pod yield per plant, green pod yield per plant, 100 seed weight, number of seed per pod and pod length exhibited high GCV accompanied by high heritability indicated a good possibility for selection for development of high yielding varieties through selection. High heritability, along with high values of genetic gain, occurred for number of pods per plant, pod yield per plant, number of pods per plant and green pod yield·ha⁻¹ indicating total variation in these characters might be due more to genetic than phenotypic variance. Selection for these characters would be effective for improvement of French bean yield. Ahmed and Kamaluddin (2013) used the same French bean characters but with different germplasm and reported high heritability, along with high genetic advance, for days to 50% flowering indicating there is the possibility to develop high yielding germplasm. The importance of genetic advance lies in determining the amount of progress that can be achieved

Table 2: Range of variation among genotypes for all the characters

Trait	High	Medium	Low
Low value < 5.73		Genotypes with high and low values for each trait	
Number of seed/pod		FB-122, FB-127, FB-133, FB-115, FB-105, FB-119, Arka Suvidha (C) ^a ,	
High value > 5.66	FB-108, FB-117, FB-119,	Arka Anoop (C) ^a , Arka Komal (C) ^a	
Mid value 2.93-5.66	FB-125, FB-126, FB-127,	FB-101, FB-115, FB-102, FB-135, FB-114, FB-106, FB-120, FB-136, FB-137,	
Low value < 2.93	FB-128, FB-132, FB-133	FB-130, FB-104, FB-105, FB-112, FB-107, FB-129, FB-124, FB-110, FB-109,	
Green pod yield (Mt·ha ⁻¹)		FB-113, FB-122, FB-103, FB-131, FB-123, FB-116, FB-134, FB-111, FB-121,	
High value > 131.70	FB-107, FB-109, FB-132	Arka Suvidha (C) ^a , Arka Anoop (C) ^a , Arka Komal (C) ^a	
Mid value 36.42-131.70		FB-127, FB-106, FB-117, FB-116, FB-105, FB-110, FB-104, FB-112, FB-135,	
Low value < 36.42		FB-131, FB-115, FB-129, FB-134, FB-128, FB-101, FB-136, FB-102, FB-133,	
100 seed weight		FB-122, FB-121, FB-124, FB-119, FB-120, FB-114, FB-137, FB-111, FB-137,	
High value > 49.86	FB-129	FB-111, FB-103, FB-130, FB-123, FB-118, FB-113, FB-126, FB-108, Arka Suvidha (C) ^a ,	
Mid value 14.44-49.86		Arka Anoop (C) ^a , Arka Komal (C) ^a	
Low value < 14.44		FB-113, FB-103, FB-111, FB-130, FB-120, FB-124, FB-121, FB-122, FB-125,	
		FB-108, FB-123, FB-128, FB-131, FB-127, FB-116, FB-104, FB-126, FB-110,	
		FB-132, FB-117, FB-136, FB-107, FB-135, FB-102, FB-133, FB-134, FB-115,	
		FB-118, FB-109, FB-137, FB-106, FB-101, FB-105, FB-114, FB-112,	
		Arka Suvidha (C) ^a , Arka Anoop (C) ^a , Arka Komal (C) ^a	
			FB-118
			FB-125
			FB-119

^ac = check variety: Arka Komal, Arka Suvidha, Arka Anoop.

Table 3: Intercharacter correlation coefficients at phenotypic (P) and genotypic (G) levels in all French Bean genotypes with values combined.

Character		Leaf length (cm)	Leaf width (cm)	Pod length (cm)	Pod width (cm)	Number of marketable pods/plant	Days to 50% flowering	Pod yield/ plant (g)	Number of pods/ plant
Plant height at 30 days	P	-0.212	-0.134	-0.146	0.182	0.188	0.131	0.154	0.139
	G	-0.228	-0.138	-0.145	0.186	0.206	0.136	0.158	0.136
Days to 50% flowering	P		-0.173	-0.149	-0.283	-0.376*	-0.292	-0.352*	-0.406*
	G		-0.187	-0.154	-0.297	-0.396*	-0.304	-0.357*	-0.414*
Leaf length (cm)	P			0.626**	0.209	0.066	0.32	0.173	0.089
	G			0.631**	0.233	0.071	0.359*	0.19	0.109
Leaf width (cm)	P				0.193	-0.075	0.213	0.192	0.082
	G				0.206	-0.1	0.249	0.216	0.097
Pod length (cm)	P					0.587**	0.421**	0.259	0.442**
	G					0.606**	0.431**	0.263*	0.453**
Pod width (cm)	P						0.179	0.24	0.339*
	G						0.175	0.256	0.367*
Number of marketable pod/plant	P							0.475**	0.615**
	G							0.489**	0.637**
Pod yield/ plant (g)	P								0.888**
	G								0.900**
Number of pods/plant	P								
	G								
Weight of marketable pods/plant (g)	P								
	G								
Days to 50% maturity	P								
	G								
Seed length	P								
	G								
Seed width	P								
	G								
Number of seed/pod	P								
	G								
100 seed weight (g)	P								
	G								

by selecting for a specific trait. Similar observation was also recorded by Singh *et al.* (1994), Asati and Singh (2008) and Pandey *et al.* (2013). The relative values of phenotypic variance, genotypic variance and coefficient of variance (PCV and GCV), give an idea about the magnitude of variability present in a population. Among morphological characters, maximum variation was observed for 100-seed weight followed by plant height for both phenotypic variance and genotypic variance. The variance was very low for characters like days to 50% flowering, germination percentage, days to first flowering and green pod yield/plot. The results get support from the findings of Johanson *et al.* (1955). Correlation studying provides better understanding of yield component that helps the plant breeder during selection. In addition, earlier researchers revealed that direct effect of number of pods per plant on seed yield was positive and highly significant (Rodrigo *et al.*, 1972; Dhiman, 1996; Amini *et al.*, 2002).

