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Neelambika
Department of Vegetable
Science, University of
Horticulture Sciences, Bagalkot,
Karnataka, India

HB Lingaiah
Department of Vegetable
Science, University of
Horticulture Sciences, Bagalkot,
Karnataka, India

Mangesh
Department of Vegetable
Science, University of
Horticulture Sciences, Bagalkot,
Karnataka, India

Anand G Patil
Department of Vegetable
Science, University of
Horticulture Sciences, Bagalkot,
Karnataka, India

Correspondence
Neelambika
Department of Vegetable
Science, University of
Horticulture Sciences, Bagalkot,
Karnataka, India

Interfamily variability studies in green long pre-breeding lines of brinjal (*Solanum melongena* L.)

Neelambika, HB Lingaiah, Mangesh and Anand G Patil

Abstract

An investigation was carried out with ten pre-breeding lines of F₄ generation of green long brinjal derived from the cross Green Long x IIHR-3 to study the interfamily variability for nine different growth and yield parameters. High PCV and GCV estimates was found only for average fruit weight in interfamily variability studies indicating there is lack of high variability between the average performance of segregating lines for these characters. Low PCV and GCV were recorded for plant height, days to 50 percent flowering, fruit length and fruit breadth. Moderate PCV and GCV was noticed for number of branches per plant, days to first flowering, number of fruits per plant and yield per plant. But the narrow difference between PCV and GCV indicated low environment effect. 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 high GAM was recorded for other traits like average fruit weight and number of fruits per plant. Estimation of percent bacterial wilt incidence in each family revealed that five lines viz., 12-36-170-11, 12-36-46-3, 12-36-170-9, 12-36-170-19 and 12-36-46-6 were found to be resistant.

Keywords: Interfamily variability, heritability, genetic advance

Introduction

Brinjal (*Solanum melongena* L.) is the most popular and widely cultivated vegetable crop in the central, southern and southeast Asia and in some African countries (Karak *et al.* 2012). It belongs to the family Solanaceae having chromosome number 2n=24. Major producing states are Orissa, Bihar, Karnataka, West Bengal, Andhra Pradesh, Maharashtra and Uttar Pradesh. Large numbers of cultivars are grown depending upon the consumer's preference for the colour, size, shape and along with better yield throughout the country. Consumer's preference varies with region to region for shape and colour. In southern Karnataka, people prefer long types whereas, in northern Karnataka region people prefer round shaped fruits. There is larger variation existing in brinjal cultivars for characters like growth habit, spiny-ness, flower colour, fruit shape, fruit colour and also response to different abiotic and biotic stresses. Among the diseases of eggplant, bacterial wilt is one of the most devastating disease, which severely hampers its cultivation. So development of improved varieties in green long segment of brinjal along with bacterial wilt resistance plays a significant role in increasing the productivity. Selection based only on phenotype is not always effective, as the trait is likely to degenerate in the advanced generations. However, some of the criteria like heritability and genetic advance of yield and its related characters do help in effective selection. High genetic advance coupled with high heritability is an indication of more additive gene action (Panse and Khargonkar, 1957) [8]. Hence, knowledge of genetic advance along with heritability is most useful. Therefore high heritability accompanied with high genetic advance gives an indication of more additive gene action, indicating the population under selection is more effective. 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 F₄ generation of Green Long x IIHR-3 for different horticultural traits.

Material and Methods

Arunkumar *et al.* (2013) [3] reported the cross Green Long x IIHR-3 as superior hybrid having higher yield and bacterial wilt resistance with all the acceptable fruit qualities. Further F₂, F₃ families were evaluated and selected ten F₃:F₄ families. In the present investigation ten F₄ families viz., 12-36-46-3, 12-36-46-6, 12-36-164-1, 12-36-164-7, 12-36-164-10, 12-36-164-11, 12-36-164-14, 12-36-170-9, 12-36-170-11 and 12-36-170-19 from the cross Green Long X IIHR-3 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* (Smith) as prescribed by Kelman (1954) [6]. Before inoculation, the roots were slightly damaged by inserting a sharp knife 1.0cm away from the stem then inoculum was drenched around the root zone on 21st day of sowing. Then during transplanting also seedlings were dipped in the bacterial suspension and planted in the main field. These populations were maintained by following package of practices (Anon., 2014) [2]. The observations on different quantitative and qualitative traits were recorded on

every plant in each family. Mean performance of each F₄ 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 percent of mean and expected mean in next generation were estimated.

Percent bacterial wilt incidence in each F₄ 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 (1952).

