

# Morphological Characterization, Trait Variability and their Association, and Diversity Analysis Among Yard Long Bean (*Vigna unguiculata* (L.) Walp. subsp. *Sesquipedalis* (L.) Verdc.) Genotypes

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## Research Article

**Keywords:** Correlation, Genetic diversity, Path coefficients, Variability, Variance, Yardlong bean

**Posted Date:** June 8th, 2021

**DOI:** <https://doi.org/10.21203/rs.3.rs-572423/v1>

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## Abstract

Genetic variability has been greatly valued in yard-long bean, due to their narrow genetic base. To diversify the genetic base, yard long bean genotypes were evaluated to quantify the variation, to assess the extent of association between the yield complaint traits, diversity and for their utilization in crop improvement programmes. High phenotypic and genotypic coefficient of variations, heritability coupled with genetic advance over mean were observed most of the traits except internodal length, days to first and 50 per cent flowering, days to first and last picking, seeds per pod. Correlation and path analysis of variables namely pod length, pod width and pods per plant contributes high positive significant association with pod yield per plant, and maximum direct and indirect effect recorded for pods per plant, green pod length and green pod width. The genotypes were grouped into 12 clusters, the maximum divergence recorded between genotypes of Cluster XI and Cluster XII for traits pod yield per plant, vine length and yield per plot and pod length contributed high towards total divergence, the genetically diverse genotype of these clusters aids in the creation of larger recombinants, and would be an aid in the genetic improvement of yard-long bean genotypes.

## Introduction

The yardlong bean or asparagus bean (*Vigna unguiculata* (L.) Walp. subsp. *sesquipedalis* (L.) Verdc.;  $2n = 2x = 22$ ) belongs to the family Fabaceae, formerly known by Leguminosae, of the genus *Vigna*. It is comprised of above 200 species and is native to either the old or new world (Fery 2002). The yardlong bean (subspecies *sesquipedalis*), catjang (subspecies *catjang*) and cowpea (subspecies *unguiculata*) were classified by Verdcourt (1970). Which were reclassified as cultivar groups *sesquipedalis*, *biflora*, and *unguiculata* respectively under *V. unguiculata* subsp. *unguiculata* (Marechal et al. 1978), further five cultivar groups enumerated namely *unguiculata*, *sesquipedalis*, *biflora* (or *catjang*), *textilis* and *melanophthalmus* (Pasquet 1999), intra-specific taxonomic nomenclature is indeed a point of contention. the association among the subspecies is obscure for characterization, however, ssp. *sesquipedalis* is likely to be derived from domesticated ssp. *unguiculata* upon subjected to intensive selection for vegetable pod qualities and climbing growth characteristics (Xu et al. 2010). The scientific literature illustrated genetic variance among and within genotypes of yardlong bean revealed by diversity, characterization, and classification (Pidigam et al. 2019). Although significant phenotypic diversity exists among cultivated germplasm, however, breeding is a particularly concerning limit by the low inherent genetic diversity as a consequence of a single domestication activity of members of genus *Vigna* (Pasquet 1999). The landraces, varieties, improved cultivars have a narrow genetic base, as a result, germplasm should be considered in breeding programs to increase genetic diversity, for long-term breeding, and genetic improvement (Xu et al. 2010). The limited number of genetic diversity in ssp. *sesquipedalis*, resultant of an unexpected constraint in genetic improvement, yardlong bean varieties from Thailand and other Asian countries (cultivar group *Sesquipedalis*) demonstrated a lack of genetic variation among accessions, corroborating the widely held belief that this cultivar group resultant of genetic variability constraint. Despite though, the existence of morphological variability in the germplasm for several traits, still genetic diversity noted to be limited in Asian ssp. *sesquipedalis* germplasm. Therefore, more exploration of germplasm resources is needed to enhance the genetic diversity for yard-long bean breeding initiatives (Fang et al. 2007).

The yardlong bean has significant economic value in many developed countries as pulse and vegetable and often used as forage, cover crops, and green manure crop. It is a trellis, intensively cultivated vegetable crop, it is widely cultivated in Southeast Asia, it is considered one of the most popular vegetable crops in Indonesia, the Philippines, Thailand, Taiwan and China, it is known by the vernaculars *sitao* bean, *bodi* bean, and snake bean are some of the names of this plant (Fery 2002; Rachie 1985). It is grown primarily for its crisp and tender green pods that can be eaten raw or roasted (Bhagavati et al. 2019), its tender long pods are used as a vegetable in eastern and southern Asia, it is regarded as one of the top ten vegetables of Asia, it is distinguished by its very long immature 'snap' pods (0.5–1 m), small kidney-shaped beans, and creeping habit (Xu et al. 2010). The pod develops 2 to 4 days after anthesis, and it is varying on the type of cultivar, it is cultivated for pulses, and for its crispy delicious immature pods of 45 to 75 cm, from 9–12 foot long indeterminate plant (Ano and Ubochi 2008), it is characterized by the long, succulent and crispy pods of 30 to 90 cm (Verdcourt 1970). Yardlong bean is mainly cultivated in Asia for its fresh, sweet, crisp, and tender pods, which are consumed as a vegetable in both fresh and cooked forms, The quality of the pods in terms of firmness and sweetness are the most important factor that decides the buyer's acceptance. Thus, the development of new varieties with novel and better quality traits paves avenues to the breeders in search of elite lines or genotypes, or varieties to increase yielding efficiency without compromising pod quality (Kongjaimum et al. 2013). It is a high-quality, low-cost source of vegetable protein, coming from immature pods, and also which are rich in vitamin A and C, fibre, and other minerals (Ano and Ubochi 2008). Despite its nutritional value, it has a narrow range of cultivation, which may be due to a lack of knowledge and improved varieties of the crop, these limits maybe lead to the underutilization of the crop. Hence, breeding needs to be focused on high pod yield varieties, with earliness, determinate and semi-determinate growth habit types for a wide range of agro-climatic adaptation.

