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Genetic Diversity Analysis in Tomato *(Solanum lycopersicum)* Genotypes

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Abstract:

Genetic diversity among 18 tomato genotypes was worked out using Mahalanobis D^2 statistic. On the basis of genetic distance, the eighteen genotypes were grouped into 6 clusters. Out of the 18 genotypes cluster I and cluster III has the highest genotypes (4 each) followed by cluster II and cluster IV (3 each) and cluster V and cluster VI had 2 genotypes each. Inter cluster distance was observed to be highest between cluster V and cluster VI indicating that these two cluster were genetically diverse. Hence, the genotypes of cluster V and VI would be utilized in hybridization program to achieve greater variability in the segregating generations. Among the different characters studied yield per plot, TSS and vitamin C contributed maximum towards divergence.

Key words: Cluster, D^2 values, Genetic divergence, Tomato

Introduction:

Tomato is one of the most popular vegetable crops widely cultivated in India after Potato. It is universally treated as 'protective food' and provides almost all types of vitamins and minerals in fair amount. It is a very good appetizer and has many medicinal values. It is highly adaptive crop having the potential to grow all the year round in mild climatic condition and can be grown in the plains as well as in hill condition. In any crop, germplasm is a valuable source of base population and provides the scope for wider adaptability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregation generations (Maurya and Singh, 1977). Therefore, the present study was carried out to analyze the genetic diversity in tomato genotypes in order to select the potential parents for breeding program.

Materials and Methods:

The present investigation was carried out in the experimental farm of Nagaland University, School of Agricultural and Rural Development, Medziphema Campus, Nagaland during September, 2014 to March, 2015. The experiment was laid out in Randomized Block Design with 18 genotypes in 3 replication. All the seeds of eighteen genotypes were obtained from Indian Institute of Vegetables Research (IIVR) Varanasi (U.P).

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Recommended Standard agronomic practices and plant protection measures were undertaken. Observations were recorded on five randomly sampled plants in each replication on plant height, Number of leaves per plant, Number of branches per plant, Days to fruit ripening, Crop duration, Fruit length, Fruit diameter, No of fruits per Plant, Fresh wt of fruit/ Plant, Vitamin C, TSS and Yield per plot. The genetic divergence was estimated using Mahalanobis's D^2 statistics (Mahalanobis, 1936). All the genotypes were grouped into clusters on the basis of D^2 values, by using Tocher's method (Rao, 1952).

Results and Discussion:

Analysis of variance revealed significant variation among the 18 genotypes for all the characters. The genetic divergence was estimated by utilizing D^2 statistic proposed by Mahalanobis (1936). Using this technique, all the genotypes were group into 6 clusters. Out of the 18 genotypes cluster I and cluster III had the highest genotypes (4 each) followed by cluster II and cluster IV (3 each) and cluster V and cluster VI had 2 genotypes each (Table 1)

The inter cluster distance were greater than intra cluster distance revealing considerable amount of genetic diversity among the genotypes studied as shown in Table: 2. The inter cluster distance was observed to be highest between cluster V and cluster VI (816.50) followed by cluster I and cluster V (670.82) indicating that these two cluster were genetically diverse. Hence, the genotypes of cluster V and VI would be utilized in hybridization program to achieve greater variability in the segregating generations. Inter cluster distance was minimum between cluster I and cluster III (179.89) followed by cluster II and cluster IV(232.48) which suggest close proximity of genotypes of one cluster with those of the other cluster in respect of their genetic constitution. These results are in accordance with the findings of Reddy *et al*. (2013), Pedapati *et al*. (2014), Janaki *et al*. (2016).

The cluster mean shown in Table- 3 revealed that there is a considerable difference between the clusters for all the characters studied. Cluster I recorded highest cluster mean for plant height (84.66), number of leaves per plant (83.26), number of fruits per plant and yield per plot. Cluster II recorded highest cluster mean for days to fruit ripening (97) and crop duration (147.78) cluster IV recorded highest cluster mean for fruit diameter (5.29), fresh weight of fruits (83.79), vitamin C (48.61) and TSS (7.33). Cluster mean of fruit length (6.29) was recorded highest in cluster V.

