



Genetic Variability in Fusarium Wilt Resistant BC₂F₁ Lines of Yard Long Bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) Variety Githika for Yield and its Related Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Yardlong bean is a highly popular and profitable vegetable traditionally cultivated in the humid tropics of Kerala and is an inexpensive source of vegetable protein. Developing sustainable host plant resistance mechanisms, such as using the backcross method to introduce single-gene resistance into susceptible crop varieties, is crucial for reducing losses due to Fusarium wilt. In the present study Thirty-five resistant backcross progenies (BC₂F₁) of Yardlong Bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) variety Githika were evaluated for various genetic parameters for yield and its related traits using Completely Randomized Design at Department of Genetics and Plant Breeding, College of Agriculture, Vellayani, Trivandrum. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for traits such as the number of pods per plant, pod weight, pod yield per plant, crude protein content. High Heritability(H) and High Genetic advance as percent mean (GAM) were observed for traits such as Number of pods per plant, Pod weight, Pod length, Number of seeds per pod, Pod Yield per plant, Crude fibre and Crude protein content. This significantly suggest that additive gene action is predominant in these traits and low reliance by environmental factors on these traits, making such character a good candidate for direct selection. The study helps in assessing genetic variability to identify traits as well as lines with maximum similarity with recurrent parent which could be used for further crop improvement program.

Keywords: Yardlong bean; Phenotypic Coefficient of Variation (PCV); Genotypic Coefficient of Variation (GCV); Heritability(H); Genetic Advance as Percent Mean (GAM).

1. INTRODUCTION

Yardlong bean, scientifically known as *Vigna unguiculata* (L.) Walp. ssp. *sesquipedalis* (L.) Verdc., with a chromosome number of $2n = 22$, is an annual leguminous plant. It holds significant importance as a vegetable crop in tropical and subtropical regions, particularly in Southeast Asia, South China, and West Africa, where it thrives in temperatures ranging from 25 to 35°C. Yardlong beans are notable for their moderate nutritional value, particularly their protein content, which ranges from 23.5% to 26.3%, earning them the nickname "meat of the poor" (Litty, 2015). It is a highly popular vegetable in Southeast Asia, contributing approximately 7% to the region's total vegetable production (Heiser, 1990; Ali et al., 2002). Yardlong beans also contribute to soil fertility by fixing atmospheric nitrogen. Due to their rapid growth, they play a vital role in sustainable agriculture, especially in the marginal lands of the tropics. However, quality and productivity decline during the monsoon season because of heavy rainfall and unfavorable conditions, which lead to increased vegetative growth and higher pest and disease incidence. The growing demand for yard long beans has prompted large-scale intensive cultivation, resulting in significant crop losses (Kuo, 2002).

Fusarium wilt is a devastating disease of cowpea caused by a soil-borne fungus (Okiror, 2002). It

can survive in the soil for several years and thrives in wet conditions and high temperatures. Severe attack by Fusarium wilt can cause significant losses in cowpea yield, ranging from 36-90% (Hussain & Usman, 2019). Yield losses depend on the stage at which the plants wilt, with losses reaching up to 100%, if the wilt occurs at the pre-pod stage (Srasvan Kumar et al., 2017). To minimize crop loss from Fusarium wilt and reduce the use of hazardous chemical fungicides, developing and utilizing sustainable host plant resistance mechanisms is essential (Saxena, 2008; Jain et al., 2015). The backcross method is commonly used to introduce resistance genes into well-adapted but susceptible varieties when resistance is controlled by single genes (Gaur et al., 2012).

PCV and GCV are widely used for assessment of variability (Rispaill & Rubiales, 2015). The expression of a trait is influenced by both genetic as well as environmental factors thereby creating variation in relationship pattern, which is highly effective for selection (Magloire, 2005). The measures of Heritability could be used for selecting elite genotypes from diverse genetic population and GAM measures the amount of progress that could be expected by the selection of characters (Selvi et al., 2003). Hence the study aimed to assess genetic variability in backcross progenies of YB for yield and yield related traits.