Commercial varieties have distinguishable morphological characteristics that make variety identification easy, and most germplasm accessions have a diverse range of morphological characters; most of them were identifiable from one another solely based on morphological traits (Tantasawat et al 2010). Dwarf types of yardlong bean genotypes are the demanding modern horticultural crop that could develop by the hybridization between yardlong bean and cowpea; it is gaining popularity due to many favourable characteristics (Laosuwan et al. 1996). The pods per plant, pod weight, pod size, seeds per pod, and seed size are the components of yield in the YardLong bean. Based on the correlation between the two characters, pod length may be a significant indicator of the seeds per pod. The pod yield per plant, pods per plant, pod weight, and seed weight were indicated the significant and positive additive effects, To manipulate the fixable components of heterogeneity, pedigree selection of breeding method was suggested (Rahman and Saad 2000). The morphological traits showed a strong positive association of seed protein content with pod length, test weight of seeds with pod length and seed protein content, pod yield with pods per cluster and pods per plant (Pidigam et al. 2019). The assessment of genetic diversity among genotypes is the ultimate goal for the evaluation of heterogeneity that can aid in the crop modification of desirable characteristics. Assessment of genetic diversity is an important part of the breeding process for selecting better genotypes. Although morphological studies can be used to characterize germplasm heterogeneity and aid in understanding the genetic diversity (Pidigam et al. 2019). The most successful way to widen the genetic base is to tap into the subspecies gene pools, especially cv. gr. *sesquipedalis*.

These would eventually accelerate long-term genetic gains either by intra- or inter-specific crosses, despite their differences in several characteristics; all cultivar groups are cross-compatible, as hybrids produced were completely fertile (Fatokun et al. 1997).

Genetic variability within asparagus bean cultivars germplasm will indicate the need for the introgression of exotic germplasm into breeding programs to increase genetic variability and diversity (Fang et al. 2007). Yield is a complex trait associated with several other characters, thus correlation and path analysis can increase selection efficacy for yield enhancement and its contributing components. The success of hybridization is largely determined by the genetically diverse parents, to produce heterotic combinations. To classify diverse parents, diversity analysis could be an aid in the breeding program. As a result, the current study was conducted for the characterization of genotypes, by the evaluation for traits heterogeneity, and their nature and magnitude of association, and genetic diversity among yard-long bean genotypes. To reveal the superior varieties with high yield potential and performance, extant genetic variability and diversity are the prime need for the execution of plant breeding programs. Characterization of genetic resources is essential to utilize and improve plant genetic resources in various breeding programs. Thus, this study could be useful for the genetic improvement and the development of new yard-long bean varieties with high pod yield and quality.

## **Materials And Methods**

### **Plant materials**

The forty yardlong bean genotypes were evaluated in the study, were collected from Indian Council of Agricultural Research (ICAR)-National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Thrissur, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, ICAR-Indian Institute of Horticultural Research (IIHR), Bangalore, Govind Ballabh Pant University of Agriculture and Technology, (GBPUAT), Pantnagar and Kerala Agriculture University (KAU), Thrissur and also included local cultivars and private sector varieties, which were listed in Table 1, and were characterized for morphological traits as per the distinctiveness, uniformity and stability guidelines (NBPGR 2005 ).

Table 1  
Collection source of yard long beans and their morphological characterization of genotypes

Sl. No.	Treatments	Source	Plant type	Growth habit	Pod colour	Pod length (cm)	Pod shape	Seed per pod	Seed colour
1	TCR122	NBPGR, RS, Thrissur	Indeterminate	Pole type	Green	Long	Straight	High	Brown
2	TCR87	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Dark green	Medium	Straight	High	White
3	TCR86	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Dark green	Medium	Curved	High	Purple
4	TCR119	NBPGR, RS, Thrissur	Indeterminate	Pole type	Green	Long	Straight	Medium	White
5	TCR117	NBPGR, RS, Thrissur	Indeterminate	Pole type	Dark green	Long	Straight	Medium	Brown
6	Pant Vegetable-20	GBPUAT, Pantnagar	Indeterminate	Pole type	Purple	Long	Straight	High	Brown
7	EC693345	ICRISAT, Hyderabad	Indeterminate	Pole type	Green	Long	Straight	High	Brown
8	TCR125	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Purple	Medium	Straight	High	White
9	TCR84	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Dark green	Medium	Straight	High	White
10	TCR79	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Dark green	Medium	Curved	High	Black
11	TCR124	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Dark green	Short	Curved	High	Black
12	TCR115	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Dark green	Medium	Straight	Medium	White
13	Arka Mangala	IIHR, Bengaluru	Indeterminate	Pole type	Green	Extra long	Straight	High	Brown
14	TCR104	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Green	Medium	Curved	High	Brown
15	EC693344	ICRISAT, Hyderabad	Indeterminate	Semi erect	Green	Long	Straight	High	Brown
16	TCR80	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Dark green	Medium	Curved	High	White
17	TCR85	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Green	Long	Curved	Medium	White
18	TCR88	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Green	Long	Curved	High	Black
19	TCR116	NBPGR, RS, Thrissur	Indeterminate	Horizontal	Dark green	Medium	Straight	Few	Brown
20	TCR89	NBPGR, RS, Thrissur	Indeterminate	Semi erect	Dark green	Long	Straight	High	Purple
21	Trivandrum Local	KAU, Thrissur	Indeterminate	Pole type	Green	Long	Straight	High	Brown
22	Khunthi Local	Khunthi, Jharkhand	Indeterminate	Pole type	Dark green	Long	Straight	Medium	Brown
23	Bhubaneswar Local	Odisha	Indeterminate	Pole type	Dark green	Extra long	Straight	High	Brown
24	Githika	KAU, Thrissur	Indeterminate	Pole type	Dark green	Long	Straight	High	Brown
25	Lola	KAU, Thrissur	Indeterminate	Pole type	Green	Long	Straight	Medium	Black
26	Bobbili Local	Sakata Seeds Pvt Ltd	Indeterminate	Pole type	Dark green	Extra long	Straight	Medium	Brown
27	Vyjayanthi	KAU, Thrissur	Indeterminate	Pole type	Purple	Long	Straight	High	Brick red
28	Vellayani Jyothika	KAU, Thrissur	Indeterminate	Pole type	Green	Long	Straight	High	Brown
29	VS-50	KAU, Thrissur	Indeterminate	Pole type	Green	Long	Straight	Medium	Brown

