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**Vinutha Patil S**

Department of Genetics and  
Plant Breeding, College of  
Agriculture, Shivamogga  
University of Agricultural and  
Horticultural Science,  
Shivamogga, Karnataka, India

**Gangaprasad S**

Department of Genetics and  
Plant Breeding, College of  
Agriculture, Shivamogga  
University of Agricultural and  
Horticultural Science,  
Shivamogga, Karnataka, India

**Dushyantha Kumar BM**

Department of Genetics and  
Plant Breeding, College of  
Agriculture, Shivamogga  
University of Agricultural and  
Horticultural Science,  
Shivamogga, Karnataka, India

**Corresponding Author:**

**Vinutha Patil S**

Department of Genetics and  
Plant Breeding, College of  
Agriculture, Shivamogga  
University of Agricultural and  
Horticultural Science,  
Shivamogga, Karnataka, India

## Studies on variability, heritability, genetic advance and transgressive segregating in brinjal (*Solanum melongena* L.)

**Vinutha Patil S, Gangaprasad S and Dushyantha Kumar BM**

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### Abstract

Significant variability is available in the F<sub>2</sub> population of brinjal. Top crosses of brinjal Biliudda badane × mullu badane produced from F<sub>1</sub> generation were in augmented design at ZARS Shimogga in Kharif 2017. They have several characteristics of plant breeding significance with sufficient scope for added improvement to growing conditions. The F<sub>2</sub> study showed significant variation for nine quantitative traits. Close estimates between GCV and PCV values indicated lesser influence of environmental factors on the expression of traits under study. In this investigation, the proportion of genetic contribution of high GCV, PCV coupled with high broad sense heritability and genetic advance to the overall phenotypic expression of the studied traits like number of fruits per plant, number primary branches, number of flowers per plant was high, indicating predominant control of additive genes, and these traits could be improved upon by selection without progeny testing. High magnitude of heritability for most of the characters suggested the progress of improvement in yield and its components. Differences in mean values of parents for various characters indicated involvement of diverse parents in the crosses studied. The F<sub>2</sub> plants exceeded either of the parents for most of the characters, which seems to be due to transgressive segregation.

**Keywords:** Transgressive segregation, kharif, skewed platykurtic, environmental factors, leptokurtic

### Introduction

Brinjal (*Solanum melongena* L.) is one of the most common, widespread and principal vegetable crops grown in India and is also considered as the king of vegetables. The **crop** is highly productive and known as the poor man's crop. It belongs to the family *Solanaceae* and is native of Indo-Burma region and China (Vavilov, 1926). It stands second in area and production after China and occupies an area of 6.69 lakh hectares with an annual production of 124.01 lakh metric tonnes and average productivity of 19 tonnes per hectare (Anonymous, 2016). Brinjal occupies an area of 15.8 thousand hectares with an annual production of 4.03 lakh metric tonnes and productivity of 25.4 tonnes per hectare in Karnataka.

Brinjal or eggplant is a perennial but grown commercially as annual crop. Inflorescence is often solitary but some time it constitutes a cluster of 2-5 flowers. Solitary or clustering nature of inflorescence is a varietal character. Flower is complete and hermaphrodite. Heterostyly is a common feature, and fruit setting flower consist of long (70-86.7%) and medium styled (12-55.6%) flower. The non-fruit setting flowers consist of short styled and pseudo styled. It ranks fair in nutritional value (carbohydrates, proteins, and fiber). It is an essential source of carbohydrate (4.0 g), protein (1.4 g), fiber (1.3 g), vitamin-A (124 IU), phosphorus (47 mg), potassium (2.0 mg) and iron (0.3 mg) and recommended for diabetes, asthma, cholera, bronchitis and it protects the brain cell membranes from damage.

### Material and Methods

The field experiment under present investigation was conducted with top two crosses from F<sub>1</sub> including 1 check from Private company seeds, Shivamogga. Crosses were made between as line × testes, among them, top crosses were selected.