2. MATERIALS AND METHODS

The plant material for the study was collected at the Department of Genetics and Plant Breeding (GPB), College of Agriculture (COA), Vellayani, Kerala, India. The experimental material consist of 35 resistant BC₂F₁ lines of YB variety Githika. The experiment was conducted at the GPB, COA, Vellayani, from April to July 2024. The resistant lines were planted in polyhouse in Completely Randomized design each with two replications. Agronomic practices were done as per the Package of Practices Recommendations Crops 2016 of Kerala Agricultural University (Kerala Agricultural University, 2016). Data were recorded for yield and yield attributing traits viz., number of primary branches per plant, days to 50% flowering, pod length, pod weight, number of pods per plant, pod yield per plant, crude fibre and crude protein content. The data thus generated were subjected to analysis of variance (ANOVA). The statistical analysis for genetic parameters were carried out using GRAPES software of KAU (Gopinath et al., 2020). The range of phenotypic and genotypic coefficient of variation data were estimated by adopting the statistical methods suggested by Sivasubramanian and Menon (Sivasubramanian & Menon, 1973) and for heritability and genetic advance by Johnson et al. (1955).

3. RESULTS AND DISCUSSION

3.1 ANOVA

Analysis of variance was done to find the significant differences among the resistant lines for the 8 characters. The results suggested that their exists significant variation among 35 resistant lines for the 8 different characters studied (Table 1).

3.2 Genetic Variability

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were categorized as low (<10%), moderate (10-20%) and high (>20%) by Sivasubramanian and Menon (Sivasubramanian & Menon, 1973). The present study revealed that high PCV and GCV were observed for traits such as the number of pods per plant, pod weight, pod yield per plant, crude protein content indicating that selection is effective for improvement of these traits (Table 2) [Fig. 1]. These results were similar to the result reported by Savithri et al. (2018) for number of pods per plant, pod weight, pod yield per plant

and Sivakumar (2012) for protein content. Moderate PCV and GCV also provide a greater scope for selection and was observed in traits such as pod length, number of seeds per pod and crude fibre content. Moderate PCV and GCV were reported for the number of seeds per pod by Thangam et al. (2020). Low PCV and GCV was observed in the trait days to 50% flowering indicating that direct selection of the trait is ineffective for crop improvement. This result was in concordance with the results of Rambabu et al. (2016) for days to 50% flowering. The values of GCV were smaller than PCV, and a slight difference was observed between PCV and GCV, which indicates minimal environmental influence towards the expression of a trait. A slight difference between PCV and GCV were also reported by Savithri et al. (2018).

3.3 Heritability and Genetic Advance

Heritability represents the proportion of phenotypic variance in a trait that is attributable to genetic variation within a population. It indicates the degree to which genetic factors influence the transmission of characters from one generation to the next generation. The selection of elite genotypes from a diverse genetic population can be evaluated using heritability estimates, by which the proportion of phenotypic variation in a trait due to genetic factors can be determined (Selvi et al., 2003). High heritability suggests that direct selection of the trait will be more effective in identifying genotypes with superior performance for breeding. Broad sense heritability (H^2) is the ratio of genotypic variance to the total observed variance in the population and heritability values were categorised as low (<30%), moderate (30-60%) and high (>60%) by Johnson et al. (1955).

Heritability and GAM for various characters under study is depicted in Fig. 2. In the present study high heritability was observed for Days to 50% flowering, Number of pods per plant, Pod weight, Pod length, Number of seeds per pod, Pod yield per plant, Crude fibre and Crude protein content, indicating the predominance of additive gene action in expression of the trait. The results were found similar to the findings of Panchta et al. (2020) for days to 50% flowering, Selvam et al. (2000) for number of pods, Kumar et al. (2013) for pod weight, pod length and pod yield per plant, Srinivas et al. (2017) for number of seeds per pod and Savithri et al. (2018) for crude protein and crude fibre content.