Sl. No.	Treatments	Source	Plant type	Growth habit	Pod colour	Pod length (cm)	Pod shape	Seed per pod	Seed colour
30	EC693333	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Long	Straight	High	Brick red
31	EC693334	ICRISAT, Hyderabad	Indeterminate	Semi erect	Green	Long	Straight	Medium	Brown
32	EC693341	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Long	Straight	Medium	Brick red
33	EC693336	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Extra long	Straight	Medium	Brown
34	EC693348	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Long	Straight	High	Black
35	EC693340	ICRISAT, Hyderabad	Indeterminate	Pole type	Green	Long	Straight	High	Black
36	EC693337	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Extra long	Straight	Medium	Brown
37	Pant Vegetable-20	GBPUAT, Pantnagar	Indeterminate	Pole type	Purple	Long	Straight	Medium	Brick red
38	EC693338	ICRISAT, Hyderabad	Indeterminate	Pole type	Dark green	Long	Straight	High	Brown
39	Avka	KAU, Thrissur	Indeterminate	Pole type	Purple	Long	Straight	High	Brown
40	Sarpan 601	Sakata Seeds Pvt Ltd	Indeterminate	Pole type	Dark green	Long	Straight	High	Brown

## Experimental details

The experiment was performed at the Department of Vegetable Science, Kittur Rani Channamma College of Horticulture, Arabhavi, University of Horticultural Sciences, Bagalkot, during *Khariif* 2019-20 in a randomized complete block pattern (RCBD) with two replications. The experimental site was located in the Northern dry region of Karnataka by a latitude of 15° 84' North and a longitude of 74° 51' East, with an altitude of 612 meters above mean sea level.

## Cultural practices

The experimental plot was ploughed twice to a fine tilth, harrowed and soil was made ready sowing of seeds. Seeds of both genotypes were sown in a row at a distance of 100 cm, with 60 cm between rows. Fertilizers were applied for maximum doses of phosphorus and potassium and half dose of nitrogen (25:50:25 kg NPK/ha). The remaining 50% of nitrogen was top-dressed 45 days after sowing. Irrigation, weed control, spraying, and other cultural activities were practiced according to the package of the practice of the University of Horticultural Sciences, Bagalkot (UHS 2013).

## Statistical analysis

The mean values of examined traits from each genotype were documented from five randomly tagged plants, and the mean data was subjected to statistical software IndoStat Version 9.3. The results of an analysis of variance were interpreted as the procedure given by Panse and Sukhatme (1967), phenotypic and genotypic variance (Wricke and Weber 1986), Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were classified as low (0–10%), moderate (10–20%) and high (> 20%) (Johnson et al. 1955; Shivasubramanian and Menon 1973), heritability ( $H^2$ ) percentage was categorised as low (0–30%), moderate (31–60%) and high (> 60) (Robinson et al. 1949; Burton and Devane 1953) and genetic advance mean was classified as low (0–10%), moderate (11–20%) and high (> 20%) (Johnson et al. 1955). Cluster analysis was carried out using Mahalanobis  $D^2$  statistic (1936) to determine genetic diversity and to group forty yard long bean genotypes into various clusters by employing Tocher's method (Rao 1952).

## Results

### Analysis of variance of traits

The analysis of variance (Table 2) revealed a very significant (both at  $p = 0.01$  and  $p = 0.05$ ) difference in growth and yield parameters among the genotypes in yard long bean. The results of the analysis of variance for different quantitative traits for 40-yard long bean genotypes demonstrated highly significant ( $P = 0.01$ ) differences, except for the number of pods per cluster, which demonstrated a significant ( $P = 0.05$ ) difference among the genotypes. It showed that there had been adequate genetic variability exist in the yard long bean genotypes for traits.

Table 2  
Analysis of variance in yard long bean genotypes for growth, yield and quality parameters

Sl. No.	Source of variation	Replications	Treatments	Error	S.Em±	CD (5%)	CD (1%)
	Degrees of freedom	1	39	39			
<b>A. Growth parameters</b>							
1.	Vine length(m)	0.002	1.71**	0.03	0.12	0.35	0.47
2.	Primary branches per plant	1.15	2.61**	0.55	0.52	1.50	2.02
3.	Internodal length (cm)	19.20	12.71**	4.64	1.52	4.35	5.83
<b>B. Flowering parameters</b>							
1.	Days to first flowering	4.60	48.29**	6.69	1.82	5.23	7.00
2.	Days to 50% flowering	4.05	47.73**	7.22	1.90	5.43	8.19
3.	Days to first picking	0.002	49.03**	4.60	1.51	4.34	5.82
4.	Days to last picking	13.28	65.17**	7.94	1.99	5.69	7.62
<b>C. Yield parameters</b>							
1.	Green pods per cluster	0.67	0.17*	0.10	0.22	0.64	1.01
2.	Green pods per plant	10.95	112.50**	17.30	2.94	8.41	11.26
3.	Green pod length (cm)	15.84	425.33**	20.71	3.21	9.20	12.32
4.	Green pod width (mm)	0.55	3.03**	0.60	0.55	1.57	2.10
5.	Green pod yield per plant (g)	1011.04	6704.30**	1807.16	30.05	85.99	115.11
6.	Green pod yield per plot (kg)	0.06	7.14**	0.13	0.25	0.74	0.99
7.	Seeds per pod	0.61	8.82**	1.51	0.86	2.49	3.33
8.	100 seed weight (g)	0.88	38.50**	0.14	0.26	0.78	1.04
**Significant at 1%, *significant at 5%							

## Morphological characterization

The forty genotypes of yardlong bean showed a wide range of morphological traits such as vine growth, pod shape and colours, and seed shape and colours with varied habits (Table 1). All the genotypes had indeterminate plant types, and horizontal spreading, pole type trailing, and semi-erect growth habits, genotypes were varied with pod colours namely green, dark green, and purple pods (Fig. 1), with variable pod length viz. short, medium, long, and extra-long pod bearing genotypes. Genotypes were varied for seed traits namely straight and curved pod shapes and medium to high seeds per pod, brown, white, purple, brick red, and black colour seeded genotypes (Fig. 2), The majority of genotypes have one or more morphological traits in common, and many features are comparable between them, indicating the existence of substantial variability.

