

## Interfamily Variability Studies in Green Round Pre-Breeding Lines of Brinjal (*Solanum melongena* L.)

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### ABSTRACT

An experiment was carried out with seven pre-breeding lines of F<sub>4</sub> generation of green round brinjal derived from the cross Raidurga Green Round x West Coast Green Round to study the interfamily variability for nine different growth and yield parameters. None of the characters had shown high PCV and GCV estimates, which revealed lack of high variability between the average performance of segregating lines for these characters. Low PCV and GCV were recorded for plant height, number of branches per plant, days to first flowering, days to 50 per cent flowering, fruit length, fruit breadth and number of fruits per plant. Moderate levels of PCV and GCV were observed for yield per plant showing the presence of moderate variability for these characters between the lines whereas average fruit weight had recorded with moderate PCV and low GCV. High heritability coupled with high GA and GAM was observed for yield per plant indicates predominant role of additive gene action whereas high heritability with moderate GAM was recorded for average fruit weight. Estimation of per cent bacterial wilt incidence in each family revealed that four lines viz., 12-23-30-1, 12-23-30-2, 12-23-249-10 and 12-23-249-12 were found to be resistant.

**Key words:** Interfamily variability, Heritability, Genetic advance

### INTRODUCTION

Brinjal is one of the most important vegetable crops in India grown throughout the country for its green, purple, white and variegated fruits. India is the origin of this crop, there exists a huge diversity in its growth habit,

flower colour, fruit shape, colour, size and consumer acceptance. In India, the consumer preference for this vegetable is mainly depends upon the shape, size and colour of the fruits, and it varied from region to region within the country.

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In northern parts of Karnataka, there is a huge demand for the green round or oval shaped fruits with purple or white stripes. So development of improved varieties in green round segment of brinjal along with bacterial wilt resistance plays a significant role in increasing the productivity. An important step in developing superior varieties in self-pollinating crops is the selection among the progenies of superior crosses. The phenotype of the plant is influenced by genotype x environmental interaction. Thus, one should identify the characters which are less influenced by the environment and highly heritable. The heritable variation can be estimated with higher degree of accuracy when heritability is studied along with genetic advance. High heritability estimates coupled with high genetic advance is an effective criteria for selection<sup>5</sup>. Heritability coupled with genetic advance would be helpful in assessing the nature of gene action. In advanced segregating generations, the variability exists between the lines plays a major role for selecting the plants having particular across the lines. With these, the present study was undertaken to estimate the interfamily variability F<sub>4</sub> generation of RGR x WCGR for different horticultural traits.

#### MATERIAL AND METHODS

Arunkumar *et al.*<sup>2</sup> reported the cross Raidurga Green Round x West Coast Green Round as superior hybrid having higher yield and bacterial wilt resistance with all the acceptable fruit qualities. Further F<sub>2</sub>, F<sub>3</sub> families were evaluated and selected seven F<sub>3</sub>:F<sub>4</sub> families. In

the present investigation seven F<sub>4</sub> families *viz.*, 12-23-30-1, 12-23-30-2, 12-23-30-12, 12-23-30-14, 12-23-249-2, 12-23-249-10 and 12-23-249-12 of Raidurga Green Round x West Coast Green Round which were raised at the research block of Department of Vegetable Science, College of Horticulture, UHS Campus, GKVK (PO), Bengaluru during the year 2016. The seedlings of segregating lines, respective parents and checks were artificially inoculated with *Ralstonia solanacearum* suspension with a concentration of 1.0 x10<sup>6</sup> cfu/ml by root injury method where the roots were slightly damaged by inserting a sharp knife 1 cm away from the stem and about five ml of bacterial suspension was inoculated to each of the seedlings by drenching around the root zone on 21<sup>st</sup> day of sowing. Then during transplanting also seedlings were dipped in bacterial suspension and planted in field. The recommended agronomic practices (Anon., 2014) were followed to raise a healthy crop. The observations on different quantitative and qualitative traits were recorded on every plant in each family. Mean performance of each F<sub>4</sub> family was analysed to get the interfamily variability estimates. Genetic parameters of variability *viz.*, mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance, genetic advance as per cent of mean and expected mean in next generation were estimated. Percent bacterial wilt incidence in each F<sub>4</sub> family was estimated and these were classified into five different groups as given below according to percent disease incidence as reported by Winstead and Kelman.

