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Genetic divergence studies in tomato (*Solanum lycopersicum* L.)

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Abstract
A study was conducted using twenty two genotypes of tomato under AICRP on Vegetable Crops, Department of Vegetable Science at Horticultural Research and Instructional Farm, IGKV, Raipur (C.G.) during 2016 - 2017. Genetic divergence analysis following Mahalanobis D^2 statistics revealed considerable genetic diversity among twenty two genotypes of tomato (*Solanum lycopersicum* L.) for all the eighteen quantitative characters. A wide genetic diversity was observed among the genotypes and was grouped into five clusters. Cluster I topped with maximum number of genotypes among cluster fanned, while maximum inter-cluster distance was observed between cluster I and II followed by cluster II and IV. Number of locules per fruit contributed maximum towards diversity followed by average fruit weight, fruit yield per plant. Hence, selection for divergent parents based on these cluster distance is recommended for getting good hybrids or segregants in tomato.

Keywords: Diversity, *Solanum lycopersicum* L., D^2 analysis, genotypes, yield

Introduction
Tomato (*Solannum lycopersicum* L.) is one of the most popular, widely grown and versatile vegetables grown in the world. Tomato is popular due to its nutritive and medicinal values. It is identified as an important horticultural crop with the highest commercial value (Nuez *et al.* 2004) [1]. Tomato is a tropical day neutral and mainly self-pollinated crop, but a certain percentage of cross-pollination also occurs. The crop is native to Central and South America (Vavilov, 1951) [2]. Globally, the area under tomato is around 4.8 million hectares with a production of 162.52 million tonnes, while in India; tomato is grown across all agro-ecological zones and occupies an area of about 801 thousand hectares with an annual production of 22.33 million tonnes, respectively (Anon., 2017) [4]. Tomato is universally treated as 'Protective Food' since it is very rich in minerals, vitamins, antioxidants, essential amino acids, sugars and dietary fibers which are important ingredients for culinary and table purpose, chutney, pickles, ketchup, soup, juice, puree etc. (Sekhar *et al.*, 2010) [5]. Fresh fruit of tomato are in great demand round the year throughout the country.
The effectiveness of techniques like Mahalanobis D^2 statistic to analyse the genetic diversity of populations has been proved useful for selection of genetically diverse parents. It is generally agreed that genetically diverse parents will show the maximum heterosis and offer the maximum chance of isolating transgressive segregants. The evaluation of germplasm is imperative, in order to understand the genetic background of the available germplasm in tomato for further utilization of specific genotypes to achieve specific objectives. Estimation of genetic divergence allows the breeder to concentrate their efforts on smaller number of diverse parents for hybridization programme.

Materials and Methods
Twenty two genotypes of tomato collected from different sources were evaluated during 2016-17 under AICRP on Vegetable Crops, Department of Vegetable Science at Horticultural Research and Instructional Farm, IGKV, Raipur (C.G.).
The experiment was laid out in Randomized Block Design (RBD) with three replications. All recommended cultural practices were followed. Observations were recorded for eighteen characters viz., days to 50% flowering, number of branches per plant, plant height, number of fruit cluster per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, days to first fruit harvest, fruit yield per plant, fruit length, fruit diameter, average fruit weight, number of locules per fruit,

pericarp thickness and fruit yield per hectare (q). Whereas, qualitative characters like, total soluble solids, ascorbic acid content, dry matter % of fruit were recorded and subjected to D^2 statistical analysis.

Results and Discussion

On the basis of D^2 analysis, twenty two genotypes were grouped into five clusters (Table 1). Maximum numbers of genotypes were grouped into cluster I included 6 genotypes whereas, cluster IV and cluster V included 5 genotypes in cluster respectively, which is followed by cluster II and cluster III having 3 genotypes respectively in cluster. The clustering pattern did not show any relationship between genetic diversity and geographic diversity.