Plant height was correlated with pod yield·ha⁻¹ indicating selection for plant height is not effective for yield improvement. Selection of short stature genotypes may be effective for better grain yield (Mumtaz *et al.*, 2014 and Mohsen *et al.*, 2012). Green pod yield·ha⁻¹ was positively, and significantly, correlated with pod yield per plant, number of pods per plant, and number of marketable pods per plant at phenotypic and genotypic levels, and significantly, and positively, correlated with days to 50% flowering (Table 3). Days to 50% flowering

were significantly, and positively, correlated with days to 50% maturity and significantly, and negatively, correlated with green pod yield·ha⁻¹ indicating that selection for earliness is effective for yield improvement, similar observation was also recorded by Singh *et al.* (1994).

Pod yield per plant was significantly, and positively, correlated with pod length, pod weight, number of pods per plant and seed weight at genotypic and phenotypic levels indicating yield may depend on these traits, which might be improved through selection. Number of pods per plant was significantly, and positively, correlated with pod length, pod width, number of marketable pods per plant and pod yield·ha⁻¹ indicating number of pods per plant was important for improvement in yield via pod length, pod width and number of marketable pods. (Malaghan *et al.*, 2014) reported a significant correlation between number of pods per plant and plant height. This is important in French bean because more pods is associated with improved pod yield.

Differences in genotypic, and phenotypic, coefficient of variations indicated existence of considerable genetic variability among French bean genotypes which were in part controlled by environment. Heritability, in combination with genetic advance, is more useful than heritability alone in predicting resultant effects for selecting the best genotype for a given trait. Direct selection for early maturing genotypes, along with more pods per plant, would be desirable to improve seed yield

Table 3: Cont.....

Character		Green pod yield (Mt-ha ⁻¹)	Weight of marketable pods/plant (g)	Days to 50% maturity	Seed length (mm)	Seed width (mm)	100 seed weight (g)	Number of seed/pod
Plant height at 30 days	P	0.002	-0.17	0.177	0.122	-0.121	-0.197	0.153
	G	0.033	-0.18	0.18	0.119	-0.122	-0.201	0.157
Days to 50% flowering	P	0.226	0.911**	-0.125	0.085	-0.13	0.267	-0.352*
	G	0.256	0.930**	-0.128	0.086	-0.143	0.271	-0.358*
Leaf length (cm)	P	0.195	-0.227	0.012	0.085	-0.005	-0.223	0.17
	G	0.195	-0.251	0.012	0.1	-0.004	-0.248	0.19
Leaf width (cm)	P	0.28	-0.182	0.115	-0.125	-0.032	-0.213	0.191
	G	0.287	-0.186	0.134	-0.124	-0.045	-0.238	0.215
Pod length (cm)	P	-0.347*	-0.163	0.322	-0.11	0.108	-0.087	0.259
	G	-0.414*	-0.187	0.325*	-0.111	0.116	-0.087	0.263
Pod width (cm)	P	-0.273	-0.321	0.035	-0.11	0.052	-0.324	0.24
	G	-0.322	0.364*	0.034	-0.127	0.047	-0.340*	0.256
Number of marketable pod/plant	P	-0.292	-0.202	0.06	-0.131	0.318	-0.406*	0.475**
	G	-0.352*	-0.222	0.059	-0.139	0.340*	-0.418*	0.489**
Pod yield/ plant (g)	P	0.177	-0.276	0.007	-0.111	0.149	-0.307	0.988**
	G	0.198	0.283	0.007	-0.113	0.157	-0.308	0.988**
Number of pods/plant	P	-0.218	-0.289	0.04	-0.206	0.253	-0.322	0.888**
	G	-0.219	-0.293	0.043	-0.212	0.276	-0.327*	0.900**
Weight of marketable pods/plant (g)	P		0.131	-0.09	0.19	-0.287	0.102	0.177
	G		0.164	-0.11	0.228	-0.357*	0.118	0.198
Days to 50% maturity	P			-0.13	-0.048	-0.071	0.278	-0.276
	G			-0.136	-0.045	-0.088	0.286	-0.284
Seed length	P				0.461**	0.052	0.05	0.005
	G				0.468**	0.057	0.05	0.005
Seed width	P					0.086	0.183	-0.112
	G					0.102	0.186	-0.114
Number of seed/pod	P						-0.218	0.148
	G						-0.228	0.156
100 seed weight (g)	P							-0.306
	G							-0.307

(Prasanth, K., 2014). Traits with a high range of various phenotypic and genotypic coefficients of variation, heritability in broad sense, expected genetic advance, and genetic advance in percent of mean, for pod yield per plant can be used to improve seed yield through indirect selection. Seed yield is also important because in some area seeds are used as a pulse. In French bean it is the immature pods that are most desired for the fresh and processed market. New genotypes can be develop in an area where no similar work has been done. Just because it has not been done in your area does not mean it needs to be done.

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