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Short communication

Genetic divergence in tomato grown in subtropical mid-hills of Meghalaya

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ABSTRACT

Genetic divergence analysis was carried out in thirty tomato genotypes using Mahalonabis D^2 statistics. These genotypes were grouped into five clusters based on nineteen characters. Maximum divergence was recorded between clusters III and IV followed by clusters IV and V. Genotype MT-4 (Oval big) of cluster III was found to be best for yield and related traits, like number of primary branches, fruit length, diameter, weight and yield per plant. Similarly, BT-10 of cluster IV was suitable for quality traits, like TSS, ascorbic acid, juice, β-carotene and lycopene content. Genotypes of cluster III and IV (MT-4, Oval Big and BT-10) can be used for the development of hybrid/variety having higher yield and better quality.

Key words: Tomato, genetic divergence, quantitative and qualitative characters.

Tomato (*Solanum lycopersicon*) is the second most important and popular vegetable crop after potato in terms of world vegetable production. It belongs to the family Solanaceae and is considered a native of Peruvian or Mexican region. It is grown world-wide both for its fresh and processed products. It is an important protective food because of its special nutritive value as it contains abundant and well balanced nutrition consisting of minerals (potassium, magnesium, calcium, iron, zinc, etc.), vitamins (A, B1, B2, C, E, etc.), dietary fibre, citric acid, etc. In addition, the red pigment of the lycopene, which tomato fruit contains in plenty, has recently attracted interest, because of its high antioxidant property.

Although tomato is a self-pollinated crop, there is genetic diversity not only in the morphological features but also in the quality attributes as reported by Abushita *et al*. (1). An improvement in yield and quality in tomato is mostly achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. The success of hybridization programme depends upon selection of suitable parents of diverse origin. Therefore, 30 tomato genotypes including advance lines were evaluated in a randomized block design with three replications at Horticultural Farm of ICAR Research Complex for NEH Region, Umiam Meghalaya for two seasons. All recommended agro-techniques were followed to raise a healthy crop. Five plants were selected at random in each plot to record the observations on 19 yield and quality related traits. Mahalanobis (4) generalized distance (D^2) was used to determine the degree of divergence and the genotypes were grouped into clusters following Tocher's method (Rao, 6). The data analysis was carried out using SPAR-1 (Statistical Package for Agricultural Data Analysis) software of Indian Agricultural Statistical Research Institute, New Delhi.

Mahalanobis D^2 statistics helped in grouping 30 tomato genotypes of into five clusters (Table 1). Cluster I had 26 genotypes, while, cluster II, III, IV and V were monogenotypic. The intra- and inter-cluster distances indicated that cluster I recorded maximum intra cluster distance of 40.67, whereas, clusters II, III, IV and V had zero intra-cluster distance because those were solitary clusters. The maximum inter-cluster D^2 values were obtained between clusters III and IV (159.23) followed by clusters IV and V (139.32). The smallest inter-cluster distance was observed between II and IV (44.03).

Among the 19 characters, average fruit weight contributed maximum (60%) towards genetic divergence followed by juice content (27.82%), lycopene (3.68%), β-carotene (2.76%), acidity (1.84%) and ascorbic acid (1.38%). Pericarp thickness and number of fruits per plant contributed 0.69% of divergence each. Days to 50% flowering, plant height and fruit length contributed 0.23% each towards genetic divergence. Remaining eight characters did not show any contribution towards genetic divergence. Ara *et al.* (2) also reported the maximum contribution of the traits like, fruit yield/plant, fruit size, fruit weight and number of primary branches towards the genetic divergence in tomato.

The results on cluster mean analysis are presented in Table 2. In case of plant height, maximum value (85.26 cm) was noticed in cluster IV and minimum (45.44 cm) in cluster V. Maximum mean values for

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Table 1. Cluster composition and average intra- (bold) and inter-cluster distance values.