Disease reaction and Percent wilt incidence

Disease reaction	Percent 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 F₄ families of Green Long x IIHR-3 are represented in the Table 1. The characters like yield per plant, plant height and average fruit weight shown considerable range of variation between the lines. Whereas, narrow range of variation was found between the F₄ families for the

parameters like number of branches per plant, days to first flowering, days to 50 percent flowering, fruit length, fruit breadth and number of fruits per plant. 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 percent flowering, fruit weight, fruit length, fruit breadth, number of fruits per plant and yield per plant which might be due to the interaction between the genotypes and the environment.

Table 1: Genetic parameters of interfamily variability for different characters of F_{3:4} populations of Green Long x IIHR-3

Characters	Grand mean ± SD	Range		PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	EMNG
		Min.	Max.						
Plant height (cm)	47.38±6.98	40.17	51.63	7.76	5.18	44.58	3.38	7.13	50.76
No. of branches/plant	6.62±1.84	4.00	7.71	10.20	6.85	45.16	0.63	9.49	7.25
Days to first flowering	35.60±6.20	30.00	41.00	10.85	9.52	76.90	6.12	17.20	41.72
Days to 50% flowering	48.10±2.80	45.00	53.00	5.84	5.04	74.61	4.31	8.97	52.41
Average Fruit weight (g)	38.64±10.51	30.93	59.38	22.64	22.05	94.89	17.10	44.26	55.74
Fruit length (cm)	10.78±2.35	10.23	11.48	4.14	0.64	2.41	0.02	0.21	10.80
Fruit breadth (cm)	1.56±0.41	1.29	1.77	9.61	5.76	35.92	0.11	7.11	1.67
No. of fruits/plant	9.59±9.74	6.64	13.07	19.03	18.30	92.50	3.48	36.26	13.07
Yield/ plant (g)	327.66±207.6	274.14	405.18	15.15	14.58	92.66	94.76	28.92	422.42

*Mean values were used for statistical analysis.

PCV – Phenotypic co-efficient of variation

GCV – Genotypic co-efficient of variation

h² – Broad sense heritability

GA – Genetic advance

GAM – Genetic advance as percent of mean

SD – Standard deviation

EMNG – Expected mean in next generation

This environment effect could be due to heterogeneity in soil fertility status between the blocks rather than within the block. PCV and GCV was low for the traits like plant height (7.76% and 5.18%), number of branches (10.20% and 6.85%), days to first flowering (10.85% and 9.52), fruit length (4.14% and 0.64%) and fruit breadth (9.61% and 5.76%) whereas, moderate level of PCV and GCV was obtained for number of fruits per plant (19.03% and 18.30%) and yield per plant (15.15% and 14.58%) and high level of PCV and GCV was obtained for average fruit weight (22.64% and 22.05%). The same results were obtained for plant height by Prabhu *et al.* (2009), Gavade and Ghadage. (2015) [5]. Low PCV and GCV for number of branches per plant were also reported by Prabhu *et al.* (2009) and Singh *et al.* (2014). The low PCV and GCV estimates for days to first flowering were supported

by the research findings of Mahaveer *et al.* (2006) and Naik *et al.* (2009) [7]. The low estimates of PCV and GCV for days to 50 percent flowering was in accordance to the result obtained by Naik *et al.* (2009) [7], Adesh *et al.* (2011) [1] and Vidya and Kumar (2015). Similar results were reported for fruit length, fruit breadth and number of fruits per plant by Prabhu *et al.* (2009). Fruit yield per plant both GCV and PCV were moderate which was in accordance with the research findings of Prabhu *et al.* (2008), Vidya and Kumar (2015) and Gavade and Ghadage (2015) [5] and high level of PCV and GCV was obtained for average fruit yield the same results were reported by Mahaveer *et al.* (2006), Adesh *et al.* (2011) [1], Balaji *et al.* (2013) and Singh *et al.* (2014). The moderate levels of PCV and GCV for these characters in segregating population indicate good scope for improvement in these traits.

High heritability was observed for all the characters except fruit length (2.41%) and similar results were obtained by Mahaveer *et al.* (2006), Prabhu *et al.* (2009), Reshmika *et al.* (2015)^[9], Gavade and Ghadage (2015)^[5] and low heritability for fruit length was also reported by Adesh *et al.* (2011)^[11] and Singh *et al.* (2014) it may be due to the use of average performance of each lines for the analysis of interplant variability. Low GA was observed for the traits like plant height (3.38), number of branches (0.63), days to first flowering (6.12), days to 50% flowering (4.13), fruit length (0.02), fruit breadth (0.11) and number of fruits per plant (3.48) similar results were obtained for plant height and days to first flowering by Gavade and Ghadage (2015)^[5], for days to 50 percent flowering by Madhavi *et al.*, (2015), fruit length by Adesh *et al.* (2011)^[11] and number of branches per plant by Adesh *et al.* (2011)^[11] and Reshmika *et al.* (2015)^[9] while moderate GA was noticed for average fruit weight (17.10). This was also observed in the study conducted by Reshmika *et al.* (2015)^[9] and high GA was found for yield per plant (94.76) same findings is reported by Chaudhary and Kumar (2014)^[4]. Low GAM was observed for plant height, number of branches, fruit length and fruit breadth whereas moderate for days to first flowering and high GAM for average fruit weight, number of fruits per plant and yield per plant this was

in agreement with Naik *et al.* (2009)^[7] and Chaudhary and Kumar (2014)^[4] for average fruit weight, number of fruits per plant and yield per plant.

