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Genetic divergence and its implication in breeding tomato (*Solanum lycopersicum*) suitable for mid-hills of Himachal Pradesh

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ABSTRACT

Genetic divergence among the 56 genotypes of tomato (*Solanum lycopersicum* L.) collected from different geographical regions of India, was quantified by Mahalanobis D^2 statistic for 14 quantitative and qualitative traits during the year 2014-15. Analysis of variance indicated that genotypes varied significantly among themselves in respect of 14 characters studied. Based on D^2 analysis using Tocher's method all 56 genotypes were grouped into 10 clusters with a maximum of 13 genotypes in cluster VIII and minimum 1 in cluster III. Maximum inter-cluster distance was observed between cluster IV and VIII (2601.53) followed by cluster III and V (1981.92). Appreciable diversity within and between the clusters was observed. No parallelism was found between geographical and phenotypic diversity. Considering the cluster mean, the genotypes of cluster IV are suitable, both as open-pollinated varieties and as parents to be used in a hybridization programme. The five traits, viz. yield/plant, plant height, number of fruits/plant, days to first picking and average fruit weight contributed 87.33% to the total divergence and played the greatest role in differentiation of germplasm. These traits can be utilized for improving yield and obtaining good segregants in tomato breeding programs.

Key words: Clusters, D^2 analysis, Dendrogram, Genetic divergence, Tomato

Tomato (*Solanum lycopersicum* L.) is one of the most important solanaceous vegetable crops grown widely throughout the world. It is mostly considered as 'Protective food' based on its nutritive value and antioxidant properties due to the presence of lycopene and flavonoids (Sepat *et al*. 2013). The crop has wide acceptance among hill farmers because of its short duration, high market value and constant demand throughout the year. In mid-hills, tomato comes during June to September which is the lean period of tomato production in plain due to the prevalence of high temperature and rainfall. An improvement in yield and quality in self-pollinated crops like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. The success of hybridization programme mainly depends upon selection of suitable parents from diverse origin because diverse parents are expected to give hybrid vigour (Harrington 1940). D^2 statistic which is based on multivariate analysis of quantitative traits is one such powerful tool for measuring divergence among a set of population using the concept of statistical distance (Mahalanobis 1936). Further, grouping of the genotypes based on Tocher's method will be more useful in choosing suitable parents for heterosis breeding. Therefore, the present investigation was carried out, to assess the proximity of accessions with each other, thus classifying them into different clusters/groups, and to identify highly divergent clusters/promising accessions for high yield and better quality.

MATERIALS AND METHODS

The experimental material consisting of 56 genotypes of tomato collected from various sources given in Table 1, were evaluated during *kharif* season of 2014 at an experimental farm in the Department of Vegetable Science, Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan (HP). The experiment was laid out in randomized complete block design with three replications at a spacing of 90 cm×30 cm. Observations were recorded for 14 characters, viz. days to first flowering, number of fruits/cluster, number of fruits/plant, average fruit weight, fruit yield/plant, plant height, inter-nodal distance, thousand seed weight, number of locules/fruit, total soluble solids, locular wall thickness, pericarp thickness, lycopene content and harvest duration in five randomly selected plants from each genotype in each

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Table 1 List of tomato genotypes studied along with their sources