Disease reaction	Per cent wilt incidence
Highly resistant (HR)	Plants do not show any wilt symptom
Resistant (R)	1-20% plants wilt
Moderately resistant (MR)	21-40% plants wilt
Moderately susceptible (MS)	41-60% plants wilt
Susceptible (S)	61-80% plants wilt
Highly susceptible (HS)	More than 80% plants wilt

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of plants infected with bacterial wilt}}{\text{Total number of plants}} \times 100$$

## RESULTS AND DISCUSSION

Genetic parameters of interfamily variability for different characters of F<sub>4</sub> families of RGR x WCGR are represented in the Table 1. A narrow range of variation was found between the F<sub>4</sub> families for the parameters like plant height, number of branches per plant, days to first flowering, days to 50 per cent flowering, fruit length, fruit breadth and number of fruits

per plant. Only fruit length and yield per plant had shown considerable range of variation between the lines. PCV was found to be higher than GCV for all the parameters studied *viz.*, plant height, number of branches per plant, days to first flowering, days to 50 per cent flowering, fruit weight, fruit length, fruit breadth, number of fruits per plant and yield per plant.

**Table 1: Genetic parameters of interfamily variability for different characters of pre-breeding lines of RGR x WCGR**

Characters	Grand mean ± SD	Range		PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA	GAM (%)	EMNG
		Min.	Max.						
Plant height (cm)	53.19 ± 3.06	48.96	57.04	5.75	2.83	24.21	1.53	2.87	54.72
No. of branches/plant	7.90 ± 0.75	7.03	8.87	9.45	5.01	28.11	0.43	5.47	8.33
Days to first flowering	35.57 ± 2.07	32.00	38.00	5.82	2.57	19.50	0.83	2.34	36.40
Days to 50% flowering	47.57 ± 2.23	45.00	51.00	4.68	3.71	62.98	2.89	6.07	50.46
Average fruit weight (g)	58.64 ± 7.33	52.22	73.43	12.50	9.98	63.72	9.62	16.41	68.27
Fruit length (cm)	5.54 ± 0.32	5.12	5.95	5.75	2.44	17.97	0.12	2.13	5.65
Fruit breadth (cm)	4.92 ± 0.18	4.67	5.14	3.63	1.78	24.10	0.09	1.80	5.00
No. of fruits/plant	5.49 ± 0.45	5.026	6.17	8.21	0.99	1.45	0.01	0.24	5.50
Yield per plant (g)	307.01 ± 38.21	252.54	357.30	12.45	11.37	83.45	65.69	21.40	372.71

\*Mean values were used for statistical analysis.

PCV – Phenotypic co-efficient of variation

GCV – Genotypic co-efficient of variation

h<sup>2</sup> – Broad sense heritability

GA – Genetic advance

GAM – Genetic advance as per cent of mean

SD – Standard deviation

EMNG – Expected mean in next generation

The difference between PCV and GCV was more for each character. This result indicated a good amount of environmental role in the expression of the character along with genetic contribution. This environment effect could be due to heterogeneity in soil fertility status between the blocks. PCV and GCV estimates were low for plant height (5.75% and 2.83%), number of branches per plant (9.45% and 5.01%), days to first flowering (5.82% and 2.57%), days to 50 per cent flowering (4.68% and 3.71%), fruit length (5.75% and 2.44%), fruit breadth (3.63% and 1.78%) and number of fruits per plant (8.21% and 0.99%) which reveals the least scope for improvement through selection between the lines for these traits (Table 1). Similar findings were reported for plant height by Gavade and Ghadage<sup>3</sup>. Low PCV and GCV for number of branches per plant were also reported by Singh *et al*<sup>7</sup>. The low PCV and GCV estimates for days to first flowering were supported by the research findings of Naik *et al*<sup>6</sup>. The low estimates of

PCV and GCV for days to 50 per cent flowering was in accordance to the result obtained by Kumar *et al.* and Vidhya and Kumar<sup>9</sup>. Fruit weight has shown moderate and low levels of PCV (12.50%) and GCV (9.98%) estimates respectively while, for fruit yield per plant both GCV (12.45%) and PCV (11.37%) were moderate (Table 1.) which was in accordance with the research findings of Vidhya and Kumar<sup>9</sup> and Gavade and Ghadage<sup>3</sup>. The moderate levels of PCV and GCV for these characters in segregating population indicate good scope for improvement in these traits. High heritability combined with low to moderate GAM was observed for days to 50 per cent flowering (62.98% and 6.07%) and fruit weight (63.72% and 16.41%). It is indicative of non-additive gene action for days to 50 per cent flowering and fruit weight. High heritability (83.45%) with high genetic advance (65.69) was observed for yield per plant indicating presence of additive effects. While, higher

value of GAM (21.40%) in this trait suggests that selection for this trait may be economical. High heritability for different traits indicated that large proportion of phenotypic variance was attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. These results were similar to the findings of Lokesh *et al*<sup>5</sup>. All other characters like plant height, number of branches per plant, days to first flowering, fruit length, fruit breadth and number of fruits per plant have shown low heritability values along with low GA and GAM which indicates that selection for such traits may not be rewarding. These results were in disagreement with the findings of Singh *et al*.<sup>8</sup> who reported high heritability for all these characters with high genetic gain. The low heritability values for these characters may be due to the use of average performance of each lines for the analysis of interfamilial variability. The very low heritability value observed for number of fruits per plant may be due to the less variation between the average performance of all seven pre-breeding lines