The intra-cluster distances indicate the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters. It is vivid from the Table 2 and Fig.1 that maximum inter cluster distance was observed between cluster I and II (6.515) followed by cluster II and IV (5.721), cluster II and III (5.709), cluster I and V (4.846), cluster I and III (4.823). The rest of the combinations for inter cluster distance varied from 4.648 to 3.809 with least distance cluster III and V (3.809). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

The intra-cluster distance varied from 2.364 to 3.188. The maximum intra-cluster distance was shown by cluster IV (3.188) followed by cluster V (2.975), cluster II (2.828) and cluster III (2.480). Cluster I (2.364) showed minimum distance. Cluster IV had maximum diverse genotypes. These results are in general agreement with the findings of Parthasarathy and Aswath (2002) [7], Sharma *et al.* (2006) [8], Shashikanth (2008) [9], Mehta and Asati (2008) [10], Rizvi *et al.* (2013) [11], Nalla *et al.* (2014) [12], Srivastava *et al.* (2014) [13], Lekshmi and Celine (2016) [14], Kaur *et al.* (2017) [15] and Patel *et al.*, (2017) [16].

The better genotypes can be selected for most of characters on the basis of mean performance in the cluster Table 3. The means of the clusters for days to 50% flowering showed the lowest mean performance for cluster V (28.40), which was followed by cluster II (28.56) and cluster I (29.33) and highest in cluster IV (35.27). No. of branches per plant showed highest cluster mean performance for cluster IV (12.69) followed by cluster III (11.77), cluster V (11.07), cluster II (9.67) and lowest for cluster I (8.27). The genotypes of cluster III recorded highest plant height (cm) (75.09) followed by cluster V (57.31), cluster II (52.37), cluster I (51.89), while lower plant height was observed in cluster IV (48.70).

Maximum no. of fruit cluster per plant was recorded in the genotypes of cluster IV (10.64) followed by cluster V (10.34) and cluster III (9.90). No. of flowers per cluster exhibited the highest mean performance for cluster II (5.69) followed by cluster V (5.35), cluster III (5.07) and cluster I (4.84). The maximum mean for no. of fruits per cluster was noted in cluster II (4.58) followed by cluster V (4.52), cluster III (4.29) whereas, the minimum was noted in cluster IV (3.88). The genotypes of cluster III recorded highest mean value for no. of fruits per plant (29.43) followed by cluster IV (29.31) and cluster II (28.86).

Days to first fruit harvest exhibited the minimum mean performance for cluster II (69.11) followed by cluster V (70.00), while the genotypes of cluster I (79.17) exhibited maximum mean performance followed by cluster IV (75.20).

The highest mean value for fruit yield per plant was recorded in the genotypes of cluster II (3.25) followed by cluster IV (2.45) and cluster V (2.32). The lowest mean value was recorded in cluster I (1.38).

Fruit length (cm) showed maximum cluster mean performance in cluster II (6.06), which was followed by cluster IV (5.64) and cluster I (4.74), while the minimum cluster mean observed in cluster III (3.94). Fruit diameter (cm) showed maximum cluster mean performance in cluster II (6.01) followed by cluster V (5.54). Average fruit wt. (g) recorded its maximum mean value in the genotypes of cluster II (104.17) followed by cluster V (79.30), cluster IV (67.40), cluster III (59.88). The minimum mean value was recorded in the genotypes of cluster I (58.23).

Number of locules per fruit showed maximum cluster mean performance in cluster V (4.80), which was followed by cluster III (3.79), cluster I & II (3.73). The minimum mean value was recorded in the genotypes of cluster IV (3.07). Pericarp thickness (mm) exhibited the highest mean performance for cluster II (5.60) followed by cluster I (5.11). Total soluble solid showed maximum cluster mean performance in cluster III (4.36), which was followed by cluster II (4.22) and cluster IV (4.13). Ascorbic acid (mg/100g) showed maximum cluster mean performance in cluster II (23.04) followed by cluster III (21.66) and cluster I & V (20.68). Dry matter % of fruit showed maximum cluster mean performance in cluster I (4.87), which was followed by cluster IV (4.53), cluster II (4.49) cluster V (4.34) and cluster III (3.62).

