The Pharma Innovation

Manoj Kumar
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Singh TH
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Reddy KM
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Lakshmana Reddy DC
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Sadashiva AT
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Samuel DK
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Corresponding Author:
Manoj Kumar
Division of Vegetable Crops, Plant Biotechnology and Plant Pathology, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India

Generation mean analysis of important yield traits in eggplant (*Solanum melongena* L.)

Manoj Kumar, Singh TH, Reddy KM, Lakshmana Reddy DC, Sadashiva AT and Samuel DK

Abstract
Generation mean analysis using basic populations like P1, P2, F$_1$, F$_2$, BC1 and BC2 is an efficient method to understand the nature of gene effects involved in the expression of a character in interacting and non-interacting crosses. The parents P1 (IIHR-711) and P2 (IIHR-127) were inter-mated to produce F$_1$ and these F$_1$s were forwarded to obtain segregating populations namely F$_2$, BC1 and BC2 to study the inheritance pattern of the characters. The crosses showed significant results for the only one scale (C) for fruit length and for average fruit weight scale A and C were significant indicating the inadequacy of simple additive-dominance model to estimate the gene effects and presence of epistasis. Whereas, non-significant results in scaling tests (A, B, C and D) for the traits plant height and average fruit weight, indicate that particular gene effect is present in the mode of inheritance of the traits i.e. additive and dominance effect of genes are sufficient to explain the mode of inheritance of character studied. The non-significant results in scaling tests (A, B, C and D) for the traits plant height and average fruit weight, indicate that particular gene effect is present in the mode of inheritance of the traits i.e. additive and dominance effect of genes are sufficient to explain the mode of inheritance of character studied. Therefore, single seed descent method and subsequent pedigree selection would be appropriate breeding method.

Keywords: Generation, eggplant, *Solanum melongena* L.

Introduction
Eggplant is an important vegetable crop and grown throughout the year in tropical and subtropical region of the country and world. Brinjal *(Solanum melongena* L. 2n = 24) is the fifth most economically important non-tuberous crop of solanaceous (nightshade) family and originated from India (Frary *et al*., 2007) [2]. The occurrence of many mineral salts and phenolic compounds in fair amount plays an important role in human nutrition (Raigon *et al*., 2008) [8]. Due to availability of larger diversity in Indian subcontinent, there is a vast opportunity for genetic improvement in this crop. Therefore, knowledge of genetic system and its relation with other parameters contributing towards yield and its related traits is must before formulation of suitable strategies to breed varieties with specific requirements. Hence, the current experiment comprises genotypes contrasting for yield and its related traits to study the components of genetic variation using generation mean analysis (GMA) (Cavalli, 1952; Mather, 1949) [1, 6]. Generation mean analysis using basic populations like P1, P2, F$_1$, F$_2$, BC1 and BC2 is an efficient method to understand the nature of gene effects involved in the expression of a character in interacting and non-interacting crosses.

Materials and Methods
The segregation populations like F$_2$, BC1 and BC2 were developed by using the cross of IIHR-711 and IIHR-127. The line IIHR-711 was used as female parent (Recipient) with good fruit quality and IIHR-127 was used as male parent (Donor) due to its high resistance against bacterial wilt with high yield potential. The parents P1 (IIHR-711) and P2 (IIHR-127) were inter-mated to produce F$_1$ and these F$_1$s were forwarded to obtain segregating populations namely F$_2$, BC1 and BC2 to study the inheritance pattern of the characters. These segregatin g populations (F$_2$ - 224), (BC1- 150) and (BC2 - 150) were planted in three replications in randomized complete block design with non- segregation populations (P1- 30), (P2- 30) and (F$_1$ - 30) for evaluation purpose at the vegetable research block of Division of Vegetable Crops, ICAR- Indian Institute of Horticultural Research, Bengaluru.