(phenotypic variance) which was found same as variation exist in the parent population (error variance/environmental variance) leading to minimum genotypic variation for this character. Reactions of seven F<sub>4</sub> families of RGR x WCGR, their parents and checks to bacterial wilt incidence is presented in the Table 2. The parent West Coast Green Round (11.11 %) and the check Arka Anand (4.16 %) were found to be resistant to bacterial wilt while, the other parent Raidurga Green Round (90.28 %) and the check Arka Kusumakar (91.67%) were shown highly susceptible reaction. Out of seven pre-breeding lines evaluated, four lines *viz.*, 12-23-30-1, 12-23-30-2, 12-23-249-10 and 12-23-249-12 were found to be resistant. The minimum wilt incidence was shown by the line 12-23-30-1 (1.39%) which was lesser than the resistant parent and the check. Two lines *viz.*, 12-23-30-12 and 12-23-30-14 were showing moderately resistant reaction while, the line 12-23-249-2 was found to be moderately susceptible with 53.33 per cent bacterial wilt incidence.

**Table 2: Reactions of F<sub>4</sub> families of RGR x WCGR, their parents and checks to *Ralstonia solanacearum* (Smith)**

Sl. No.	Line number/ Parents/ Checks	Percentage wilt	Reaction
1.	12-23-30-1	1.39	R
2.	12-23-30-2	13.89	R
3.	12-23-30-12	20.83	MR
4.	12-23-30-14	22.22	MR
5.	12-23-249-2	53.33	MS
6.	12-23-249-10	13.89	R
7.	12-23-249-12	19.44	R
8.	West Coast Green Round	11.11	R
9.	Raidurga Green Round	90.28	HS
10.	Arka Anand	4.16	R
11.	Arka Kusumakar	91.67	HS

R – resistant

MR – moderately resistant

MS – moderately susceptible

HS – highly susceptible DAT – Days after transplanting

Results on frequency distribution of F<sub>4</sub> families for six qualitative characters are presented in the Table 3. Among 341 plants in F<sub>4</sub> generation of the cross Raidurga Green Round x West Coast Green Round, 79.18 per cent of the plants (270) had spreading growth habit, 19.06 per cent (65) had semi spreading growth habit and remaining 1.76 per cent of the plants (6) had erect growth habit. Hundred per cent of the plants were free of spines and

produced purple colour flowers. The shape of the fruits varied from round (53.96% plants) to oval (46.04% plants), whereas most of the plants (95.31%) produced green fruits with white stripes and very few segregated in to green fruits with purple stripes (46.92%). Sixty-nine point five per cent plants (237) produced fruits in cluster, while the remaining (30.49%) were exhibited solitary bearing habit.

**Table 3: Frequency distribution of F<sub>4</sub> segregating population of RGR x WCGR for six qualitative characters out of 341 plants**

Sl. No.	Qualitative characters	Categories	Frequency
1.	Growth habit	Erect	6
		Semi spreading	65
		Spreading	270
2.	Spiny	Non spiny	341
		Spiny	0
3.	Flower colour	Purple	341
		White	0
4.	Fruit shape	Round	184
		Oval	157
5.	Fruit colour	Green with white stripes	325
		Green with purple stripes	16
6.	Fruit bearing habit	Clustering	237
		Solitary	104

### CONCLUSION

The pre-breeding lines under evaluation were shown very narrow range of variability, low to moderate PCV and GCV values, low heritability and genetic advance for almost all the characters. The direct selection of superior plants across different pre-breeding lines may be effective for days to 50 per cent flowering, average fruit weight and fruit yield per plant as these characters having high heritability estimates. Average performance of different pre-breeding lines didn't varied greatly but variation within family indicates good scope for selection. The superior plants in the resistant families viz., 12-23-30-1, 12-23-30-2, 12-23-249-10 and 12-23-249-12 can be selected for the evaluation in further generation to get bacterial wilt resistant superior varieties in green round segment.

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