## Genetic variability, heritability and genetic advance over percentage mean

The study showed a significant amount of variability in the research data. The genotypic variance was smaller than the phenotypic variance for many of the characters studied. Range, mean, genotypic variation (GV), phenotypic variation (PV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ) in a broad sense, phenotypic coefficient of variation (PCV), genetic advance (GA), and genetic advance as per cent of mean (GAM) were calculated and presented in Tables 3 for better define the degree of total variations due to genetic factors.

Table 3  
Genotypic and phenotypic correlation coefficients of growth, yield attributes and yield among the yard long bean genotypes

CC	Traits	1	2	3	4	5	6	7	8	9	10	11	12	13
G	1	1	-0.033	0.019	0.053	0.100	0.067	0.303**	0.000	-0.019	0.120	0.035	-0.216	0.353**
P		1	-0.046	0.015	0.033	0.068	0.062	0.260*	-0.019	-0.016	0.099	0.029	-0.157	0.349**
G	2		1	-0.664**	0.086	0.032	0.051	-0.482**	0.208	0.421**	-0.258*	-0.199	0.127	0.096
P			1	-0.357**	0.000	-0.018	0.034	-0.261*	0.007	0.381**	-0.138	-0.120	0.099	0.069
G	3			1	0.063	0.131	0.121	0.106	-0.194	-0.743**	0.277*	0.256*	-0.258*	0.195
P				1	-0.103	-0.054	-0.031	0.125	-0.003	-0.356**	0.198	0.117	-0.144	0.134
G	4				1	0.998**	0.993**	0.212	-0.114	0.375**	-0.390**	-0.030	-0.035	-0.063
P					1	0.986**	0.921**	0.089	-0.020	0.225*	-0.343**	-0.035	-0.006	-0.057
G	5					1	0.997**	0.229*	-0.110	0.334**	-0.362**	-0.032	-0.064	-0.034
P						1	0.917**	0.094	-0.018	0.184	-0.316**	-0.032	-0.009	-0.330**
G	6						1	0.091	-0.066	0.260*	-0.369**	-0.150	-0.051	-0.038
P							1	0.044	-0.035	0.181	-0.333**	-0.127	-0.012	-0.035
G	7							1	-0.422**	0.194	0.227*	0.251*	0.038	0.099
P								1	-0.236*	0.194	0.229*	0.164	0.023	0.090
G	8								1	-0.265*	-0.027	-0.818**	0.390**	-0.202
P									1	0.026	-0.050	-0.354**	0.275*	-0.118
G	9									1	-0.358**	-0.161	0.368**	-0.326**
P										1	-0.309**	-0.142	0.304**	-0.285*
G	10										1	0.512**	-0.270*	0.260*
P											1	0.427**	-0.222*	0.250*
G	11											1	-0.587**	0.382**
P												1	-0.364**	0.307**
G	12												1	-0.323**
P													1	-0.270*
G	13													1
P														1
G/P	14													

Genotypic (g) correlation coefficient (CC),  $r_g$  @ 0.05 is 0.2198,  $r_g$  @ 0.01 is 0.2864, and Phenotypic (P) correlation coefficient ( $r_p$ ) @ 0.05 is 0.2198,  $r_p$  @ 0.01 is 0.2864, \*significant at 5%, \*\*Significant at 1%, 1. Vine length, 2. Primary branches per plant, 3. Inter nodal length, 4. Days to first flowering, 5. Days to 50% flow, 6. Days to first picking, 7. Days to last picking, 8. Number of green pods per cluster, 9. Green pods per plant, 10. Green pod length, 11. Green pod width, 12. Seed pod, 13. 100 seed weight, 14. Green pod yield per plant.

The variance of yardlong bean genotypes characters varied from low to high (Table 3), with high GCV and PCV for yield and yield contributing factors were vine length, primary branches per plant, green pods per plant, green pod length, green pod yield per plot, green pod width, green pod yield per plant, and 100 seed weight, revealed the presence of substantial variation among genotypes for genetic improvement yardlong bean. Further, internodal length and seeds per pod were traits with moderate GCV and PCV, indicating the presence of considerable variability for desired traits, can also be used in the breeding. GCV and PCV estimates were highly unaffected by the environment, although PCV is higher than GCV, traits with high phenotypic variability can also be employed in breeding.

The high heritability and high genetic advance revealed for yield and yield attributing traits (Table 3), the high heritability ( $h^2$ ) was noted for all traits, except inter-nodal length of the plant. Further, high  $h^2$  with a high genetic advance mean (GAM) was noted for 100 Seed weight, seeds per pod, green pod yield per plot, green pod yield per plant, green pod width, green pod length, green pods per plant, days to the last picking, and primary branches per plant and vine length. Since the traits are highly heritable and high GAM may contribute to additive gene action, thus yardlong bean genotypes can be improved more successfully by selection. However, non-additive gene action is expected to be influenced by the traits with low GAM, as resultant traits were governed by high  $h^2$  with high genetic advance mean emphasizing that selection may have only a modest influence on improvement.

## Association of growth and yield attributing traits with pod yield

The yield-related traits interact in a desirable or undesirable path, thus association studies reveal the magnitude and pattern of interactions among yield and its contributing characters. It is an appropriate test for crop yield augmentation. As a result, understanding the relationships between traits is required to establish a suitable breeding strategy, for better perceptive the genotypic and phenotypic correlation variables presented in Table 4. The trait association details aid in the indirect selection of trait for genetic improvement of economic traits. At the genotypic level, green pod yield per plant revealed highly significant (both at  $p = 0.01$  and  $0.05$ ) and positive relationship with green pod length ( $r_g = 0.537$ ;  $r_p = 0.490$ ) and green pod width ( $r_g = 0.418$ ;  $r_p = 0.353$ ) whereas, positive but non-significant association with the number of seeds per pod (0.194) and number pods per plant (0.191). It also showed a negative and significant (both at  $p = 0.01$  and  $0.05$ ) relationship with the number of pods per cluster (-0.338) however negative and non-significant correlation with the number of primary branches (-0.212). It was also significant (at  $p = 0.05$ ) and negative connection with days to first flowering ( $r_g = -0.224$ ;  $r_p = -0.227$ ), days to 50% flowering ( $r_g = -0.229$ ;  $r_p = -0.220$ ) and days to first picking ( $r_g = -0.248$ ). Phenotypic association indicates the magnitude correlation among the traits; because of its genetic and environmental effects, it does not ensure a holistic overview of association. The genotypic association estimates the innate association between traits of phenotypes. It is more important and may be used to create an effective selection strategy.

