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Analysis of Genetic Proximity in Tomato (*Solanum lycopersicum* L.) Genotypes

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Abstract: To devise a judicious breeding program, acquisition of significant improvement in tomato productivity requires information on magnitude of genetic diversity mainly in quantitative traits of interest. The rationale of this article is to sort out the genetic proximity of 29 tomato genotypes on the basis of 6 quantitative characters through heritability and cluster analysis. Mean comparison revealed significant differences in tomato genotypes for different vegetative and reproductive traits. Worth of genetic variability was also observed for plant height, fruit length, fruit width, fruit weight, number of fruit per plant and yield per plant due to highly significant genotypic mean square. Number of fruits per plant, fruit weight, plant height and fruit length exhibited high genetic advance and high heritability indicating possibility of improvement at early stages through selection in these traits because of meager influence of environment. Cluster analysis grouped test genotypes into four clusters using Euclidean distance comparison. The genotypes grouped in cluster-II were desirable to bring about improvement for plant height, fruit length and single fruit weight. Suitable parent mates could be made by hybridizing these genotypes with genotypes of cluster-III, better for fruit width and fruit yield to develop superior combinations either in F_1 or in succeeding generations.

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1. Introduction

Tomato is a model species for fruit development and composition and is also a vegetable of high economic importance grown all over the world. Its production has continuously increased over the last 50 years (Causse et al., 2013). It is an autogamous species with narrow genetic base. In Europe, the cultivation of tomato under protected conditions was crucial in decreasing the genetic base because of controlled action of wind and insect pollinators that culminated the maintenance of wild forms through autogamy only (Foolad, 2007). Development of cultivars with improved yield potential, disease and insect pest resistance and better adapted to wide range of environmental conditions are major objectives of tomato breeding in Pakistan. So far the number of varieties released for general cultivation is not great. Three open pollinated (Pakit, Nagina and Naqeeb) and one hybrid (Salar) varieties are low yielder to meet domestic demand. An amount of Rs. 224 million was spent on the import of 85 tonne quality seed of tomato (Anonymous, 2010) which is expected to increase in future. Less compatibility with the local agroclimatic conditions and dissemination of new insect pests and diseases are serious threats with imported seed.

The average yield of tomato is very low in the tune of 10.1 tonne per hectare in Pakistan (Anonymous, 2011a) as compared to 33.6 tonne per hectare of modern agricultural systems of the world (Anonymous, 2011b). Of yield limiting factors, lack of reliable categorization of genotypes chosen for crossing is one of the core issues to be addressed. The hybrids (F_1s) or recombinants (selected in F_2/later generations) very often, do not express full spectrum of genetic variability owing to inappropriate selection of the parents. To mitigate this situation, systematic evaluation of tomato germplasm for understanding the extent of genetic variability and genetic relationships between and among different groups of breeding material is indispensable for the conservation and characterization of cultivated tomato genetic resources as emphasized earlier (Corrado et al., 2014).

The biological variations in an organism are combined response of genotypic, phenotypic and environmental components. Of which the genotypic variation is of great importance from crop

improvement point of view (Mazzucato et al., 2008) and consists of heritable (additive) and non-heritable (dominance and epistatic components). It therefore becomes essential to differentiate observed variability into heritable and non-heritable portion in term of phenotypic and genotypic coefficient of the variation, heritability and genetic advance (Saleem et al., 2013b). Having done this, breeder needs additional information on how to choose parent lines to bring about real time genetic improvement in targeted crop? Biometrical tool like D^2 statistics is applied for this purpose which measures the force of differentiation at intra and inters cluster levels and determines the relative contribution of each component trait to the total divergence. The clusters being separated by the largest statistical distance show maximum divergence (Iqbal et al., 2014). Breeder can select genetically divergent parents for hybridization on the basis of such information with higher level of precision and confidence aiming to develop elite cultivars or new genetic resources. There are several reports that hybrids between lines of diverse sources generally display a broader spectrum of heterosis in yield and yield attributed traits than those between closely related parents. The present study was therefore carried out to appraise the extent of genetic proximity in available tomato germplasm and choose parents suitable for hybrid variety development.

2. Material and Methods

Seeds of 29 local tomato genotypes were sown in nursery and 35 days after sowing, seedlings were manually transplanted at experimental field of Nuclear Institute of Agriculture and Biology (NIAB) Faisalabad, Pakistan during November, 2011-12. The experimental design was randomized complete block with three replications. Plants of each genotype were transplanted maintaining plant and bed spacing of 50×150 cm.