The data of characters like plant height, fruit length, fruit diameter and average fruit weight were recorded and subjected to Mather scale; joint scaling test and generation mean analysis to work out the inheritance pattern of the traits. The data was subjected to A, B, C and D scaling tests developed by Mather (1949) and estimation of various genetic various genetic components was done by adopting six parameter model as suggested by Hayman (1958) [3] and Jinks and Jones (1958) [4].

Result and discussion
The knowledge of gene action, interaction and inheritance pattern of the traits plays important role for planning the appropriate breeding strategy during crop improvement program.

Means and variances of six generations for the cross IIHR-711 X IIHR-127
The analysed data of six generation *viz.,* P1, P2, F_1, F_2, BC1 and BC2 of the cross IIHR-711 x IIHR-127 which includes mean values along with standard error and variance are mentioned in Table 1.
1. **Plant Height (cm):** The results showed that, F_1 having

highest mean value for plant height (104.59 cm) followed by BC2 (92.34 cm) while lowest was recorded in P2 populations. The highest value for variance was recorded in F_2 population (189.00) whereas lowest was recorded in P2 (37.11).
2. **Fruit length (cm):** Among all generations, P2 was having maximum fruit length (17.56 cm) whereas minimum was observed in P1 (12.78 cm). The segregating generations (F_2, BC1 and BC2) were having the plant height between the range of both P1 and P2.
3. **Fruit Diameter (cm):** Among the six generations, maximum fruit diameter was recorded in parent P1 with the value of 6.87 cm whereas lowest was recorded in P2 (4.20 cm). The population F_1, F_2, BC1 and BC2 showed increased trend of mean value and variance as compare to P1. The highest variance reported in BC2 (1.20) while lowest was in P2 (0.16).
4. **Average fruit weight (cm):** F_1 showed the highest average fruit weight among six generation with mean value of 226.54 g. Among parents, IIHR-711 was having maximum fruit weight of 211.50 g while IIHR-127 showed minimum value for this trait which was lowest among all six generations.

Table 1: Mean and variances of six generation for yield attributing traits in IIHR-711 x IIHR-127

Generations	Plant Height (cm)		Fruit length (cm)		Fruit Diameter (cm)		Average Fruit weight (g)	
	Mean ±SE	Variance	Mean ±SE	Variance	Mean ±SE	Variance	Mean ±SE	Variance
P1	79.79±3.88	75.17	12.78±0.75	2.81	6.87±0.38	0.72	211.50±9.77	477.38
P2	84.52±2.72	37.11	17.56±1.52	11.58	4.20±0.18	0.16	63.28±5.74	164.74
F_1	104.59±3.36	56.44	16.19±0.93	4.32	6.71±0.24	0.29	226.54±5.60	156.96
F_2	89.10±3.63	197.56	14.25±0.68	7.02	6.28±0.27	1.10	152.77±12.35	2,287.26
BC1	86.25±5.20	189.00	14.39±0.85	5.17	6.44±0.40	1.12	192.31±10.32	745.22
BC2	92.34±3.97	110.16	14.96±0.95	6.29	5.35±0.41	1.20	128.56±21.29	3,173.91

Scaling test for yield related traits
Table 2 contains the results of estimates of scaling tests for yield attributing traits in brief. The crosses showed significant results for the only one scale (C) for fruit length and for average fruit weight scale A and C were significant indicating the inadequacy of simple additive-dominance model to estimate the gene effects and presence of epistasis. The similar results were obtained by Vaghasia *et al.* (2000) [9] and Patil *et al.* (2000) [7] in brinjal. Whereas, non-significant results in scaling tests (A, B, C and D) for the traits plant

height and average fruit weight, indicate that particular gene effect is present in the mode of inheritance of the traits i.e. additive and dominance effect of genes are sufficient to explain the mode of inheritance of character studied. There is no epistasis effect present in the cross i.e. absence of inter-allelic interaction. These crosses referred as non-interacting crosses. So, three parameter model is sufficient to explain the gene action present in all these traits for the particular trait. These finding were at par with Kamini *et al.* (2008) [5].