Table 4  
Cluster composition of 40 yard long bean genotypes based on  $D^2$  statistics.

Cluster	Members	Genotypes
I	18	Pant Vegetable-20, EC693345, EC693334, TCR85, EC693344, Avka, Serpan 601, EC693340, VS-50, EC693336, Vyjayanthi, EC693337, Githika, Trivandrum Local, TCR89, Vellayani Jyothika, EC693348, TCR124
II	12	TCR104, TCR80, TCR87, TCR86, TCR119, TCR115, TCR84, TCR125, TCR122, TCR79, Pant Vegtable-21, EC693341
III	1	Lola,
IV	1	TCR88
V	1	Bobbili Local
VI	1	Bhubaneswar Local
VII	1	EC693333
VIII	1	Araka Mangala
IX	1	Khunthi Local
X	1	TCR116
XI	1	TCR117
XII	1	EC693338

## Path coefficients of growth and yield attributing traits with pod yield

The correlation coefficients define the principal association between the independent and dependent variables, without defining causes and effects. The path coefficient analysis can be used to determine the correlation of traits with causes and effects, by exposing the correlation matrix to path analysis for separating their variables into indirect and direct effects, Fresh pod yield per plant was considered as the dependent variable and the rest of the traits were independent traits were presented in Fig. 3.

The genotypic path analysis depicted that, the length of the pod (0.769) had the highest significant direct influence on fresh pod yield per plant (Fig. 3a), followed by days to first harvest (0.728), seeds per pod (0.663), green pods per plant (0.258), green pod width (0.218), days to first flowering (0.189), and vine length (0.106). The indirect positive outcome on the fresh pod yield per plant via internodal length (0.175), days to first picking (0.189), seeds per pod (0.244), number of branches per plant (0.123), days required for 50% flowering (0.297), green pod width (0.111), pods per cluster (0.408) and fresh pod length (0.394). Similarly, the results phenotypic path analysis demonstrated that internodal length (0.061), days to first picking (0.137), pods per plant (0.602), days to 50% flowering (0.201), green pod length (0.581), green pod width (0.238), and seeds per pod had a direct positive influence on pod yield per plant (0.273). The traits such as pods per plant (0.117) and green pod length (0.113) had a positive indirect influence on the pod yield per plant. The fresh pod length (0.248) has an indirect influence on the pod yield per plant via green pod width (Fig. 3b).

## Genetic divergence

The genotypes were divided into 12 divergence groups through  $D^2$  analysis of 40-yard long bean genotypes based on growth and yield characteristics data, as shown in Table 4. Cluster I had the highest genotypes (18), followed by Cluster II (12), while the other clusters were solitary with only one genotype each. The intracluster such as Cluster II, which included 12 genotypes, had the highest intra-cluster distance (90.33), followed by Cluster I (75.98), indicating that genotypes in Cluster II and Cluster I were diverse for the majority of the features. The Intercluster namely Cluster XI and Cluster XII (1243.35) showed the greatest inter-cluster distance, followed by Cluster X and Cluster XII (1243.46), Cluster VII and Cluster XII (1145.86), and Cluster II and Cluster XII (1145.71), indicating that the genotypes in these clusters had the greatest genetic diversity (Fig. 4).

The relative contribution of different characteristics to total divergence indicated that pod yield per plant (60.51%) was the major character contributing the most to divergence in Table 5, followed by vine length (19.23%), pod yield per plot (5.64%), green pod length (4.36%), and days to last picking (3.46%). These qualities may be more effective in the efficient grouping. Divergent mean values across the clusters produced for 12 diverse traits indicated the substantial diversity in cluster means presented in Table 5. The greatest cluster means value for pod yield per plant (990 g) and pod yield per plot (10.43 Kg) was found in cluster XII, followed by cluster VIII (890.9 g and 9.29 Kg) and cluster IX (890.9 g and 9.29 Kg). The higher cluster mean values for days to the last picking,

seeds per pod were noted in cluster IV, for inter-nodal length in Cluster VI, vine length in Cluster XI, primary branches per plant, green pods per plant and green pod length in Cluster VIII, days to first flowering in Cluster XII and days to first picking in Cluster VII, green pod width reported in Cluster X was noted. The genotypes from different clusters that performed better in terms of yield and yield contributing attributes might be employed in future hybridization programs to recombine the desired features, resulting in increased pod yield in yard long beans.

Table 5  
Cluster mean values for growth and yielding traits of yard long bean genotypes, and their contribution to the total divergence.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	Contribution (%)
Vine length	3.52	3.48	4.96	2.99	4.49	4.33	5.59	3.43	3.59	3.3	6.86	2.75	19.23
Primary branches per plant	3.47	4.51	3.2	2.8	2.9	3.7	3.3	7	3	5.4	3.4	3.1	0.77
Inter-nodal length	16.21	14.34	16.32	15.95	15.75	15.24	16.65	14.24	15.31	15.58	16.62	15.79	0.26
Days to first flowering	56.01	55.62	52.5	65.6	57	53.8	48.2	51.5	55.3	68.6	61	47.5	1.41
Days to first picking	68.77	68.23	65.8	76.4	70.9	68	61.7	64.2	68.2	80	74.1	59	0.26
Days to last picking	116.81	113.99	116.5	132.9	127.5	116.8	116.4	107.9	119.6	111.9	119.7	111.8	3.46
Green pods per plant	35.24	39.08	43.2	46.6	41.7	30	30.4	48.1	41.1	42.4	32	39.9	1.41
Green pod length	45.89	31	34.7	35.8	65.3	64.7	40.9	74.4	50.24	24.7	44.71	39.2	4.36
Green pod width	6.5	5.17	6.34	5.6	7.62	6.17	6.13	5.89	7.25	10.17	5.81	5.83	0.64
Green pod yield per plant	583.15	336.1	548.2	510	737.4	685.4	325.9	890.9	852.9	430.8	369.4	990.6	60.51
Seeds per pod	15.84	15.64	12.9	19.2	13.4	16	15.9	16.4	14.5	8.9	13.3	18.1	2.05
Pod yield per plot	6.04	3.54	5.54	5.25	7.62	6.95	3.42	9.29	9.06	4.44	3.99	10.43	5.64