Genotypes	Sources	Genotypes	Sources
EC-5205	IIVR, Varanasi	Solan Tomato-3	UHF, Nauni, Solan
EC-521079	IIVR, Varanasi	Solan Lalima	UHF, Nauni, Solan
EC-5863	IIVR, Varanasi	97/754	UHF, Nauni, Solan
EC-538146	IIVR, Varanasi	Arka Abha	IIHR, Bangalore
EC-521038	IIVR, Varanasi	Arka Alok	IIHR, Bangalore
EC-526146	IIVR, Varanasi	Arka Saurabh	IIHR, Bangalore
EC-531804	IIVR, Varanasi	Arka Meghali	IIHR, Bangalore
EC-129604	IIVR, Varanasi	Arka Vikas	IIHR, Bangalore
EC-531803	IIVR, Varanasi	VRT-87	V P K A S, Almora
EC-620398	IIVR, Varanasi	VL-Tamatar 4	V P K A S, Almora
EC-620378	IIVR, Varanasi	VTG-93	V P K A S, Almora
EC-126903	IIVR, Varanasi	Punjab Varkha Bahar-2	PAU, Ludhiana
EC-620424	IIVR, Varanasi	Punjab Ratta	PAU, Ludhiana
EC-620383	IIVR, Varanasi	Punjab Tropic	PAU, Ludhiana
EC-392693	IIVR, Varanasi	Punjab Upma	PAU, Ludhiana
EC-620396	IIVR, Varanasi	Castle Rock	PAU, Ludhiana
EC-620434	IIVR, Varanasi	Punjab Kesri	PAU, Ludhiana
EC-620410	IIVR, Varanasi	Punjab Chhuhara	PAU, Ludhiana
EC-535580	IIVR, Varanasi	Rodade	RHRS, Bajjura
Palam Pride	HPKV, Palampur	EC-2491	RHRS, Bajjura
BT-12	OUAT, Bhubneshwar	EC-164660	RHRS, Bajjura
BT-18	OUAT, Bhubneshwar	Best of All	IARI, Katrain
BC-333-1	UHF, Nauni, Solan	Roma	IARI, Katrain
DC-1	UHF, Nauni, Solan	Marglobe	IARI, Katrain
S-208	UHF, Nauni, Solan	S-12	PAU, Ludhiana
UHF-II	UHF, Nauni, Solan	HADT-294	CHES, Ranchi
Solan Tomato-1	UHF, Nauni, Solan	KS-254	CSAUAT, Research station Kalyanpur
Solan Tomato-2	UHF, Nauni, Solan	KS-7	CSAUAT, Research station Kalyanpur

Table 2 Analysis of variance (Mean Sum of Squares) for different characters

Character	Abbre-viation	Replica-tion	Genotype	Error
	DF	2	55	110
Days to first picking	DFP	78	27.91**	4.055
Number of fruits/ cluster	NFPC	0.007	1.47**	0.132
Number of fruits/ plant	NFPP	20.956	514.73**	3.267
Average fruit weight (g)	AFW	0.501	1077.09**	2.049
Plant height (cm)	PH	437.032	1688.58**	150.089
Inter-nodal distance (cm)	ID	1.391	2.878**	0.622
Pericarp thickness (mm)	PT	1.242	2.094**	0.231
Locular wall thickness (mm)	LWT	0.023	1.684**	0.125
Number of locules/ fruit	NFLP	0.446	2.043**	0.213
Total soluble solids (^{0}B)	TSS	0.60	1.111**	0.169
Thousand seed weight (g)	TSW	0.018	0.461**	0.043
Lycopene content (mg/100g)	LC	1.322	13.593**	0.353
Harvest duration (days)	HD	27.810	85.603**	10.446
Yield/plant (g)	YPP	31680.59	734931.30**	5543.22

** Significant at 5% level of probability; DF- Degree of freedom

Table 3 Composition of different clusters in tomato

Cluster	Number of genotypes	Genotypes
I	7	Arka Vikas, Solan Tomato -3, EC-164660, BT-18, EC-2491, 97/754, Rodade
II	3	EC-521038, EC-531804, UHF-II
III	1	Best of All
IV	5	VTG-93, KS – 254, VL - Tamatar 4, Solan Tomato -1, Solan Lalima
V	9	EC-521079, EC-538146, EC-5863, EC-129604, EC-126903, BC-333-1, EC-392693, S-208, EC-535580
VI	3	EC-620434, Punjab Varkha Bahar-2, Punjab Tropic
VII	3	HADT-294, KS-7, VRT-87
VIII	13	EC-531803, EC-5205, Palam Pride, EC-526146, DC-1, S-12, BT-12, Punjab Upma, Castle Rock, Punjab Kesri, Arka Abha, Arka Saurabh, Arka Meghali
IX	6	EC-620396, EC-620383, EC-620424, EC-620378, Punjab Ratta, Roma
X	6	Punjab Chhuhara, EC-620410, EC-620398, Marglobe, Solan Tomato -2, Arka Alok