The high heritability indicates that characters were less influenced by the environment. High heritability with low genetic advance reveals the major role of non-additive gene action in the transmission of the character. High heritability with moderate genetic advance over mean indicates high influence of favourable environment rather than the genotype, selection of such traits may not be effective and high heritability with high genetic advance shows the major role of additive gene action of those characters and would be improved through simple selection.

The bacterial wilt disease resistance reaction in ten F_{3:4} pre-breeding lines of the cross Green Long X IIHR-3 was evaluated along with parent, IIHR-3 and check Arka Anand. The present study revealed that the lines *viz.*, 12-36-46-3, 12-36-46-6, 12-36-164-1, 12-36-170-9, 12-36-170-11 and 12-36-170-19 were shown resistant reaction. The lines like 12-36-164-10, 12-36-164-11 and 12-36-164-14 were moderately resistance whereas the line 12-36-164-7 had shown moderately susceptible reaction (Table 2). The parent Green Long and check Arka Kusumakar were highly susceptible to this disease.

Table 2: Reactions of F_{3:4} pre-breeding lines of Green Long x IIHR-3, their parents and checks to *Ralstonia solanacearum* (Smith)

S. No.	Line number/ Parents / Checks	Percentage wilt	Reaction
1.	12-36-46-3	10.00	R
2.	12-36-46-6	20.00	R
3.	12-36-164-1	17.50	R
4.	12-36-164-7	46.66	MS
5.	12-36-164-10	30.00	MR
6.	12-36-164-11	27.50	MR
8.	12-36-164-14	27.50	MR
9.	12-36-170-9	17.50	R
10.	12-36-170-11	7.40	R
11.	12-36-170-19	12.50	R
12.	Green Long	90.28	HS
13.	IIHR-3	20.00	R
14.	Arka Anand	4.16	R
15.	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 F₄ families for six qualitative characters are presented in the Table 3.

Among 327 plants in F₄ segregating population of the cross Green Long X IIHR-3 the interfamily variability was estimated and the results revealed that 3.97 percent plants (13) were erect, 4.5 percent plants (15) were having spreading growth habit whereas, 91.43 percent plants (299) were having semispreading growth habit. About 95.41 percent of the plants (312) were nonspiny and 4.5 percent plants (15) were spiny in nature. 45.25 percent of the plants (148) beared purple colour flowers whereas, 54.74 percent plants (179) had white flower

and the fruit shape was long in 98.77 percent population (323) whereas 1.22 percent population (4) had oblong shaped fruits. The fruit colour was found to be green in 318 plants (97.24%), green with white stripes in 4 plants (1.23%), green with purple stripes in 4 plants (1.23%) and purple with green stripes in 1 plant (0.30%). Fruit bearing habit was found to be cluster in 326 plants (99.69%) and solitary in 1 plant (0.30%) (Table 3).

Table 3: Frequency distribution of F_{3:4} pre-breeding lines of the cross Green Long x IIHR-3 for six qualitative characters out of 327 plants

Growth habit	Spinyness	Flower colour	Fruit shape	Fruit colour	Fruit bearing habit
Erect '13' Spreading '15' Semi spreading '299'	Non spiny '312' Spiny '15'	Purple '148' White '179'	Long '323' Oblong '4'	Green '318' Green with white stripes '4' Green with purple stripes '4' Purple with green stripes '1'	Clustering '326' Solitary '1'

Conclusion

The pre-breeding lines under evaluation were shown very narrow range of variability for almost all characters. Low to moderate PCV and GCV values for all characters except for

average fruit weight, high heritability and low genetic advance for almost all the characters except for fruit length which had low heritability and low GA. The direct selection of superior plants across different pre-breeding lines may be

effective for average fruit weight, number of fruits per plant and fruit yield per plant as these characters having high heritability estimates with high GAM. 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., 12-36-170-11, 12-36-46-3, 12-36-170-9, 12-36-170-19 and 12-36-46-6 can be selected for the evaluation in further generation to get bacterial wilt resistant superior varieties in green long segment.

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