Table 1. Analysis of variance for 8 characters in 35 resistant BC₂F₁ lines of Yardlong bean

Character	Mean sum of squares		S.E.m	C.D@5%
	Treatment	Error		
Days to 50% flowering	2.925	0.014	0.083	0.239
Number of pods per plant	37.268	1.625	0.901	2.585
Pod weight	27.334	0.268	0.366	1.05
Pod length	30.461	0.418	0.457	1.311
Number of seeds per pod	8.411	1.236	0.786	2.255
Pod yield per plant	25255.680	641.564	17.91	2.028
Crude fibre content	4.907	0.197	0.314	0.90
Crude protein content	38.783	0.23	0.342	0.981

Table 2. Estimates of genetic variability parameters of various characters in 35 resistant lines of Yardlong bean

Characters	Mean	PCV (%)	GCV (%)	H ² (%)	GAM (5%)
Days to 50% flowering	44.292	2.737	2.724	99.0	5.584
Number of pods per plant	12.625	34.929	33.438	91.6	65.942
Pod weight	17.75	20.930	20.726	98.1	42.278
Pod length	30.94	12.700	12.527	97.3	25.453
Number of seeds per pod	14.708	14.932	12.878	74.4	22.878
Pod yield per plant	228.278	49.848	48.597	95.0	97.599
Crude fibre content	8.529	18.730	17.993	92.3	35.606
Crude protein content	18.239	24.216	24.070	98.8	49.286

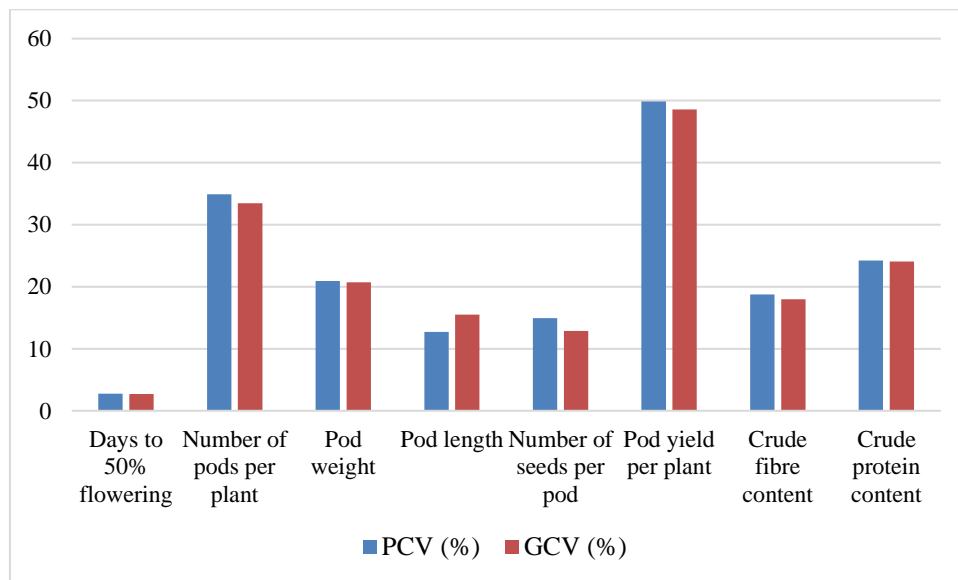


Fig. 1. PCV & GCV for selected biometric characters

Genetic advance measures the amount of progress which could be expected by the selection of characters. The traits coupled with high heritability and high genetic advance could be improved through direct selection by Tefera et al. (2017). GAM values are classified as high (>20), moderate (10-20) and low (<10) by Johnson et al. (1955).