This experiment was conducted at ZAHRS, Shivamogga. The experimental material consisted of the F<sub>2</sub> population and checks. Sowing was carried out at 3<sup>rd</sup> week of July 2017. The seedlings were transplanted in main field after 22 days at a spacing of 90 cm between rows and 60 cm between plant to plant. The crop was raised by following recommended package of practices.

Portrays were filled with a mixture of vermicompost and coco peat; seeds were sown and watered. These portray were covered with black polythene to build up humidity for better and early germination of seeds. After germination, polythene cover was removed, and watering was done either in the morning or evening hours. The main field was prepared to fine tilt by repeated ploughing and harrowing, and the FYM @ 25 t/ha was incorporated into the soil. Ridges and furrows were prepared at a spacing of 90 cm. Seedlings were planted on ridges at a spacing of 60 cm (Anon., 2012). A total of 24 plants were planted on each ridge with a plot area of 6.75 m<sup>2</sup>. A healthy crop was laid by adopting standard agronomic practices.

Observations were recorded from all plants. The characters studied were days to first flowering, plant height (cm), number of primary branches per plant, number of flowers/plant, fruit length (cm), fruit width (cm), number of fruits/plant, number of fruits per cluster, fruit yield/plant (kg).

### Results and Discussion

The study of distribution properties such as coefficients of skewness (third-degree statistic) and kurtosis (fourth-degree statistic) provides insight about the nature of gene action (Fisher *et al.*, 1932) and a number of genes controlling the traits (Robson, 1956), respectively.

Platykurtic and positively skewed distribution suggested the involvement of relatively large number of segregating genes with majority of them having decreasing effects and dominance based complementary type of interaction in the inheritance of number of flowers per plant, number of primary branches per plant, number of fruits per plant, fruit length (cm) exhibiting this kind of inheritance. Maximizing the genetic gain in respect of the traits with positively skewed

distribution requires eminence selection from the existing variability (Roy, 2000) [13].

Negatively skewed platykurtic distribution like days to first flowering, plant height, number of fruits per plant, fruit width is evidence for the involvement of a large number of dominant genes with the majority of them having increasing effects and duplicate type of epistasis in the inheritance. These traits have evolved with dominance and dominance based duplicate epistasis which helps to protect the individual plant from deleterious alleles arising from existing variability (Roy, 2000) [13].

Positively skewed leptokurtic distribution suggested the involvement of a relatively fewer number of segregating genes with the majority of them having decreasing effects in the inheritance of a number of fruits per cluster.

### Phenotypic coefficient of variation

The PCV estimates were relatively high for numbers of flowers, number of fruits per cluster, number of primary branches, number of fruits per plant, fruit yield per plant. This indicates the higher magnitude of variability present in the populations. Moderate PCV values were observed plant height, fruit width, fruit length. Low values of PCV were observed for days to first flowering followed by days to 50 percent flowering.

Present results are in accordance with high PCV for number of fruits per cluster similar findings were also reported by several investigators like Lokesh *et al.* (2013) [7], number of primary branches Arunkumar *et al.* (2014) [3], number of fruit Arunkumar *et al.* (2014) [3], Samlindsujin *et al.* (2017) [17], fruit yield per plant Swaroop and Sharama (2000), Negi *et al.* (2000) [9].

**Table 1:** Descriptive statistics for nine characters in F<sub>2</sub> generation of cross Biliudda badane × Mullu badane