The highest mean value for fruit yield per hectare (q) was recorded in the genotypes of cluster II (629.25) followed by cluster V (435.84), cluster III (366.59), cluster IV (292.72). The lowest mean value was recorded in cluster I (280.95). Cluster mean values showed a wide range of mean values among the characters studied indicating presence of wide variation among the genotypes studied.

The percentage contributions towards genetic divergence are presented in Table 4. The results showed that the character number of locules per fruit contributed maximum (22.94%) towards diversity by taking first ranking 53 times, followed by average fruit wt.(g) (19.93%), fruit yield per plant (13.85%), total soluble solid (°Brix) & dry matter % of fruit (7.79%), plant height(cm) & fruit diameter (cm) (7.36%), fruit yield per hectare (q) (5.63%), number of branches per plant, fruit length (cm) and pericarp thickness (mm) contributed (2.16%),whereas ascorbic acid (mg/100g) (0.87%) contribute lowest to divergence. This contribution is an important consideration for the purpose of further selection and choice of parents for hybridization. The results of the present study was close agreement with findings of Parthasarathy and Aswath (2002) [7] who reported that plant height, number of fruits and fruit size contributed the most of the total genetic divergence, Reddy *et al.* (2013a) [17] for fruit weight, number of fruits per plant and plant height, Srivastava *et al.* (2014) [13] for plant height, yield per plant and pericarp thickness. Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration as they appears as desirable for inclusion in tomato improvement.

The inter-cluster distances in present investigation were higher than the intra-cluster distance reflecting the wider diversity among the breeding lines of the distant group. Hence, it is suggested that intercrossing of genotypes from diverse clusters showing high mean performance will be

helpful in obtaining better recombinants with higher genetic variability.

Genetic divergence is one of the useful tools for selection and efficient use of parents for hybridization to develop high yielding potential cultivars/hybrids. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining stronger heterosis and gives broad spectrum of variability in segregating generations.

Table 1: Composition into various clusters of tomato genotypes during rabi, 2016-17

Cluster Number	Number of genotypes included	Name of genotypes
I	6	2014/TOLCVRES-5, 2015/TOLCVRES-3, 2015/TOLCVRES-5, 2014/TOLCVRES-2, 2014/TOLCVRES-4, 2015/TOLCVRES-1
II	3	H-86, 2014/TOLCVRES-3, 2015/TOLCVRES-4
III	3	Pusa Ruby, Arka Vikash, Punjab Chhuhara
IV	5	2014/TODVAR-2, 2014/TODVAR-3, 2014/TODVAR-4, 2014/TODVAR-5, 2014/TODVAR-6.
V	5	2015/TOLCVRES-2, 2014/TOLCVRES-1, 2014/TODVAR-1, Kashi Anupam, H-24

Table 2: Intra (bold) and Inter cluster distance values in cluster formed of tomato genotypes

Cluster Number	I	II	III	IV	V
I	2.364				
II	6.515	2.828			
III	4.823	5.709	2.480		
IV	4.648	5.721	4.440	3.188	
V	4.846	3.883	3.809	4.445	2.975