Cluster	No. of genotype(s)	Compositions/ Genotype(s)	Average intra- and inter-cluster distance values				
			I	II	III	IV	V
I	26	MT-3 grooved green top, MT-11, MT-7 (1), KT-15, TLBRH-5, Floradade, MT-4 Long big, MT-1 round grooved big, Sel-2, MT-10, MT-4 round grooved green top, LE-2, BWT-3, Sel-3, Shakti, MT-7 (2), KT-10, BT-10, BT-1 long oval, TLBRH-6, Arka Sherestha, MT-6, MT-9, MT-2 big, MT-3 round grooved and Sel-1	**40.67**	62.05	89.65	84.58	78.99
II	1	Cherry tomato cv. Arunachal		**00.00**	138.56	44.03	106.20
III	1	MT-4, Oval big			**00.00**	159.23	85.99
IV	1	BT-10				**00.00**	139.32
V	1	MT-5					00.00

Tocher's cut-off value 3430.57

Table 2. Cluster mean values of characters in different tomato genotypes.

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
	Plant height (cm)	No. of branches per plant	Days to 50% flowering	Days to 1st harvest	No. of flowers per cluster	Fruit length (mm)	Fruit dia. (mm)	Av. fruit weight (g)	Locules per fruit	No. of fruits per cluster	No. of fruits per plant	Yield/ plant (kg)	Pericarp thickness (mm)	TSS. (°Brix)	Ascorbic acid (mg)	Acidity (%)	Juice (%)	β−carotene (mg/g)	Lycopene (mg/g)
I	61.26	5.34	37.31	77.58	9.70	46.12	51.70	68.21	4.44	4.44	31.48	1.08	5.19	5.11	17.32	1.08	63.59	3.00	77.58
II	75.01	6.22	34.00	82.67	9.40	26.38	28.18	20.35	3.00	6.53	67.78	0.14	2.64	4.77	14.71	1.02	64.56	3.73	82.67
III	73.21	5.52	36.67	76.00	8.87	55.27	56.74	150.19	4.67	4.45	24.32	1.88	6.36	5.13	15.09	0.63	55.85	2.41	76.00
IV	85.26	5.08	31.67	73.33	11.81	27.88	22.65	7.30	2.00	6.45	83.41	0.26	2.68	5.50	24.64	1.62	75.58	5.55	73.33
V	45.44	2.78	27.00	58.00	6.62	34.39	44.80	92.36	5.00	0.37	18.45	1.97	3.74	2.57	11.18	0.23	37.56	1.73	58.00

number of primary branches per plant (6.22) was observed in cluster II. Minimum number of days to 50% flowering (27) and days to first harvesting of fruits (58) was noticed in cluster V. The mean value for number of flowers per cluster was maximum (11.81) in cluster IV. Mean value for number of fruits per plant was highest (83.41) in cluster IV. In case of yield per plant, cluster III exhibited maximum (1.88 kg) followed by cluster V (1.71 kg). Cluster III values recorded the highest mean value (6.36 mm) for pericarp thickness.

Cluster means in Table 2 reveals the best cluster for various characters. If a breeding programme is aimed at higher fruit yield with thick pericarp then genotype (MT-4 oblong) from cluster III can be selected as parent in hybridization programme as it showed highest mean yield per plant, fruit length, fruit diameter and average fruit weight. If a breeding programme is aimed at earliness, then genotype in cluster V (MT-5) showing least days to 50% flowering and days to first fruit harvest can be selected. Similarly, to improve quality parameters like TSS, ascorbic acid, juice percentage, β-carotene, and lycopene content then genotype in cluster IV (BT-10) can be utilized.

The selection of parents to be included in hybridization programme should be based on genetic distance. Parental lines selected from clusters III, IV, V and II may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama, 6). Such recommendations by which genotypes from the diverse cluster can be utilised as promising parents for hybridization programme to obtain high heterotic response and thus better segregants in tomato for industrial purpose was also reported by Mehta and Asati (5).

The above findings illustrated that, the smallest inter-cluster distance was observed between clusters II and IV (44.03) followed by cluster I and II (62.05). The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. Such analysis was meant to avoid selection of parents from genetically homogeneous clusters, and maintain a relatively broad genetic base. Moreover, genotype MT-4 Oval big of monogenotypic cluster III can be utilized in the development of hybrids/varieties for the yield and related traits like number of primary branches, fruit length, fruit diameter, average fruit weight and fruit yield per plant. Similarly, BT-10 of cluster IV can be utilized for quality traits, *viz.*, TSS, ascorbic acid, juice, β-carotene and lycopene content. These quality traits are important help in metabolite profiling of the germplasm (Lee *et al.*, 3).

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