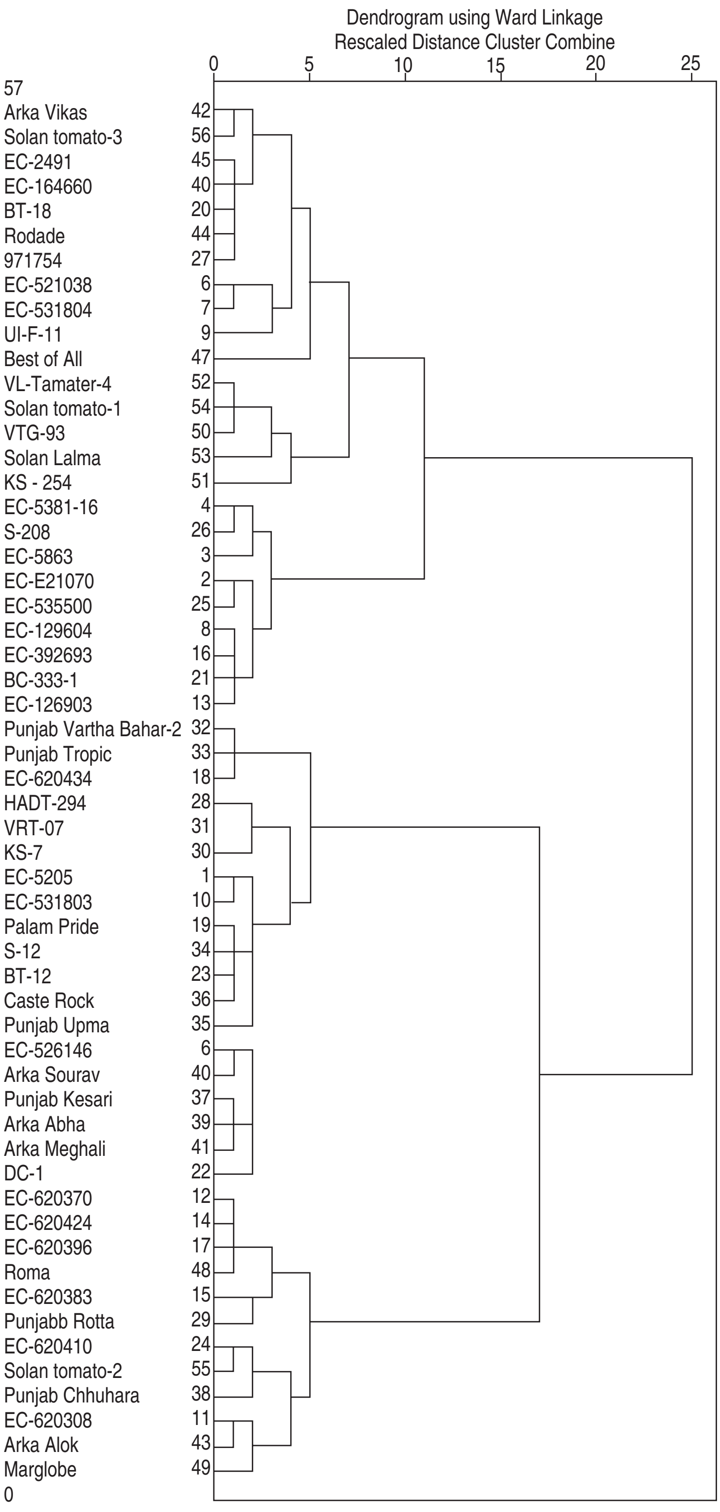

Fig 1 Dendrogram of 56 genotypes of tomato based on evaluation of 14 characters

replication. The data were subjected to multivariate analysis. Multivariate analysis was done utilizing Mahalanobis D^2 statistic and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that, the genotypes belonging to the same cluster should show a smaller D^2 value than those belonging to different clusters.

The data analysis was carried out using SPAR-1 (Statistical Package for Agricultural Data Analysis) software of Indian Agricultural Statistical Research Institute, New Delhi and SPSS 19.0 version.

RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences among the genotypes for all the characters studied (Table 2). The analysis of plot means revealed significant differences among 56 genotypes for each of 14 characters suggesting appreciable variability among the genotypes. The D^2 values estimated for 56 germplasm lines in n(n-1)/2 = 1540 combination varied from 245.82 to 2601.53 indicating the presence of substantial amount of genetic diversity in the population. The 56 genotypes were grouped into 10 clusters depending upon their morphological similarity (Table 3). Among these, cluster VIII was the largest having 13 genotypes followed by cluster V, cluster I, cluster IX and X, cluster IV, cluster II, VI and VII and cluster III with 9, 7, 6, 5, 3 and 1 genotypes respectively. Genotypes from different geographical regions were also grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence. Present results are in line with the findings of Kumar *et al.* (2013) and Srivastava *et al.* (2014). This means that geographical diversity though important may not be factor in determining genetic divergence. The genotypes originating from one place as in present study were scattered in to ten clusters. No parallelism between geographical distribution and genetic diversity might be due to some forces other than geographical distance like genetic architecture of population, heterogeneity, history of selection, proximity of development of traits etc. (Sureja and Sharma 2001, Sanwal *et al.* 2015). The dendrogram was generated using Wards method (Fig 1) with an aim to visualize the best representation of the phenetic (overall similarity) or phylogenetic relationship among individuals, cultivars, populations, or species. At smaller measures of dissimilarity (i.e., 5), ten clusters can be seen, which indicates the presence of considerable amount of variability in the studied genotypes because clusters formed are based only on few traits. At higher measures of dissimilarity (i.e. 25), most of the traits are taken into consideration for cluster formation. Therefore, as the measure of dissimilarity increased to 25 it broadly grouped the 56 genotypes into two clusters comprising of 25 (from cluster I to V) and 31(from cluster VI to X) genotypes respectively. Dendrogram (Fig 1) depicted the clear picture of diversity present in the population and subsequently also aids in the selection of suitable parents for hybridization because it ultimately narrowed the number of diverse clusters to two. Finally, the selection of suitable parents for hybridization from these clusters is easy based on their mean performance (Shushay *et al.* 2014).

Table 4 Inter (upper half diagonal) and intra (diagonal) cluster D^2 and D values

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**1140.58 (33.77)**	368.41 (19.19)	1474.64 (38.40)	1647.08 (32.51)	546.45 (23.48)	424.19 (20.59)	613.16 (24.76)	712.38 (26.69)	533.64 (23.10)	467.42 (21.62)
II		**584.42 (24.17)**	549.89 (23.45)	984.50 (31.38)	947.15 (30.78)	314.92 (17.75)	255.19 (15.97)	340.15 (18.44)	297.96 (17.26)	268.25 (16.38)
III			**589.09 (24.27)**	480.82 (21.93)	1981.92 (44.52)	1077.75 (32.83)	299.54 (17.31)	490.09 (22.14)	751.71 (27.42)	892.29 (29.87)
IV				**262.01 (16.18)**	675.02 (25.98)	1558.42 (39.48)	633.11 (25.16)	2601.53 (51.01)	1298.06 (36.03)	1310.67 (36.20)
V					**847.17 (29.11)**	911.92 (30.20)	1397.53 (37.38)	1436.36 (37.89)	1135.75 (33.70)	966.95 (31.10)
VI						**745.81 (27.31)**	613.39 (24.76)	534.45 (23.12)	433.30 (20.82)	245.82 (15.68)
VII							**207.44 (14.40)**	328.31 (18.12)	540.39 (23.25)	520.17 (22.81)
VIII								**862.63 (29.37)**	498.92 (22.34)	479.75 (21.90)
IX									**597.77 (24.45)**	475.62 (21.81)
X										583.73 (24.16)