Table 2: Estimates of scaling tests for yield attributing traits characters in in eggplant for the cross IIHR-711 x IIHR-127

Sl. No.	Traits	A	B	C	D
1	Plant Height (cm)	11.88±6.69	-4.43±5.21	17.10±9.63	-0.39±5.64
2	Fruit length (cm)	-0.20±1.21	-3.82±1.50	-5.74*±2.15	-0.86±1.08
3	Fruit Diameter (cm)	-0.71±0.53	-0.22±0.51	0.62±0.73	0.78±0.46
4	Average Fruit weight (g)	-53.42**±13.57	-32.70±25.02	-116.77**±29.96	-15.33±19.75

**p= 0.01, *p = 0.05

All the estimates of additive and dominance parameters for plant height were non-significant except m̂ (143.34) which indicates that this trait is quantitatively inherited and having good genetic diversity. While, the trait fruit diameter having good significant value for the gene component m̂ in positive direction indicates this trait is quantitatively inherited i.e. good genetic diversity and ĥ in negative direction indicates alleles responsible for less value of trait, where dominant over alleles controlling high values. (Table 3).

Table 3: Estimates of additive and dominance parameters for yield attributing characters in eggplant for the cross IIHR-711 x IIHR-127

Traits	(m̂)	(d̂)	(ĥ)
Plant Height (cm)	143.34**±10.91	-2.36±1.37	7.70±28.54
Fruit Diameter (cm)	8.83**±0.87	1.34**±0.12	-2.88±2.39

**p= 0.01, *p = 0.05

For the trait fruit length, among main crosses the significant result was found only for mean effect (m̂) with positive

magnitude of 14.25 indicates the trait is quantitatively inherited i.e. existence of genetic diversity. Whereas in case of interacting crosses, only additive x dominance (ĵ) was significant while, other two were non-significant. The components dominance effect (ĥ) and dominance x dominance (Î) having the similar sign indicates the presence of complementary epistasis. On the other side, the significant results for average fruit weight were observed for all main crosses as well as interacting crosses except additive x additive which was non-significant in six parameter model. The results showed the significant values of m̂ (155.77) with positive sign indicates that this trait is quantitatively inherited

i.e. existence of genetic diversity. The significant values of d̂ (28.35) with positive magnitude were reported which indicate the presence of additive effect; hence selection of this trait in early generation is not possible. The ĥ component was also found significant and positive value indicates the presence of good dominance effect (119.81). The components of interacting crosses *viz.*, additive x dominance (-10.36) and dominance x dominance (55.47) were significant while additive x additive (30.65) was non-significant. The components dominance effect (ĥ) and dominance x dominance (Î) having the similar sign indicates the presence of complementary epistasis (Table 4).

Table 4: Estimates of additive, dominance and non-allelic genetic parameters for yield attributing characters in eggplant for a cross between IIHR-711 x IIHR-127

Traits	(m̂)	(d̂)	(ĥ)	(î)	(ĵ)	(Î)	Type of epistasis
Fruit length (cm)	14.25**±0.39	-0.57±0.74	2.74±2.28	1.72±2.16	1.81*±0.89	2.30±3.65	Complementary
Average Fruit weight (g)	152.77**±7.13	63.75**±13.66	119.81**±39.76	30.65±39.49	-10.36*±14.05	*55.47±63.32	Complementary

**p= 0.01, *p = 0.05

As the scaling tests were not significant for any of the yield attributing trait (plant height and fruit diameter) indicating that particular gene effect is present in the mode of inheritance of the traits i.e. additive and dominance effect of genes are sufficient to explain the mode of inheritance of character studied. There is no epistasis effect present in the cross i.e. absence of inter-allelic interaction. These crosses known as non-interacting crosses. So, three parameter model is sufficient to explain the gene action present in all these traits for the particular trait. Therefore, following paragraphs reveals the probable gene effects occurring for the respected traits in cross IIHR-711 x IIHR-127 along with their role in selection of breeding methods for the particular trait improvement.

