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Interfamily variability studies in F_{2:3} population of tomato (*Solanum lycopersicum* L.)

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Abstract

An experiment was carried out with seventeen F_{2:3} families of tomato derived from the cross IIHR 2201 x C-13-1-2-1 to study the interfamily variability for different growth, yield and quality parameters. None of the characters had shown high estimates of PCV and GCV. Which revealed that lack of variability between the average performance of segregating families for these characters. Low estimates of PCV and GCV were recorded for plant height, days to first flowering, average fruit weight, fruit length, fruit width, pericarp thickness, number of locules per fruit and total soluble solids (TSS). Moderate level of PCV and GCV were observed for number of fruits per plant showing the presence of moderate variability for number of fruits per plant between the families. This shows the selection of families is in positive direction. The magnitude of difference between the PCV and GCV was more for all the parameters, this shows the influence of environmental factors on the expression of these traits. Moderate to low heritability coupled with low GAM was observed for all the traits, indicating non additive gene action for the expression of these traits.

Keywords: Genetic variability, GCV, PCV, heritability and genetic advance

Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most popular vegetable widely grown in India. It belongs to the family Solanaceae and having a diploid chromosome number of 24. Tomato has its origin in Peru, Equador and Bolivia. The most likely ancestor of tomato is the wild cherry tomato, *Solanum lycopersicum* var *cerasiformae*. Fruits are rich source of vitamin A, B, C and antioxidants, they are consumed in various forms; raw, cooked and also in processed forms like puree, paste, sauces, ketchup etc. Tomato is a herbaceous, day neutral and self pollinated crop, but cross pollination occurs to an extent of five per cent due to exerted stigma at high temperature. It is a warm season crop reasonably resistant to heat, drought and it can be grown under a wide range of soil and climatic conditions.

It's adaptation to fit many diverse uses and environments is a reflection of the great wealth of genetic variability existing in the genus *Solanum*, which can be exploited in applied breeding programs. Systematic study and evaluation of tomato germplasm is of great importance for current and future agronomic and genetic improvement of the crop.

The entire success of plant breeding programme mainly depends upon the magnitude and extent of variability present in the germplasm. Variability is nothing but amount of variation present in the germplasm at genotypic or phenotypic level. It is pre-requisite in any breeding programme for effective selection of plants or particular genotype. Adequate variability present in the early segregating generation provides an opportunity for genetic improvement through selection. Thus the current study deals with evaluating the F_{2:3} families of IIHR 2201 x C-13-1-2-1 for growth, yield and quality attributes.

Material and methods

Sureshkumar *et al.* 2015^[11], reported the cross IIHR 2201 x C-13-1-2-1 as a superior hybrid having higher yield and tomato leaf curl disease resistance with all acceptable fruit qualities. Further F₂ generation were evaluated and selected seventeen F_{2:3} families. In the present investigation seventeen F_{2:3} families viz., 18, 29, 33, 35, 43, 64, 81, 88, 89, 133, 134, 144, 158, 224, 248, 253, and 261 of IIHR 2201 x C-13-1-2-1 which were raised at the research block of department of Vegetable Science, College of Horticulture, Bengaluru during 2017. 30 days old healthy seedlings of seventeen F_{2:3} families of tomato derived from the cross IIHR 2201 x

C-13-1-2-1 along with the parents IIHR 2201, C-13-1-2-1 and checks Arka Vikas, Arka Rakshak were transplanted in paired row system by following a spacing of 90 x 60cm. In each family fourty plants were maintained, observations were recorded from each individual plant for all the qualitative and quantitative parameters. The genotypic and phenotypic

coefficients of variation were calculated using the formula of Allard (1960) [2]. Heritability in broad sense was estimated according to the method of Hanson *et al* (1956) [3]. Genetic advance and genetic advance as per cent mean was calculated by the formula used by Johnson *et al* (1955) [4].

Table 1: Genetic parameters of interfamilial variability for different characters of F_{2:3} populations of the cross IIHR 2201 x C-13-1-2-1