Table 1. Mean performance of different characters in tomato genotypes

Designated No.	Genotype	Plant height (cm)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Number of fruit per plant	Fruit yield per plant (kg)
A	AL-1	64.3 dg	5.6 ad	4.63 h	61.3 gi	89.7 bc	3.9 ab
B	AL-2	66.7 dg	6.7 a	5.00 c	86.7 ac	64.7 ch	3.1 af
C	AL-3	65.7 dg	6.1 ab	4.80 eg	72.0 de	38.7 hk	2.3 eg
D	AL-5	172.3 ab	4.4 d	4.40 jk	47.3 lm	74.0 be	2.9 ag
E	AL-6	64.0 dg	5.6 ad	4.80 eg	80.7 c	54.7 dk	4.1 a
F	AL-7	74.3 de	5.0 bd	5.03 c	67.7 dg	72.0 bf	3.6 ad
G	AL-8	187.0 a	2.5 e	2.70 p	11.0 o	211.7 a	2.1 eg
H	AL-9	179.0 ab	2.8 e	2.93 o	14.3 o	225.7 a	3.2 ae
I	LB-3	74.7 de	4.5 d	5.83 a	85.7 bc	27.0 k	2.0 fg
J	NT-2	61.3 dg	4.5 d	4.90 ce	68.7 df	52.7 dk	3.2 ae
K	NT-3	63.3 dg	5.7 ad	4.97 cd	71.0 de	63.0 ci	3.5 ad
L	NT-4	70.0 df	4.8 bd	5.37 b	88.0 ab	45.0 ek	3.2 ae
M	NT-7	60.3 dg	5.3 bd	4.70 fg	63.7 fh	47.0 dk	2.6 cg
N	NT-8	62.3 dg	4.9 bd	4.63 gh	57.7 hk	43.7 fk	2.2 eg
O	NT-9	68.3 dg	4.9 bd	4.57 hj	54.7 ik	51.7 dk	2.8 b-g
P	NT-10	71.7 df	4.5 d	4.57 hj	51.3 kl	41.7 gk	1.9 g
Q	NT-11	77.7 cd	4.6 cd	4.43 ik	52.0 jl	59.7 di	2.9 bg
R	NT-13	55.7 fg	4.6 cd	3.67 n	38.7 n	98.7 b	3.0 ag
S	NT-14	66.0 dg	5.0 bd	4.63 gh	58.7 hj	61.0 ci	2.8 bg
T	NT-15	58.0 eg	6.0 ac	4.20 l	57.0 hk	65.3 ch	2.8 bg
U	NT-16	58.3 eg	5.3 bd	4.83 df	69.3 de	55.3 dk	3.2 ae
V	NT-18	90.0 c	4.4 d	5.23 b	74.3 d	33.7 ik	2.2 eg
W	NT-19	52.0 g	5.5 a-d	3.90 m	44.7mn	58.0 dj	2.0 eg
X	NT-21	164.7 b	5.0 b-d	5.23 b	70.3 df	76.7 bd	3.8 ac
Y	NT-22	71.3 df	4.4 d	4.03 m	40.0 n	66.3 ch	2.4 dg
Z	NT-23	164.3 b	5.2 b-d	5.33 b	92.3 a	28.7 jk	2.7 cg
A1	GALIA	91.7 c	4.5 d	4.43 jk	67.3 dd	57.7 dj	3.0 ag
B1	NAQEEB	65.7 dg	5.5 a-d	4.60 hi	66.7 eg	43.0 fk	2.8 bg
C1	AS2565	63.7 dg	5.5 a-d	4.37 k	57.3 hk	71.7 bg	3.2 ae

Values having similar letter's are not significantly different at 5% level of significance.

Table 2. Analysis of variance and estimates of genetic parameters for different characters in tomato genotypes

Source	d.f	Plant height (cm)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Number of fruits per plant	Fruit yield per plant (kg)
Genotypes	28	5251.62**	2.16**	1.38**	1117.97**	6043.63**	1.026**
Replications	2	159.66	0.47	0.02	24.88	797.84**	1.914**
Error	56	76.94	0.50	9.00	14.02	228.32	0.36
Mean ± S.E	86	85.67 ±5.0	4.94 ±0.4	4.58 ±0.1	61.05 ±2.2	68.22 ±8.7	2.87 ±0.3
$\sigma^2 g$		1724.89	0.55	0.46	367.99	1938.44	0.22
$\sigma^2 p$		1801.83	1.05	0.47	382.00	2166.75	0.58
GCOV		48.84	15.08	14.75	31.42	64.54	16.45
PCOV		49.55	20.77	14.89	32.02	68.23	26.55
h^2(b.s)%		96	53	98	96	89	38
G.A(% of mean)		98	23	2.2	57	126	21

*,**=Significant at 0.05 and 0.01 level of probability, respectively.