## Discussion

The examined traits for analysis of variance indicated extremely significant ( $P = 0.01$ ) differences across 40 genotypes of yard-long beans, except for the number of pods per cluster, which exhibited significant ( $P = 0.05$ ) variations among the genotypes. The morphological characteristics of the yard-long beans revealed a wide range of variation. Different quantitative traits such as pod yield per plant, plant height, pods per plant, pod length, and clusters per plant were established the significant differences among the genotypes of yard-long beans (Resmi et al. 2004; Rambabu et al. 2016, Gul et al. 2019). The yard-long bean genotypes showed a considerable variation in terms of morphological traits, particularly in terms of pod and seed characteristics with various patterns (Fig. 1; 2), the genotypes exhibited an indeterminate plant growth, with other varied growth traits (Table 1). Although, noted different plant type like determinate and semi-indeterminate types (Tantasawat et al. 2010), with varied plant traits of leaf shape, flower colours, seed colours and lusters were the most frequently found characters among these yardlong bean accessions. The lucid variation was revealed for pod colours namely light green, green and white, seed colour was dark red, red, and brown, other traits like plant height, pods per cluster, pod length, pods per plant, seeds per pod, 100 seed weight, and yield per plant were varied among the genotypes (Pidigam et al. 2019)

Variance, heritability and genetic advance are key tools for the development of plant idiosyncratic phenotypes. The large variance in GCV and PCV indicates the presence of genetic and phenotypic diversity for diverse growth and yield traits. The high heritability and high genetic advance indicate the presence of additive gene action; under selection, genetic advance refers to an increase in the mean genotypic value over the base population, thus a simple selection breeding method would be effective in improving traits. In the present study, a considerable degree of variance was observed, as demonstrated in the summary of variances, heritability and genetic advance statistics by the continuous variables of all the characteristics in Table 2. Most of the traits are high variability, high heritability with high GAM, which is the total of heritable and non-heritable elements. High heritability (> 60 per cent) indicates a degree of genetic determination. Higher estimates of heritability combined with a strong genetic advance as per cent of mean (> 20%) were recorded for characters (Table 2) vine length, number of primary branches per plant, number of green pods per plant, green pod length, green pod width, pod yield per plant, fresh pod yield per plot, 100 seed weight. These attributes were possibly influenced by additive gene action, hence selection could be effective for genetic improvement of yard-long bean genotypes. This finding support by vine length, primary branches per plant, intermodal length, pods per plant, length of the pod, green pod width, pods per plant, green pod yield per plant, the yield of pod per plot, seeds per pod, and 100 seed weight by Aghora et al. (1998), Manju (2006), Rambabu et al. (2016) and Asoontha et al. (2017). The efficiency of selection is largely determined by the magnitude of variation inherent in a population. Because observed variability in a population is the total deviation created by genotypic and environmental factors, the GCV and PCV variables for all parameters revealed by estimates of PCV were greater than GCV estimates. This revealed a significant level of heterogeneity across the genotypes studied, which might be improved further by selection. These findings are consistent in yard-long beans of previous findings for the number of pods present in plant and seed weight (Sivakumar and Celine 2014), for pod length and pod yield per plant (Jithesh 2009), for the number of primary branches per plant and pod weight (Pravin et al. 2013).

The relevance of the traits associated with each other being determined by the degree of phenotypic and genotypic interaction. Plant breeders should pay close attention to characteristics that are closely associated with pod yield while making selection decisions. In correlation analyses of the study, the genotypic correlation coefficient was higher than the phenotypic correlation coefficient for the majority of the traits, indicating that these features had a

stronger inherent association of traits with pod yield (Table 3). On both a genotypic and phenotypic level, fresh pod production per plant demonstrated a strong positive significant relationship with pod length and pod breadth. At the phenotypic level solely, green pod production per plant revealed a strong positive relationship with the number of pods per plant. Selection for these linked traits may improve pod output per plant since they are in the desired direction, reported similar findings for pod length, pod width, and the number of pods per plant positively associated with pod yield (Lovely 2005, Manju 2006, Jithesh 2009, Vavilapalli and Celine 2014, Rambabu et al. 2016, Bhagavati et al. 2019). Plant height and pods per cluster had a significant positive association with each other, and pods per cluster had a highly significant positive association with pods per plant and pod production. Pod length had a highly significant positive relationship with seed weight, pods per plant had a positive association with seed weight and seed yield (Pidigam et al. 2019). Pod yield per plant was highly positive significant with pods per plant and pods per cluster, and seed weight was positively significant with pods per cluster and pods per plant (Ullah et al. 2011; Lovely and Radhadevi 2006). As we all know, correlation merely demonstrates the correlation between characters without taking into account the cause and effect of that association. By exposing the correlation matrix to path analysis for separating their variables into indirect and direct effects, the true relationship may be determined using path coefficient analysis. Figure 3 represents the path analysis findings using yield attributing traits as independent variables and fresh pod yield per plant as the dependent variable. Among traits, the green pods per plant, followed by green pod length, number of seeds per pod, and green pod width, had a strong positive direct influence on plant pod yield. This implies that when other variables remain constant, genetic improvement of such traits will result in higher yields (Lovely 2005, Manju 2006). Increased pod yield can be achieved by increasing the pods per cluster, and per plant. As a result, these traits can play a significant role in crop improvement, and the better-performing accessions aided the advance into the breeding program.