High GAM were recorded for characters such as Number of pods per plant, Pod weight, Pod

length, Pod yield per plant, Crude fibre and Crude protein content. This suggest that additive gene action is predominant in these traits and direct selection improves the crop performance. The results were in line with the findings of Savithri et al. (2018) for Number of pods per plant, Pod weight, Pod length, Number of seeds per pod, Pod yield per plant and Crude protein content; Srinivas et al. (2017) for number of seeds per pod in cowpea. Moderate GAM was observed by Savithri et al. (2018) for crude fibre

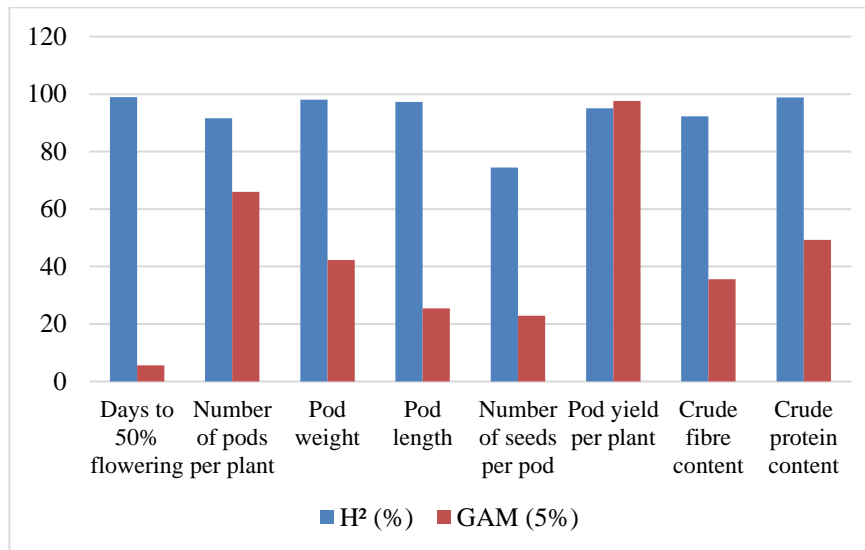


Fig. 2. Heritability & GAM for selected biometric characters

content. Low GAM was obtained for days to 50% flowering which indicates that the traditional selection method is not significant for improvement of such traits due to the presence of non-additive gene action. Similar result was obtained by Rambabu et al. (2016).

The broad-sense heritability, combined with genetic advance enhances the precision in assessing the success of trait selection by Johnson et al. (1955). High estimates of heritability, along with significant genetic advance as a percentage of the mean, were observed for traits such as Number of pods per plant, Pod weight, Pod length, Pod yield per plant, Crude fibre and Crude protein content which suggests that these traits were predominant in additive gene action. Similar findings were reported by Savithri et al. (2018) for Number of pods per plant, Pod weight, Pod length, Pod yield per plant and Crude protein content. High heritability with low GAM was observed for days to 50% flowering which indicates that environment play a significant role in controlling this trait. Similar result were observed by Savithri et al. (2018).

4. CONCLUSION

The study concluded that high PCV and GCV were observed for traits such as the number of pods per plant, pod weight, pod yield per plant, crude protein content and Low PCV and GCV was observed in the trait days to 50% flowering. The difference in PCV and GCV is due to additive and nonadditive gene action. High PCV and GCV indicates that phenotypic variation is

largely due to genetic factors and trait could be improved through selection. Low PCV and GCV indicates that limited variation is present in the trait making it a poor candidate for selection. High Heritability and High Genetic advance as percent mean (GAM) were observed for traits such as Number of pods per plant, Pod weight, Pod length, Number of seeds per pod, Pod Yield per plant, Crude fibre and Crude protein content which concludes that traits are highly controlled by additive genetic factors and could be improved through selection as environment factors have less impact on such traits. The results suggest substantial variability is present in BC₂F₁ lines of Yard long bean in which selection is effective for crop improvement.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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