Standard cultural and plant protection measures were followed till harvest of the crop. Five plants per genotype in each replication were selected randomly at fruit ripening to record data on following traits; plant height (cm), fruit length (cm), fruit width (cm), single fruit weight (g), number of fruits per plant and fruit yield per plant (kg). Data was subjected to analysis of variance (Steel and Torrie et al., 1997). Heritability in broad sense [$h^2_{(b.s)}$] and genetic advance (*GA*) in term of percentage of mean were calculated as per standard procedure Lush (1940). Afterwards, cluster analysis later on, was performed following Hierarchical Cluster technique (Ward, 1963). Euclidean distance between groups was used as a unit to measure the genetic relationship among the genotypes.

3. Results and Discussion

Mean comparison indicated considerable variations in tomato genotypes for different traits (Table1) as reported earlier (Dar et al., 2012). Analysis of variance revealed highly significant genotypic mean square for each character among all genotypes (Table 2). The prospects of further genetic improvement using such material could therefore be enormously predicted as reported elsewhere (Goncalves et al., 2009; Saleem et al., 2013a).

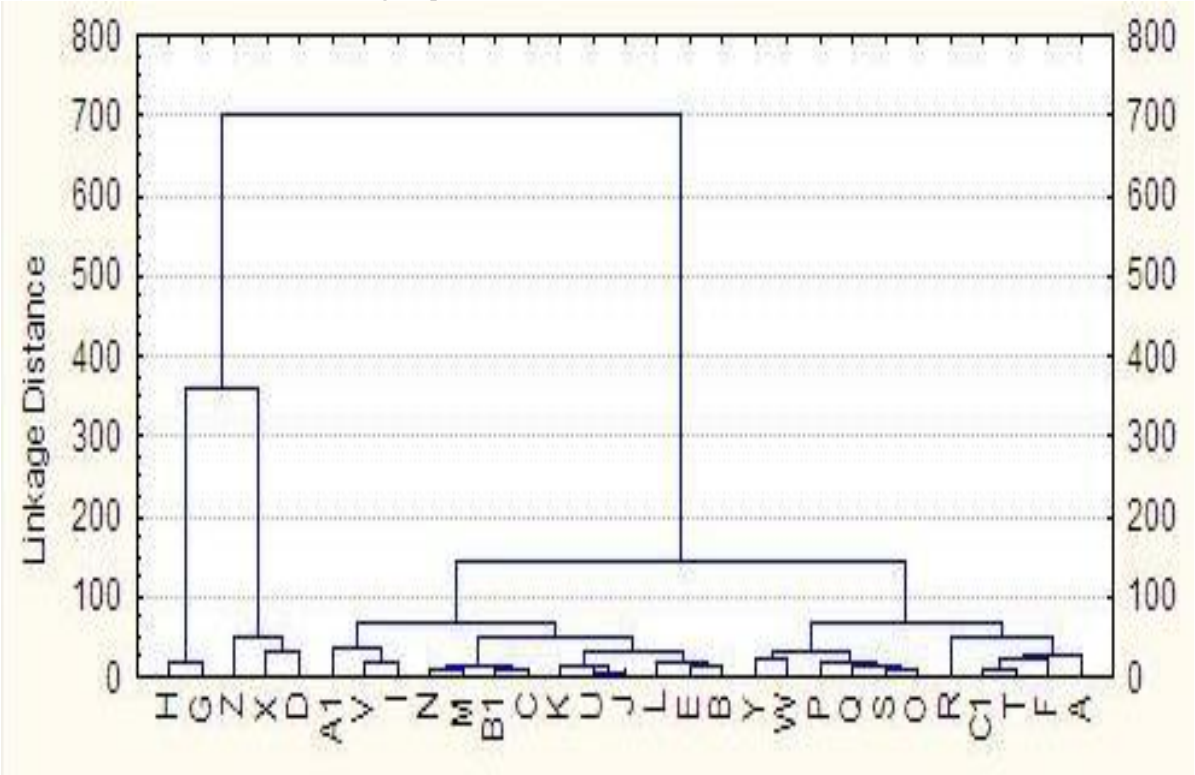

Figure 1. Tree diagram ofbased on different traits in tomato genotypes.

Table 3. Average Intra and Inter-Cluster distance (D^2) for tomato genotypes

Cluster	I	II	III	IV
I	(26.50)	35.00	108.39	196.77
II		(23.25)	104.123	214.73
III			(32.67)	170.16
IV				(17.0)

Value in parenthesis presents intra cluster distance.