The percent contributions by each character of the genotypes to total genetic divergence are presented in Table- 4. Among the different characters studied, yield per plot (53.59 %), TSS (15.03%) and vitamin C (11.11%) contributed maximum towards divergence.

Conclusion:

Based on genetic divergence studies it is concluded that the genotypes of cluster V i.e. 2014/TODVAR-4 and 2014/TODVAR-5 and cluster VI i.e. 2014/TODVAR-2 and H-86 (C) should be utilized in hybridization program to achieve greater variability in the segregating generations.

Table No. 1. Clustering pattern of 18 genotypes of tomato on the basis of genetic divergence

Cluster number	Number of genotypes	Genotypes
Cluster 1	4	2012/TODVAR-1 2012/TODVAR-2 2012/TODVAR-5 2012/TODVAR-6
Cluster 2	3	2012/TODVAR-3 2012/TODVAR-7 2013/TODVAR-3
Cluster 3	4	2012/TODVAR-4 2012/TODVAR-8 2013/TODVAR-2 2014/TODVAR-6
Cluster 4	3	2013/TODVAR-1 2013/TODVAR-4 2014/TODVAR-3,
Cluster 5	2	2014/TODVAR-4 2014/TODVAR-5
Cluster 6	2	2014/TODVAR-2 H-86 (C)

Table No. 2. Average inter and intra cluster between 18 tomato genotypes

Cluster number	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	249.39 **(15.79)**	403.09 **(20.08)**	179.89 **(13.41)**	473.39 **(21.76)**	670.82 **(25.90)**	300.43 **(17.33)**
Cluster 2		298.43 **(17.27)**	313.79 **(17.71)**	232.48 **(15.25)**	444.69 **(21.09)**	470.47 **(21.69)**
Cluster 3			145.66 **(12.07)**	379.96 **(19.49)**	481.93 **(21.95)**	242.20 **(15.56)**
Cluster 4				149.83 **(12.24)**	391.22 **(19.78)**	498.76 **(22.33)**
Cluster 5					228.38 **(15.11)**	816.50 **(28.57)**
Cluster 6						277.94 **(16.67)**

The values in parenthesis are square root of D^2 values

Table No. 3. Cluster wise mean value of twelve characters in tomato

Characters / Cluster	Plant height (cm)	No of leaves/ plant	No of branches/ Plant	Days to fruit ripening	Crop duration	Fruit length (cm)	Fruit diameter (cm)	No of fruits per Plant	Fresh wt of fruit/ Plant(g)	Vit C (mg/100g of fruit)	TSS (°Brix)	Yield/ Plot (kg)
Cluster 1	84.66	83.26	13.05	83.92	128.00	3.82	4.46	50.05	56.47	40.94	6.35	22.92
Cluster 2	71.33	57.29	10.97	97.00	147.78	4.72	4.42	38.57	61.82	43.04	6.53	18.80
Cluster 3	71.32	62.84	9.41	86.92	127.42	4.39	4.65	38.76	62.16	35.48	5.84	19.21
Cluster 4	77.80	53.81	8.91	89.56	144.67	4.32	5.29	28.66	83.79	48.61	7.33	16.94
Cluster 5	59.55	42.35	7.18	86.83	130.67	6.29	4.58	24.46	82.56	30.34	7.07	17.32
Cluster 6	66.47	67.00	10.90	91.00	124.50	4.17	5.17	30.39	65.88	48.48	5.05	15.49

Table No. 4. Contribution of different characters towards divergence in tomato

Characters	% Contribution
Plant height (cm)	1.31
No of leaves per plant	0.65
No of branches per plant	0.00
Days to fruit ripening	0.00
Crop duration	5.22
Fruit length (cm)	0.00
Fruit diameter (cm)	5.88
No of fruits per plant	4.57
Fresh weight of fruit (g)	2.61
Vitamin C (mg/100 g of fruit)	11.11
TSS (°Brix)	15.03
Yield per plot (kg)	53.59

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