Table 5 Cluster mean for fourteen different traits in tomato

Traits \ Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
DFP	77.67	82.78	79.33	76.07	77.37	82.89	77.67	78.08	81.33	82.06
NFPC	3.14	2.81	2.96	3.52	4.06	2.42	2.00	2.82	3.00	2.70
NFPP	39.12	19.21	32.84	29.15	52.68	15.15	22.94	25.90	24.33	23.85
AFW	35.49	34.40	27.68	68.87	18.79	24.38	42.07	33.57	50.17	64.33
PH	90.12	94.29	108.70	117.80	99.64	52.33	51.40	60.55	70.86	76.33
ID	5.81	6.01	8.16	6.55	5.55	3.93	4.76	4.48	5.25	5.31
PT	3.88	4.03	3.18	4.14	2.97	4.14	3.58	3.43	5.47	4.50
LWT	2.47	2.92	1.97	2.14	1.67	2.51	2.08	1.92	3.33	3.49
NFLP	3.30	2.43	3.37	3.15	2.84	3.86	4.93	3.58	2.58	3.70
TSS	4.29	4.59	5.26	4.71	4.40	4.30	3.99	4.18	4.90	3.92
TSW	2.83	2.64	2.44	2.78	2.86	2.73	2.08	2.87	2.83	3.00
LC	4.70	3.27	13.26	5.29	4.64	7.01	2.55	5.37	7.34	4.24
HD	29.14	27.11	31.00	36.20	28.89	17.78	24.33	25.33	24.33	26.56
YPP	1386.90	624.80	909.75	1919.09	958.84	365.71	956.15	894.65	1210.28	1501.49

Abbreviation of traits provided in Table 2.

The intra-cluster value was found to vary from 207.44 to 1140.58 (Table 4), the maximum being in cluster I (1140.58) followed by cluster VIII (862.63) and cluster V (847.17). Sanwal *et al.* (2015) also observed maximum intra-cluster variation among genotypes in their studies. The maximum inter-cluster distance was noticed between cluster IV and VIII (2601.53), followed by III and V (1981.92) and I and IV (1647.08). This indicates that the genotypes of these clusters are much diverse from each other. The magnitude of heterosis largely depends on degree of diversity in the parental lines. The higher distance between two clusters, the greater genetic diversity between genotypes. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and release of desirable transgressive segregants (Singh and Mishra 2008, Nisar *et al.* 2008).

Table 6 Percent contribution of each character to the total divergence

Characters	Times Ranked 1st	Percent contribution (%)	Rank
Days to first picking	177	11.49	III
Number of fruits/cluster	9	0.58	X
Number of fruits/plant	177	11.49	III
Average fruit weight(g)	140	9.09	V
Yield/plant(g)	531	34.48	I
Inter-nodal distance(cm)	3	0.19	XIII
Pericarp thickness(mm)	8	0.52	XI
Locular wall thickness(mm)	2	0.13	XIV
Number of locules per fruit	36	2.34	VIII
Plant height(cm)	320	20.78	II
Total soluble solids(oB)	16	1.04	IX
Thousand seed weight(g)	7	0.45	XII
Lycopene content(mg/100g)	66	4.29	VI
Harvest duration(days)	48	3.12	VII

Several researchers also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of different traits following Mahalanobis D^2 statistic by Shashikanth *et al.* (2010), Basavaraj *et al.* (2010), Narolia and Reddy (2012) and Thapa *et al.* (2014). Average inter and intra-cluster distances revealed that, in general, inter-cluster distances were much higher than those of intra-cluster distances, suggesting homogeneous and heterogeneous nature of the germplasm lines within and between clusters, respectively. These results are in accordance with the findings of Mahesha *et al.* (2006) and Sekhar *et al.* (2008) in tomato.