Characters	Grand mean± SD	Range		PCV	GCV	h ² (%)	GA	GAM (%)	EMNG
		Min.	Max.						
Plant height (cm)	69.73±4.57	61.30	75.70	6.55	2.01	9.43	0.89	1.27	70.62
No. of branches/plant	5.33±0.67	4.33	7.03	12.61	5.97	22.43	0.31	5.83	5.64
Days to first flowering	29.38±0.71	27.98	30.45	2.40	1.07	19.80	0.29	0.98	29.67
No. of fruits/plant	34.70± 5.76	25.18	49.18	16.59	12.09	53.10	6.30	18.15	41.00
Average fruit weight (g)	66.89±3.59	60.27	73.38	5.37	1.20	5.02	0.37	0.55	67.26
Fruit Yield/plant (Kg)	2.22±0.39	1.55	3.02	17.63	3.37	3.66	0.03	1.33	2.25
Fruit length (cm)	4.58±0.22	4.14	5.03	4.79	1.97	16.98	0.08	1.68	4.66
Fruit width (cm)	4.48±0.19	4.09	4.85	4.34	0.68	2.48	0.01	0.22	4.49
Fruit firmness(Kg/cm ²)	1.54±0.19	1.22	2.07	12.69	5.91	21.66	0.09	5.66	1.63
Pericarp thickness(mm)	5.05±0.25	4.35	5.39	5.01	3.37	45.26	0.24	4.67	5.28
Number of locules per fruit	3.18±0.31	2.71	3.80	9.86	5.28	28.72	0.19	5.84	3.36
TSS(⁰ Brix)	5.02±0.16	4.70	5.29	3.38	1.87	0.31	0.11	2.13	5.13

PCV – Phenotypic co-efficient of variation

h² – Broad sense heritability

GAM – Genetic advance as per cent of mean

EMNG – Expected mean in next generation

GCV – Genotypic co-efficient of variation

GA – Genetic advance

SD – Standard deviation

Results and discussion

The extent of variability with respect to different qualitative and quantitative characters in F₃ generation is measured in terms of mean performance, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, genetic advance as per cent mean and expected mean in next generation are given in table 1.

Average performance of each family for different qualitative and quantitative characters was considered for analysis of interfamilial variability studies of F_{2:3} families derived from IIHR 2201 x C-13-1-2-1. Analysis of interfamilial variability studies gave the information about the variation exist between the families. A narrow range of variation has been observed between the F_{2:3} families for plant height, days to first flowering, fruit length, fruit width, pericarp thickness, number of locules per fruit, total soluble solids, average fruit weight. It is mainly due to the consideration of mean values for analysis. The number of branches per plant, yield per plant and number of fruit per plant had shown considerable range of variation between the families. This shows the selection of families is in positive direction. The magnitude of PCV is higher than GCV for all the traits like plant height, number of branches per plant, days to first flowering, number of fruits per plant, fruit weight, yield per plant, fruit length, fruit width, firmness, number of locules per fruit and total soluble solids (TSS). Difference between PCV and GCV is more for almost all the traits except for days to first flowering. This result indicates that influence of environmental factors on the expression of these characters. Environmental effect mainly includes heterogeneity in fertility status of the soil between the blocks.

Low estimates of PCV and GCV is observed for the traits like plant height (6.55, 2.01) days to first flowering (2.40, 1.07), fruit weight (5.37, 1.20), fruit length (4.79, 1.97), fruit width (4.34, 0.68), pericarp thickness (5.01, 3.37), number of locules(9.86, 5.28), total soluble solids (3.38, 1.87), indicates less scope for improvement of these traits through selection between the families, similar results were reported for plant height by Suresh Kumar (2015) [11], for days to first flowering

Rai *et al.* (2016) [2], Ligade *et al.* (2017) [5], for fruit length Ahmad *et al.* (2016) [1], and for fruit width Rajolli *et al.* (2017) [10], for total soluble solids(TSS) Manna and Paul (2012) [6], Rajolli *et al.* (2017) [10]. Moderate level of PCV and low GCV is found for fruit firmness (12.69, 5.91), yield (17.63, 3.37) and number of branches per plants (12.61, 5.97) similar results were reported by Prashanth (2003) [8] for number of branches per plant. Moderate PCV and GCV was found for number of fruits per plant, similar to findings of Meena and Bahadur (2014) [7]. Low heritability coupled with low genetic advance was found for all the characters like plant height (9.43%, 0.89) number of branches per plant (22.43%, 0.31), days to first flowering (19.80, 0.29), fruit weight (5.02%, 0.37), yield of a plant (3.66%, 0.03), fruit length (16.98, 0.08), fruit width (2.48, 0.01), fruit firmness(21.66, 0.09), number of locules (28.72, 0.19) and total soluble solids(TSS) (0.31, 0.11), except for the character like number of fruits per plant (53.10%, 6.30) and pericarp thickness (45.26, 0.24) posses moderate heritability with low genetic advance, this indicates influence of non additive gene action and environmental factors on the expression of these traits, hence selection for these traits may not be effective. Low estimate of PCV and GCV, heritability and genetic advance for these characters may be due to use of average performance of each family for the analysis of interfamilial variability.

Conclusion

The F_{2:3} families under evaluation were shown very narrow range of variability, low to moderate PCV and GCV values, low to moderate heritability coupled with low genetic advance for all the characters. Number of fruits per plant had shown considerable range of variation. Average performance of different F_{2:3} families didn't varied greatly but variation within the family indicates good scope for selection.

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