The divergences among yard long bean genotypes revealed by D<sup>2</sup> analysis, thus genotypes were grouped into 12 divergence clusters (Table 4), namely Cluster I (18 genotypes), Cluster II (12) and other clusters were solitary with one genotype each. The maximum intra-cluster distance of cluster II (90.33) and cluster I (75.98) indicated genotypes grouped were diverse for most of the characters among them, indicated to advance for selection of superior types. The maximum inter-cluster distance was recorded between Cluster XI and Cluster XII (1243.35), Cluster X and Cluster XII (1243.46), Cluster VII and Cluster XII (1145.86) and Cluster II and Cluster XII (1145.71) Intermating between diverse clusters would be anticipated to yield better recombinants. In the Yardlong bean, clusters might be employed as the best parents in a crop enhancement program to create optimal segregants for yield and yield traits (Rambabu et al. 2016)

The relative contribution of different characters to the total divergence revealed (Table 5) that pod yield per plant (60.51%), followed by vine length (19.23%), pod yield per plot (5.64%), green pod length (4.36) and days to last picking (3.46%). These traits might be more useful in the efficient grouping of the genotypes and thus can be used in determining genetically diverse parents for hybridization programmes (Lal et al. 2018). The wide variation in cluster means values were confirmed for traits in Table 5 for Cluster XII, Cluster VIII and Cluster IX (pod yield per plant and pod yield per plot) respectively, Cluster IV (days to last picking and seeds per pod), Cluster VII (internodal length), Cluster XI (vine length), Cluster VIII (primary branches per plant, green pods per plant and green pod length, Cluster X (green pod width). The genotypes among various cluster which showed better performance for yield and their attributing traits could be used in future hybridization programmes to recombine the desirable characters leading to enhancement in pod yield of yard long bean (Rambabu et al. 2016). The most divergent genotypes revealed might be used as parents to derive superior recombinants for maximizing pod yield, based on cluster pattern, the magnitude of genetic distance, degree of cluster means, and relative contribution of traits to overall divergence. Hybridization of such genotypes with other genotypes from other clusters aids in improving vegetable pod yield.

## Conclusions

The estimates of variables among the genotypes include variance, heritability, genetic advance, genotypic and phenotypic association and interaction of traits that contribute to the degree of diversity and variability among yard-long bean genotypes. The GCV, PCV was shown to have a considerable genetic background for growth and yield traits (High estimates of GCV, PCV,  $h^2$  and GAM for vine length, primary branches per plant, green pods per plant, green pod length, green pod width, pod yield per plant, fresh pod yield per plot, 100 seed weight), which will be important in future selection breeding, these traits could be improved through selection. Because additive gene action is influenced by high estimates of heritability combined with high values of the genetic advance mean of characteristics, selection would be more successful in the improvement of yard-long bean genotypes. The correlation and path coefficient analysis identified pod length, number of pods per plant, and pod width as the most important traits for improving pod yield of yard long beans in a selection program. The cross of the genetically diverse genotype of several clusters aids in the creation of larger recombinants. Crop improvement would be aided by crossing divergent parents to produce heterotic hybrids, to produce yielding recombinants with significant divergence.

## Declarations

### Acknowledgement

We acknowledge the University of Horticulture Sciences, Bagalkot, Karnataka, India for providing facilities and financial support.

### Declarations

### Conflict of Interest

The authors declare that there is no conflict of interest.

### Funding

Not applicable

### Compliance with ethical standards

## Conflict of Interest /Competing interests

The authors declare that there is no conflict of interest

## Availability of data and material

The data and its related data sets presented in the manuscript

## Code availability

Not applicable

## Authors' contributions

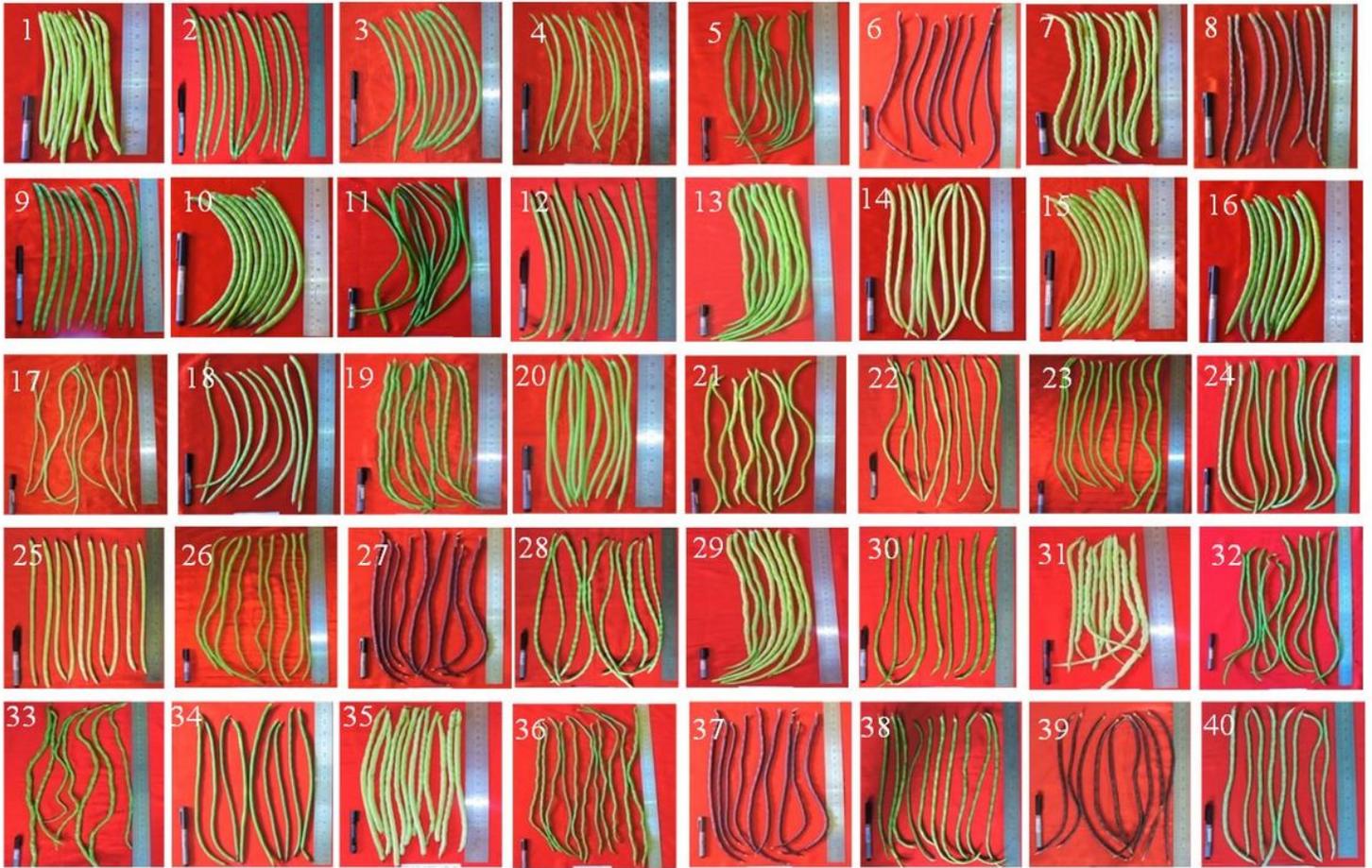
SRD, KNC and VR conceived, designed the research, conducted experiments, SRD, KNC, DCM, NS, MA, drafted, compiled, analyzed and wrote the manuscript. SRD, KNC, VR, TNL and GP performed genetic analysis. PK, RSR, AK provided suggestion and revised the manuscript. NS, MA, DCM edited and proofread the final manuscript. All authors read and approved the manuscript