The diversity present in the material was also supported by the appreciable amount of variation among cluster means for different characters. Further, for crop improvement, inter-crossing among genotypes with the outstanding mean performance was suggested by Roy and Sharma (1996). Germplasm accessions in clusters IV, V, I and VII were the earliest in days to first picking, whereas those in clusters VI, II and X were of late type (Table 5). For the traits, viz. number of fruits/cluster (4.06) and number of fruits/plant (52.68), cluster V had the highest value. Maximum average fruit weight (68.87 g), plant height (117.80 cm), harvest duration (36.20 days) and yield/plant (1919.09 g) was recorded in cluster IV followed by cluster III (72.90 g). Inter-nodal distance was noted minimum in cluster VI (3.93 cm) followed by cluster VIII (4.48 cm). The maximum pericarp thickness was observed in cluster IX (5.47 mm) followed by cluster X (4.50 mm). In case of locular wall thickness, cluster X (3.49 mm) followed by cluster IX (3.33 mm) had the maximum value. The minimum value for number of locules/fruit was observed in cluster II (2.43) followed by cluster IX (2.58). Total soluble solids were recorded maximum in cluster III (5.26 ^{o}B) followed by cluster IX (4.90 ^{o}B). Thousand-seed weight had the highest value in cluster X (3.00 g) followed by cluster VIII (2.87 g). Cluster III (13.26 mg) followed by cluster IX (7.34 mg) recorded highest value for lycopene content. Cluster I and VII did not possess superiority for any character, but cluster IV exhibited superiority for days to first picking, average fruit weight, plant height, harvest duration and yield/plant. Significantly higher cluster mean for fruit yield/plant has been observed in the cluster IV and minimum in cluster VI. The lower cluster mean for yield in cluster VI could be ascribed to less number of fruits/plant, low fruit weight and less plant height, the main yield contributing characters. Therefore, for a better understanding of yield and its components in this crop, crosses between genotypes of cluster IV and cluster VI will be highly useful. Similarly, the genotypes having a wide genetic base and desirable characteristics can be involved in intra-specific crosses which would lead to transmission of good genetic gain for various putative traits including yield for practical utility. To have better recombinants, the hybridization between genotypes in cluster IV and cluster V which depicts more inter-cluster distance, will be useful to improve most of the traits. Therefore, crosses between the genotypes belonging to these respective clusters may be worthwhile to isolate superior genotypes.

The analysis of the contribution of each character towards the expression of genetic divergence (Table 6) indicated that yield/plant contributed maximum (34.48%) towards genetic divergence followed by plant height (20.78%), number of fruits/plant (11.49%) and days to first picking (11.49%) and average fruit weight (9.09%). Singh *et al.* (2008), Ara *et al.* (2009), Reddy *et al.* (2013) and Pedapati *et al.* (2014) also observed such maximum contribution of yield/plant, plant height, number of fruits/plant and average fruit weight to total divergence of tomato germplasm. De *et al.* (1988) opined that traits contributing maximum towards D^2 values needed to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization.

In genetic improvement for higher yield, the choice of parent and desirable component characters of yield should be taken into consideration for breeding appropriate plant type (Mohammad *et al.* 2009, Sanwal *et al.* 2015). The genotypes belonging to cluster IV showed earliness for days to first picking (76.07 days) and recorded maximum value for average fruit weight (68.87 g), plant height (117.80 cm), harvest duration (36.20 days) and yield/plant (1919.09 g). The maximum inter-cluster distance was observed between IV and VIII (2601.53), followed by III and V (1981.92) and I and IV (1647.08). This indicates that the genotypes of these clusters are much diverse to each other. Inter-crossing among genotypes of these divergent clusters selected for specific component traits would lead to greater opportunity for crossing over, which may release hidden variability by breaking linkage (Thoday 1969) and may be helpful in bringing new genepool and expanding the range of adaption. Continuous selection in advance generation may lead to development of lines with high yield combining desirable component traits.

REFERENCES

Ara A, Narayan R, Ahmed N and Salim T. 2009. Estimation of genetic divergence for yield and quality traits in tomato (*Lycopersicon esculentum* Mill.). *Vegetable Science* **36**(3): 293–6.

Basavaraj N S, Patil B C, Salimath P M, Hosamani R M and Krishnaraj P U. 2010. Genetic divergence in tomato (*Solanum lycopersicon* [Mill.] Wettsd.). *Karnataka Journal of Agricultural Sciences* **23**(3): 508–39.

De R N, Seetharaman R M, Sinha T and Banerjee S P. 1988. Genetic divergence in rice. *Indian Journal of Genetics and Plant Breeding* **48**: 189–94.

Harrington J B. 1940. Yielding capacity of wheat crosses as indicated by balk hybrid tests. *Canadian Journal of Research* **18**: 5–584.

Kumar M, Buckseth T, Thakur M S and Thakur K S. 2013. Genetic divergence and cluster analysis in tomato (*Solanum lycopersicum*). *Progressive Agriculture* **13**(1): 114–7.

Mahalanobis P C. 1936. On the generalized distance in statistic. *Proceedings of National Academy of Science* **2**: 79–85.

