

Studies on Gene Action for Yield and Quality Traits in Yardlong Bean (*Vigna unguiculata* (L.) Walp. ssp. *Sesquipedalis* Verdc.)

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ABSTRACT

Gene action of fruit yield and quality traits in yardlong bean (*Vigna unguiculata* (L.) Walp. ssp. *Sesquipedalis* Verdc.) were studied through half diallel analysis of 21 F_1 hybrids derived by crossing seven parental lines. The ratio of *gca* to *sca* variances revealed that non-additive gene action was predominant over additive gene action in the inheritance of all the characters studied except for number of primary branches per plant and days to first picking. Hence, heterosis breeding is suggested for exploitation of these traits.

Keywords: Diallel, Fruit yield, Gene action, Variance, Yardlong bean.

Yardlong bean (*Vigna unguiculata* (L.) Walp. ssp. *Sesquipedalis* Verdc.) belongs to the family, Fabaceae with chromosome number, 2n=2x=22. Yardlong bean has a typical leguminous flower and is predominantly a self pollinated crop. This legume is also known as poor man's meat as it is a rich and inexpensive source of vegetable protein (3.5-5%) and 100 g of pod contains 941 IU vitamin A, 13 mg vitamin C, 2.5 mg iron, 80 mg calcium, 74 mg phosphorous and 2 g dietary fibre making it an excellent vegetable (Singh *et al.*, 2001). Besides immature pods, tender leaves and green seeds are also used as vegetable in certain parts of the country.

For developing promising hybrids through hybridizations, the choice of parents is a matter of great concern to the plant breeder. A high yielding genotype may or may not transmit its superiority to its progenies. Therefore, the success of a breeding programme is determined by useful gene combinations in the form of high combined inbred. The knowledge of nature of gene action governing the expression of various traits could be helpful in predicting the effectiveness of selection. The efficient partitioning of genetic variance into its components *viz*; additive, dominance and epistasis will help in formulating an effective and sound breeding programme.

The success of a breeding programme is determined by useful gene combinations in the form of high combining inbred. The knowledge of the relative importance of additive and non-additive gene action is essential to a plant breeder for the development of an efficient hybridization programme (Dudley and Moll, 1969). The present investigation was therefore, undertaken with a set of half -diallel crosses to elicit information about the nature and magnitude of gene action for yield and its components in yardlong bean so as to formulate suitable breeding strategy.

MATERIAL AND METHODS

Seven yardlong bean genotypes viz., Geethika, Babli, Vizianagaram Local, Bobbili Local, Lola, Trivendram Local, Bhuvaneswar Local were chosen in this study to represent substantial amount of genetic diversity for different quantitative and quality traits. These genotypes were maintained through selfing during 2018 and were involved in 7×7 half-diallel to develop 21 F₁ hybrids during Rabi, 2018-19. All the F_1 's along with their parents were evaluated in a Randomized Block Design with three replications during Summer, 2019. The crop was raised in row and plant spacing of 2 and 1 m, respectively. All recommended package of practices were followed to raise a successful crop. Five randomly selected plants from each entry were tagged in each replication for recording observations on different characters viz., vine length (cm), number of primary branches per plant, average leaf area (cm²), days to 50 percent flowering, days to first picking, duration of harvest, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), pod girth (mm), number of seeds per pod, 100 seed weight (g), pod yield per plant (kg), TSS (⁰Brix), protein (%). The data recorded on five plants per treatment was averaged for use in statistical analysis. Data were analyzed according to ANOVA techniques, as outlined by Panse and Sukhatme (1978), to determine the significant differences among genotypes for all the characters. Components of genetic variance were

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mber of ds per luster	.008	512**	827**	399**	869**	.081	452**	**060	027	
(umber Nu of bu husters c	0.675 (.931** 0.	.795** 0.	.284** 0.	.671** 0.	0.709 (.176** 0.	.777** 0.	0.236 (
Duration of harvest c	0.087	8.258** 10	14.566** 3	6.428** 13	7.000* 6	1.364	7.088** 10	1.514** 1	0.455	
Days to first I picking	2.769	5.521**	3.47	6.334**	1.579	1.696	5.377**	0.83	0.565	
Days to 50% flowering	1.667	7.524**	10.800^{**}	6.815**	2.036	1.034	7.370**	1.119**	0.345	
Average leaf area (cm ²)	23.65	674.389**	351.072**	690.259**	2296.891**	54.473	483.569**	150.861**	18.158	
Number of primary branches	0.044	1.711**	1.475^{**}	1.828^{**}	0.778^{**}	0.063	1.965^{**}	0.172**	0.021	
Vine length (cm)	75.05	4883.691**	3545.565**	5511.189**	362.472*	69.889	4548.045**	793.569**	23.296	
Df	2	27	9	20	1	54	6	21	54	
Source	Replicates	Treatments	Parents	Hybrids	Parent Vs.Hybrids	Error	GCA	SCA	Error	