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## Figures



**Figure 1**

Variability of pod traits among the collections, namely 1) TCR 122, 2) TCR87, 3) TCR86, 4) TCR119, 5) TCR117, 6) Pant Vegetable-20, 7) EC 693345, 8) TCR125, 9) TCR84, 10) TCR79, 11) TCR124, 12) TCR115, 13) Arka Mangala, 14) TCR104, 15) EC693344, 16) TCR80, 17) TCR85, 18) TCR88, 19) TCR116, 20) TCR89, 21) Trivendrum Local, 22) Khunthi Local, 23) Bhubaneswar Local, 24) Githika, 25) Lola, 26) Babli, 27) Vyajyanthi, 28) Vellavaini Jyothika, 29) VS-50, 30) EC693333, 31) EC693334, 32) EC693341, 33) EC693336, 34) EC693348, 35) EC693340, 36) EC693337, 37) Pant Vegetable-21, 38) EC693338, 39) Avak, 40) Serpan 601



**Figure 2**  
 Variability of seeds traits among the collections, namely 1) TCR 122, 2) TCR87, 3) TCR86, 4) TCR119, 5)TCR117, 6) Pant Vegetable-20, 7) EC 693345, 8) TCR125, 9) TCR84, 10) TCR79, 11) TCR124, 12) TCR115, 13) Arka Mangala, 14) TCR104, 15) EC693344, 16) TCR80, 17) TCR85, 18) TCR88, 19) TCR116, 20) TCR89, 21) Trivendrum Local, 22) Khunthi Local, 23) Bhubaneswar Local, 24) Githika, 25) Lola, 26) Babli, 27) Vyajyanthi, 28) Vellavaini Jyothika, 29) VS-50, 30) EC693333, 31) EC693334, 32) EC693341, 33) EC693336, 34) EC693348, 35) EC693340, 36) EC693337, 37) Pant Vegetable-21, 38) EC693338, 39) Avak, 40) Serpan 601

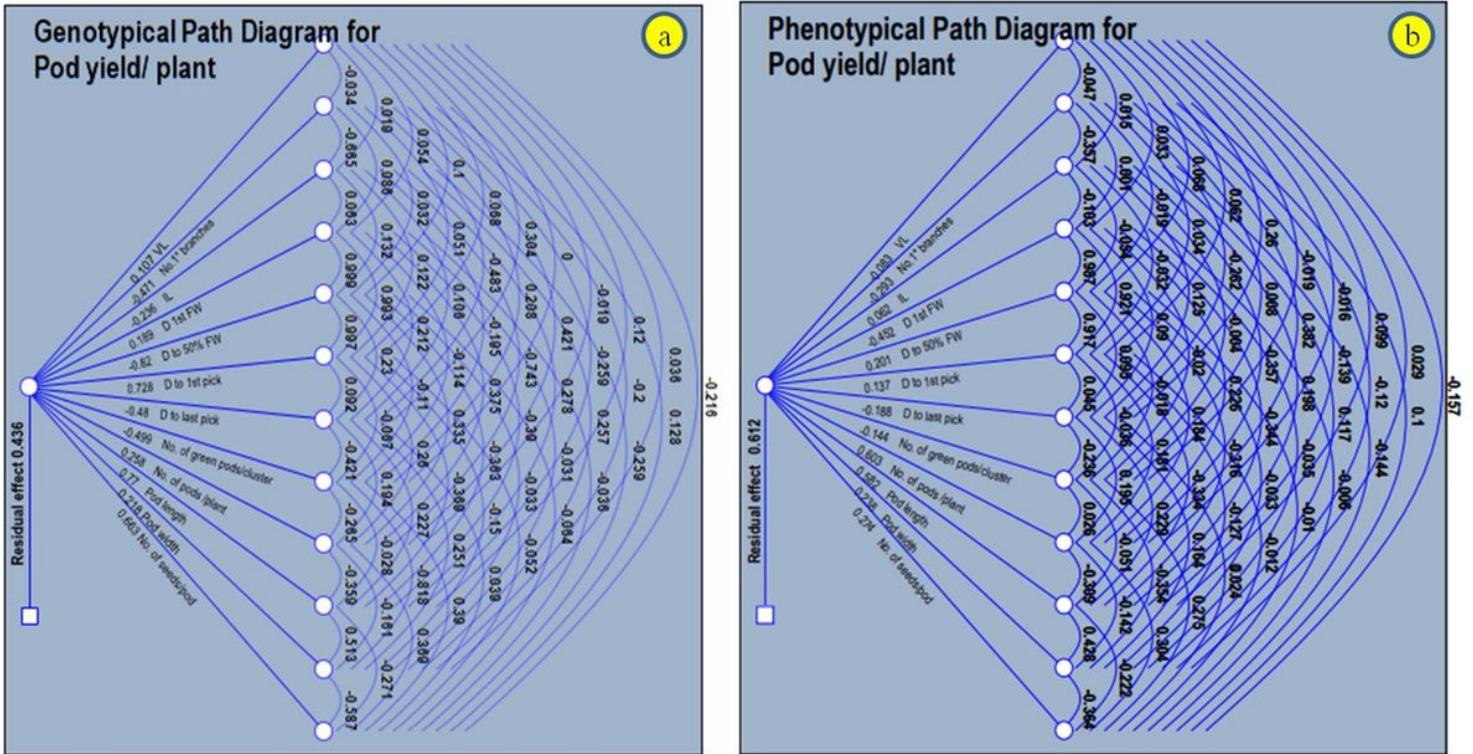


Figure 3

Direct and indirect effect growth and yield attributing traits on pod yield per plant, a) genotypic path coefficients, and b) phenotypic path coefficients of parameters among the yard long bean genotypes