Sl. No.	Characters	Mean of Bilichandu Badane	Mean of Mullu badane	Mean of F <sub>2</sub>	Range		Skewness	Kurtosis	Kurtosis type
					Min.	Max.			
1	Days to first flowering	51.60	45.00	50.04	43.00	57.00	-0.27	-1.26	P
2	Plant height (cm)	86.60	87.80	78.66	46.00	107.00	-0.18	-0.29	P
3	Number of flowers per plant	26.00	27.80	28.21	11.00	54.00	0.64	0.66	P
4	Number of fruits per cluster	1.00	1.60	1.22	1.00	3.00	2.23	4.17	L
5	Number of primary branches	3.00	5.60	3.91	3.00	13.00	1.39	2.51	P
6	Fruit yield per plant (g)	1047.06	976.71	1063.75	657.13	2210.76	-1.63	5.05	L
7	Number of Fruits per plant	31.00	27.80	27.55	11.00	54.00	0.67	0.97	P
8	Fruit width (cm)	4.31	4.21	4.32	3.12	5.23	-5.93	41.41	L
9	Fruit length (cm)	6.86	5.31	6.47	3.14	10.37	-1.21	7.32	L

**Table 2:** Estimates of genetic variability parameters for yield and its attributing traits in F<sub>2</sub> generation of Cross Biliudda badane × Mullu badane

Sl. No.	Characters	Co-efficient of variation		h <sup>2</sup> bs	GAM
		PCV (%)	GCV (%)		
1	Days to first flowering	9.12	8.40	84.81	15.94
2	Plant height (cm)	14.91	12.68	72.37	22.22
3	Number of flowers per plant	23.14	18.09	61.08	29.12
4	Number of fruits per cluster	41.62	27.07	42.31	36.27
5	Number of primary branches	58.07	49.59	72.93	87.24
6	Fruit yield per plant (g)	23.28	19.58	70.74	33.92
7	Number of Fruits per plant	23.95	19.07	63.39	31.27
8	Fruit width (cm)	13.84	13.10	89.61	1.37
9	Fruit length (cm)	18.87	17.57	65.86	0.72

Moderate PCV for fruit length, the findings of Ansari *et al.* (2010) [1] are in conformity with the present findings, Plant height Several workers *viz.*, Ramesh kumar *et al.* (2013) [11], reported similar findings. These results suggest that influence of environment was low or little. Therefore, phenotypic

variability may be a good measure of genotypic variability. Low PCV for days to first flowering are in conformity with the present findings of Ansari *et al.* (2010) [1] and Patel *et al.* (2013).

### Genotypic coefficient of variation

High values of GCV were observed for a number of fruits per cluster and number of primary branches per plant. This indicates the higher magnitude of variability present in the populations.

Moderate GCV values were observed for a plant height, numbers of flowers, fruit width and fruit yield per plant and numbers of fruits per plant. Low values of GCV were observed for days to first flowering followed fruit length, and fruit length,

Present results are in accordance with high GCV for number of primary branches per plant Muniappan *et al.* (2010) [8], Arunkumar *et al.* (2014) [3], all got same results and for number of fruits per plant Mehta (2009) [12] and Kumar *et al.* (1998) a observed high values for number of fruits per plant. Moderate GCV for number of fruits per cluster these findings are in close agreement with the results obtained by Ansari *et al.* (2000). Low GCV days to first flowering was got by Ansari *et al.* (2000), Sao and Dahatonde *et al.* (2010) [5], Shekar *et al.* (2012) [15], Das *et al.* (2002), Sabeena *et al.* (2011) [14] and Vandana *et al.* (2014) [18], Patel *et al.* (2013), and fruit yield per plant was got similar results by Das and Mishra. (1995) [4] and Ansari *et al.* (2000) in both the experiment they observed high for fruit yield which is in contrast with results.

### Heritability

The degree to which the phenotypic variation that can be explained as variation in genotype is estimated as the ratio of genotypic variability to the total phenotypic variability and is called heritability in a broad sense, which is otherwise known as “degree of genetic determination.” Estimation of heritability for each character in all the crosses will guide for opting selection for different traits. It is necessary to estimate heritability for each character. This will give an exact idea of the heritable portion of variability. Broad-sense heritability gives an idea about portion of observed variability attributable to genetic differences. In other words, heritability indicates the accuracy with which a genotype can be inferred from its phenotype.