Mahesha D K, Apte U B and Jadhav B B. 2006. Studies on genetic divergence in tomato (*Lycopersicon esculentum* Mill.). *Crop Research* **32**(3): 401–2.

Mohammad S, Bacha S, Arshad M, Din R and Ghafoor A. 2009. Genetic diversity for determining yield potential and selection criteria in *Pisum sativum* genetic resources. *Pakistan Journal of Botany* **41**:2 987–93.

Narolia R K and Reddy R V S K. 2012. Genetic divergence studies in tomato (*Lycopersicon esculentum* Mill.). *Crop Research Hisar* **44**(1/2): 125–8.

Nisar M, Ghafoor A, Ahmad H, Khan M R, Qureshi A S, Ali H and Islam M. 2008. Evaluation of genetic diversity of pea germplasm through phenotypic trait analysis. *Pakistan Journal of Botany* **40**: 2081–6.

Pedapati A, Reddy R V S K, Babu J D, Kumar S S and Sunil N. 2014. Genetic diversity analysis in tomato (*Solanum lycopersicum* L.). *Electronic Journal of Plant Breeding* **5** (3): 517–25.

Rao C R. 1952. *Advanced Statistical Methods in Biometrical Research,* pp 357–63. John Willey and sons Inc., New York.

Reddy B R, Begum H, Sunil N and Reddy T M. 2013. Genetic divergence studies in exotic collections of tomato (*Solanum lycopersicum* L.). *International Journal of Agricultural Sciences* **9**(2): 588–92.

Roy A and Sharma R N. 1996. Multivariate analysis in chilli (*Capsicum annuum* L.). *Annals of Agricultural Research* **17**(1): 30–2.

Sanwal S K, Singh B, Singh V and Mann A. 2015. Multivariate analysis and its implication in breeding of desired plant type in garden pea (*Pisum sativum*). *Indian Journal of Agricultural Sciences* **85**(10): 1 298–1 302.

Sekhar L, Prakash B G, Salimath P M, Sridevi O and Patil A A. 2008. Genetic diversity among some productive hybrids of tomato (*Lycopersicon esculentum* Mill.). *Progressive Horticulture* **34**: 77–9.

Sepat N K, Sepat S R, Sepat S and Kumar A. 2013. Energy use efficiency and cost analysis of tomato under greenhouse and open field production system at Nubra valley of Jammu and Kashmir. *International Journal of Environment Science* **3(**4): 1 233–41.

Shashikanth B N, Patil B C, Salimath P M, Hosamani R M and Krishnaraj P U. 2010. Genetic divergence in tomato (*Solanum lysopersicon* Mill.). *Karnataka Journal of Agricultural Sciences* **23**(3): 538–9.

Shushay C, Derbew B and Fetien A. 2014. Genetic diversity studies for quantitative traits of tomato (*Solanum lycopersicum* L.) genotypes in Western Tigray, Northern Ethiopia. *Journal of Plant Breeding and Crop Science* **6**(9): 105–13.

Singh A K, Sharma J P, Kumar S and Chopra S. 2008. Genetic divergence in tomato (*Lycopersicon esculentum* Mill.). *Journal of Research SKUAST* **7**(1): 1–8.

Singh D and Mishra V K. 2008. Studies on genetic divergence in pea (*Pisum sativum* L.). *Agricultural Science Digest* **28**: 77–8.

Srivastava M K, Agarwal V K and Agarwal R K. 2014. Estimation of genetic divergence among indigenous and exotic accessions of tomato (*Solanum lycopersicum* L.). *Asian Journal of Biosciences* **9**(1): 30–4.

Sureja A K and Sharma R R. 2001. Genetic divergence in garden pea (*Pisum sativum* L.). *Vegetable Science* **28**: 63–4.

Thapa R P, Jha A K, Deka B C, Reddy A N K, Verma V K and Yadav R K. 2014. Genetic divergence in tomato grown in subtropical mid-hills of Meghalaya. *Indian Journal of Horticulture* **71**(1): 123–5.

Thoday J M. 1960. Effects of disruptive selection III coupling and repulsion. *Heredity* **14**: 35–9.