The phenotypic variance ($\sigma^2 p$) and phenotypic coefficient of the variance (*PCOV*) were greater than their corresponding genotypic variance ($\sigma^2 g$) and genotypic coefficient of the variance (*GCOV*) for all characters, in particular, for number of fruits per plant and fruit yield per plant which showed a strong influence of environment on the expression of such traits. The result was in close harmony to Mohamed et al. (2012) in tomato. All characters showed high values of broad sense heritability however, fruit yield had moderate heritability as categorized elsewhere (Lush et al., 1940). Higher values of genetic advance were recorded for all the characters except for fruit width which showed lower value. The heritable variation could be well exploited in association with genetic advance (Saleem et al., 2011). Number of fruits per plant, fruit weight, plant height and fruit length exhibited high genetic advance in association with high heritability indicating the least influence of environment and predominance of additive gene action on these characters, thus improvement could be made through selection in early generations (Manna and Paul, 2012; Gaikwad and Bhalekar, 2012).

3.1 Cluster analysis

Cluster analysis distributed twenty nine genotypes into four clusters as per Euclidean distance comparison (Fig.1). Eleven genotypes (AL-1, AL-7, NT-9, NT-10, NT-11, NT-13, NT-14, NT-15, NT-19, NT-22 and AS2565) amounting to 37% of entire genotypes, were grouped in cluster-I. Cluster-II was the largest among all the four clusters, where thirteen (45%) genotypes (AL-2, AL-3, AL-6, NT-2, NT-3, NT-4, LB-3, NT-7, NT-8, NT-16, NT-18, Galia and Naqeeb) were grouped together.

Cluster-III comprised of three (10%) genotypes (AL-5, NT-21 and NT-23), while only two (7%) genotypes (AL-8 and AL-9) were grouped in Cluster-IV. Our results were comparable to findings of Krasteva et al. (2010) wherein they grouped determinate accessions of tomato using cluster analysis.

The Intra-cluster distances (17.00-32.67) were smaller compared to those of inter-cluster distances (35.00 - 214.73) in all cases (Table 3) which could be attributed to different origin of genotypes and prevailing climatic conditions (Krasteva, 2001).

Genotypes of cluster-III displayed maximum intra cluster diversity (32.67) whereas those of cluster-IV showed minimum intra cluster diversity (17.00) meaning by that genotypes grouped in cluster-III were more heterogeneous as compared to those of cluster-IV being more closely related. So far as inter cluster distances were concerned, cluster-II and cluster-IV were most distant (214.73) followed by the genetic distance between cluster-I and cluster-IV (196.77) and between cluster-III and cluster-IV (170.16). However, lowest genetic distance was found between cluster-I and cluster-II (35.0) pursued by the genetic distance between cluster-I and cluster-III (104.13). According to the cluster mean performance (Table 4), all high yielding (3.13 kg per plant) genotypes were grouped in cluster-III whereas minimum low yielding (2.65 kg per plant) in cluster-IV. Genotypes with short stature (65.73) were grouped in cluster-I and cluster-II (68.77).

For fruit length fruit width and single fruit weight, genotypes of cluster-II had the highest mean values (5.21, 4.93 and 73.16, respectively) in contrast to the genotypes of cluster-IV with the lowest mean values (2.65, 2.81 and 12.65, respectively) indicating the degree of diversity among cluster-II and cluster-IV for these traits. Genotypes of cluster-IV possessed the highest number of fruits per plant (218.7) over the genotypes of all clusters.

Table 4. Cluster means for different characters in tomato genotypes

Trait	Cluster Mean			
	Cluster-I	**Cluster-II**	**Cluster-III**	**Cluster-IV**
Plant height	65.73	68.77	167.10	183.00
Fruit length	5.01	5.21	4.87	2.65
Fruit width	4.37	4.93	4.99	2.81
Fruit weight	53.04	73.16	69.97	12.65
Number of fruits per plant	65.30	48.17	59.80	218.70
Fruit yield per plant	2.84	2.88	3.13	2.65

It was also clear that fruit length, single fruit weight and number of fruits per plant contributed maximum towards genetic divergence between cluster-II and cluster-IV. Character with maximum contribution towards genetic divergence should be preferred to decide cluster suitable for further selection and to choose parents for hybridization (Zia-ul-Qamar et al., 2012). In present study, genotypes grouped in cluster-II being superior for plant height, fruit length and single fruit weight with respect to per se performance, heritability and genetic advance could be crossed with genotypes of cluster-III having greater values for fruit width and fruit yield to develop superior combinations. Furthermore, genotypes with extreme expression of trait (s) could be chosen from different clusters to study gene action either by way of diallel or Line x Tester analysis (Saleem et al., 2009).

4. Conclusion

Present study showed significant variability in tomato genotypes in targeted traits. The breeders can include genotypes grouped in cluster-II and III to make a sensible hybridization strategy with more reliability and confidence to evolve superior combinations either in F_1 or in succeeding generations. This would ultimately lead to release high yielding variety better adapted to local environment.

Competing Interests

Authors declare that they have no competing interests about the contents of this article.

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