The difference between PCV and GCV estimates indicates the relative influence of environment on the characters, which in turn decides the extent of their heritability. If the difference for any character is low, the environmental effect is low, and

hence it results in high heritability, while wide differences between PCV and GCV indicates considerable influence by the environmental factors leading to low heritability estimates. Heritability estimates represent the relative strength of the characters and indicate the efficiency of selection systems. Broad-sense heritability gives an idea of about observed variability attributable to genetic difference.

In the population, Biliudda badane × Mullu badane high heritability was observed for all the characters studied *viz.*, number of primary branches per plant followed by days to first flowering, plant height, fruit width, number of flowers and number of primary branches per plant, and fruit yield indicating predominance of additive gene component. Thus, there is ample scope for improving these characters with direct selection. moderate heritability observed for number of fruits per cluster and low heritability observed for fruit length. Present results are in accordance with high heritability for plant height got for Rajeshkumar *et al.* (1998) [10], Lolesh *et al.* (2013), fruit width and fruit yield per plant was also conformed by Rajeshkumar *et al.* (1998) [10], Negi *et al.* (2009), Muniappan *et al.* (2010) [8], Samlindsujin *et al.* (2017) [17], Kumar *et al.* (2000) [6], numbers of branches per plant was having same results as that of Muniappan *et al.* (2010) [8], number of flowers per plant by Kumar *et al.* (2000) [6], for fruit width similar findings were also reported by several investigators like Vandana *et al.* (2014) [18] and Vidhya and Kumar (2015) [19], number of fruits per plant Negi *et al.*, (2009). Low heritability for fruit length and number of fruits per clusters similar findings were also reported by Ansari *et al.* (2010) [1].

### Genetic Advance as percent mean (GAM)

In the population Biliudda badane × Mullu badane, high GAM was observed for number of primary branches followed for number of flowers per plant, number of fruits per plant, number of fruits per cluster and plant height and it was moderate for characters like days to first flowering. Low heritability coupled with GAM was observed for fruit width, fruit length. Present results are in accordance with genetic advance as per cent mean for plant height by Patel *et al.* (1999) and Lokesh *et al.* (2013) [7], days to first flowering by Ambade, R. (2008) [2], number of fruits per plant by Kumar *et al.* (2000) [6].

**Table 3:** Desirable transgressive segregants in F<sub>2</sub> population in cross of Biliudda badane × Mullu badane in Brinjal

Sl. No	Plant number	Number of fruits per plant	Fruit yield per plant (g)
1	P-14	28	1983.80
2	P-15	26	1387.79
3	P-17	20	1118.56
4	P-29	34	1283.50
5	P-33	24	1318.29
6	P-73	26	1691.99
7	P-94	23	1594.23
8	P-96	26	1416.38
9	P-132	20	1381.31
10	P-152	21	1159.56

Transgressive segregants are those plants, which surpassed the limits of both the parents in desirable direction for any of the character in segregating generations, especially in F<sub>2</sub> generation. Combinations of favorable genes (positive alleles) from different parents and additive gene action are the main reasons for the occurrence of transgressive segregants.

The significant superior performance of segregants may be due to the contribution of some component characters. Plant number 14 exhibited highest fruit yield per plant which may be due to contribution of component characters like number of fruits per plant, number of flowers per plant and fruit yield per plant. While the superior performance of plant number 29

due to component traits like number of fruit per plant, fruits width, fruit length and fruit yield per plant. Whereas superior performance of plant number 132 may be due to component traits like number of fruits per plant, number of branches, fruit width and fruit yield per plant.

The present investigation leads to the identification of superior promising individual plants in F<sub>2</sub> segregating generation in the cross Biliudda badane × Mullu badane. It would be worthwhile to evaluate the performance of progenies derived from desirable transgressive segregants in future generations for their further use in breeding programmes.

### Conclusion

The present investigation leads to the identification of superior promising individual plants in F<sub>2</sub> segregating generation in the cross Biliudda badane × Mullu badane. It would be worthwhile to evaluate the performance of progenies derived from desirable transgressive segregants in future generations for their further use in breeding programmes.

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