** 1% level of significance, * 5% level of significance

		Number of	Pod lenoth	Pod airth	Pod weight	Number	100 seed	Pod yield	TSS	Protein
Source	Df	node ner nlant			T UU WUIGUI	of seeds	weight	per plant		10/1
		pous put plain			(गान्नि)	per pod	(gm)	(kg)	(DTIX)	(0/)
Replicates	2	15.703	3.101	0.005	0.299	0.495	0.039	0.045	0.002	0.001
Treatments	27	867.170**	204.942**	0.169**	24.500**	7.671**	16.116**	1.091**	0.396**	0.309**
Parents	9	342.725**	279.403**	0.076^{**}	22.599**	8.477**	17.538**	0.279**	0.112**	0.289**
Hybrids	20	847.359**	186.168**	0.199**	11.860^{**}	7.799**	15.010^{**}	0.690**	0.346**	0.299**
Parent Vs.Hybrids	1	4410.070**	133.664**	0.114^{**}	288.707**	0.267	29.726**	13.968**	3.085**	0.620**
Error	54	16.869	2.056	0.005	1.4	0.281	0.204	0.022	0.006	0.008
GCA	9	745.552**	193.156**	0.123^{**}	13.934**	7.042**	10.946^{**}	0.552**	0.127^{**}	0.215**
SCA	21	158.629**	32.645**	0.037**	6.519**	1.276^{**}	3.780**	0.310**	0.133**	0.071**
Error	54	5.623	0.685	0.002	0.467	0.094	0.068	0.007	0.002	0.003
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* 1% level of significance, * 5% level of significance

Source	Vine	Number of	Average leaf area	Days to	Days to	Duration	Number of	Number of pods
Source	(cm)	primary branches	(cm^2)	flowering	picking	of harvest	clusters per plant	per cluster
$\sigma^2 gca$	417.164	0.199	36.968	0.695	0.505	0.619	0.933	0.04
$\sigma^2 sca$	770.273	0.151	132.703	0.774	0.265	1.059	1.541	0.063
σ^2 gca/ σ^2 sca	0.542	1.322	0.279	0.897	1.908	0.585	0.606	0.635

Table 2. Combining ability variances and gene action for yield and quality traits in yardlong bean

Source	Number of pods per plant	Pod length (cm)	Pod girth (cm)	Pod weight (gm)	Number of seeds per pod	100 seed weight (gm)	Pod yield per plant (kg)	TSS (⁰ brix)	Protein (%)
$\sigma^2 gca$	65.214	17.835	0.01	0.824	0.641	0.796	0.027	-0.001	0.016
$\sigma^2 sca$	153.006	31.96	0.036	6.052	1.182	3.711	0.302	0.131	0.068
$\sigma^2 gca / \sigma^2 sca$	0.426	0.558	0.267	0.136	0.542	0.215	0.09	-0.005	0.235

estimated from the data obtained on the diallel crosses by the method given by Griffing's Method-II and Model-I (Griffing, 1956) as outlined by Singh and Chaudhary (1979).

RESULTS AND DISCUSSION

The analysis of variance was carried out for different traits of yardlong bean and are presented in Table 1. The analysis of variance revealed significant differences for all attributes among the parents except for days to first picking. Significant differences were also observed among the hybrids for all the seventeen attributes. Further significant differences were observed among the parents vs. hybrids for fourteen characters, while for the characters, days to 50% flowering, days to first picking and number of seeds per pod the recorded differences were not significant.

This indicates the existence of wide variability in the material studied and there is a good scope for identifying promising parents and hybrid combinations, and improving the yield through its components. These results are in accordance with the earlier findings of Pallavi *et al.* (2018) in cowpea, Farag and Afiah (2012) in faba bean, Das *et al.* (2014) in dolichos bean.

The estimates of *gca* and *sca* variances, their ratios and gene action are presented in Table 2. General combining ability is genetically associated with additive gene action while specific combining ability is due to dominance and epistasis. The ratio of s^2gca and s^2sca is an index of additive and non-additive gene action. The ratio of *gca* and *sca* variance if less than unity, predominance of non-additive gene action is indicated whereas the ratio of more than unity indicates predominance of additive gene action. In the present investigation, the magnitude of *sca* variance was greater

than that of *gca* variance and suggests the predominance of the non-additive gene action for majority of the traits. However, for number of primary branches per plant and days to first picking, the greater magnitude of *gca* variance than that of *sca* variance suggests the predominance of additive gene action.

The results for this kind of gene action are in conformity with earlier findings of Owusu *et al.* (2018) in cowpea, Askander and Osman (2018) in pea.

CONCLUSION

The presence of non-additive gene action and additive gene action revealed that heterosis breeding can be utilized for the experimental material of yardlong bean studied. However information on levels of heterosis and combining ability are required in addition to the evaluation of hybrids over seasons and locations prior to their potential commercial exploration.

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Received on 03.11.2020 and revised on 23.12.2020