The results showed that all the estimates of additive and dominance parameters for plant height were non-significant except m̂ (143.34) which indicates that these traits are quantitatively inherited and having good genetic diversity. Whereas, for fruit diameter mean effect (m̂) as well as additive effects (d̂) were significant and positive in magnitude implies selection in early generation is not possible. Therefore, single seed descent method and subsequent pedigree selection would be appropriate breeding method. While, the significant values of gene component ĥ with positive magnitude indicates presence of dominance gene effect for these traits. So, the most effective method in genetic improvement of these traits would be heterosis breeding or recurrent selection for SCA.

The crosses showed significant results for the only one scale (C) for fruit length, it indicates the presence of dominance x dominance effects and for average fruit weight scale A and C were significant indicating the inadequacy of simple additive-dominance model to estimate the gene effects and presence of epistasis. Hence, simple six parameter model (m̂, d̂, ĥ, î, ĵ and Î) was applicable for detecting the interactions.

The significant values of m̂ with positive sign indicates that fruit length is quantitatively inherited i.e. existence of genetic diversity. The significant values of m̂ with positive sign indicate that average fruit weight was quantitatively inherited i.e. existence of genetic diversity. The significant values of d̂ with positive magnitude were reported which indicate the presence of additive effects; hence selection of this trait in early generation was not possible. Therefore, single seed

descent method and subsequent pedigree selection would be appropriate breeding method.

Conclusion
The non-significant results in scaling tests (A, B, C and D) for the traits plant height and average fruit weight, indicate that particular gene effect is present in the mode of inheritance of the traits i.e. additive and dominance effect of genes are sufficient to explain the mode of inheritance of character studied. Therefore, single seed descent method and subsequent pedigree selection would be appropriate breeding method. On the other side, the significant results for average fruit weight were observed for all main crosses as well as interacting crosses except additive x additive which was non-significant with significant values of m̂ indicates that this trait is quantitatively inherited i.e. existence of genetic diversity. The estimation of different types of gene effects played a key for pertaining the knowledge of gene action which was useful for analysing genetic architecture of different characters.

References
1. Cavalli LL. An analysis of linkage in quantitative inheritance. In: Quantitative Inheritance, E. C. Reeve and C. M. Waddington (eds.) HMSO, London, 1952, 135-144.
2. Frary A, Doganlar S, Daunay MC. Eggplant, in Vegetables SE - 9, Genome Mapping and Molecular Breeding in Plants, ed C. Kole (Berlin: Springer), 2007, 287-313. DOI: 10.1007/978-3-540-34536-7_9.
3. Hayman BI. Separation of epistatic from additive and dominance variation in generation means. Heridity. 1958;12:371-390.
4. Jinks JL, Jones RM. Estimation of components of heterosis. Genetics. 1958;43:223-34.
5. Kamini JM, Monpara BA, Dhameliya HR. Genetic analysis for the yield attributing traits in brinjal (*Solanum*

melongena L.), inheritance and association. Natnl. J Pl. Improv. 2008;10(2):88-91.

6. Mather K. Biometrical Genetics. Dover Publications, Inc., New York, 1949.

7. Patil SD, Warade SD, Badgujar CD, Chaudhary SM. Generation mean analysis in Brinjal. J Maharashtra. Agric. Uni. 2000;25:37.

8. Raigon MD, Prohens J, Munoz-Falcon J, Nuez F. Comparison of eggplant landraces and commercial varieties for fruit content of phenolics, minerals, dry matter and protein. Journal of Food Composition and Analysis. 2008;21:370-376.

9. Vaghasiya MH, Kathiria KB, Bhalala MK, Doshi KM. Gene action for yield and its components in two crosses of brinjal (*S. melongena* L.). Indian J Genet. 2000;60:127.