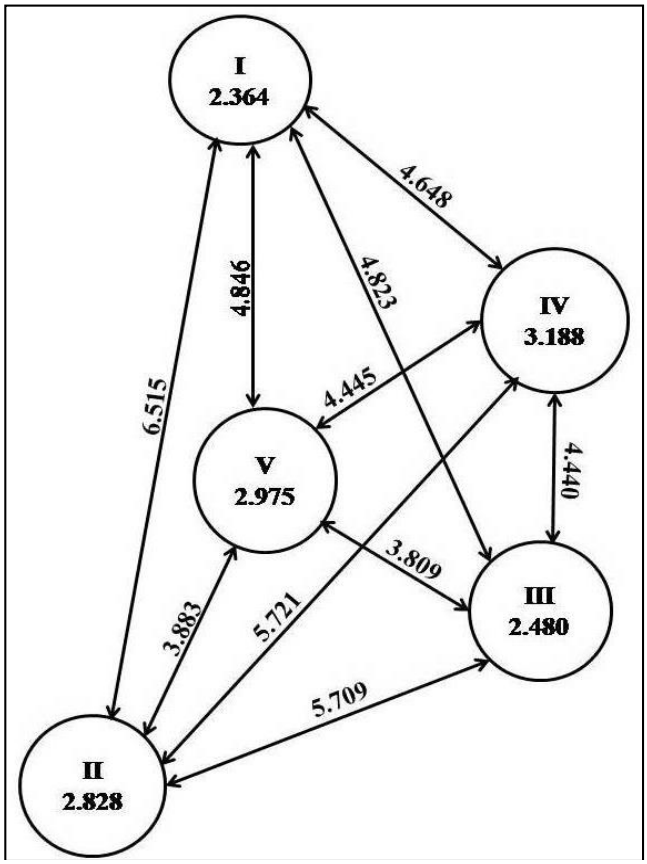

Fig 1: Statistical distance among 22 tomato genotypes (not to scale)

Table 3: Mean performance of genotypes in individual cluster for fruit yield and its components in tomato during *rabi* 2016-17

Characters Clusters		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
I	6	29.33	8.27	51.89	7.90	4.84	3.98	19.65	79.17	1.38	4.74	3.84	58.23	3.73	5.11	3.59	20.68	4.87	280.95
II	3	28.56	9.67	52.37	9.44	5.69	4.58	28.86	69.11	3.25	6.06	6.01	104.17	3.73	5.60	4.22	23.04	4.49	629.25
III	3	29.67	11.77	75.09	9.90	5.07	4.29	29.43	71.78	1.56	3.94	4.02	59.88	3.79	5.07	4.36	21.66	3.62	366.59
IV	5	35.27	12.69	48.70	10.64	4.64	3.88	29.31	75.20	2.45	5.64	4.70	67.40	3.07	4.85	4.13	20.06	4.53	292.72
V	5	28.40	11.07	57.31	10.34	5.35	4.52	27.38	70.00	2.32	4.63	5.54	79.30	4.80	4.35	3.74	20.68	4.34	435.84

1. Days to 50% flowering
2. No. of branches per plant
3. Plant height (cm)
4. Number of fruit cluster per plant
5. Number of flowers per cluster
6. Number of fruits per cluster
7. Number of fruits per plant
8. Days to first fruit harvest
9. Fruit yield per plant (kg)
10. Fruit length (cm)
11. Fruit diameter (cm)
12. Average fruit weight (g)
13. Number of locules per fruit
14. Pericarp thickness (mm)
15. Total soluble solids (ºBrix)
16. Ascorbic acid content (mg/100g)
17. Dry matter % of fruit
18. Fruit yield per hectare (q)

Table 4: Contribution of each character to divergence in tomato

S. No.	Characters	Number times appearing first time	Percent contribution
01	Days to 50% flowering	0	-
02	Number of branches per plant	5	2.16
03	Plant height (cm)	17	7.36
04	Number of fruit cluster per plant	0	-
05	Number of flowers per cluster	0	-
06	Number of fruits per cluster	0	-
07	Number of fruits per plant	0	-
08	Days to first fruit harvest	0	-
09	Fruit yield per plant (kg)	32	13.85
10	Fruit length (cm)	5	2.16
11	Fruit diameter (cm)	17	7.36
12	Average fruit wt. (g)	46	19.93
13	Number of locules per fruit	53	22.94
14	Pericarp thickness (mm)	5	2.16
15	Total soluble solid (°Brix)	18	7.79
16	Ascorbic acid (mg/100g)	2	0.87
17	Dry matter % of fruit	18	7.79
18	Fruit yield per hectare (q)	13	5.63
	Total	231	100

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