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Morphological Markers based Assessment of Genetic Diversity in Cultivated Tomato (*Solanum Lycopersicon* L.) Genotypes

Supneet Kaur*, A. K. Singh, Sreshti Bagati, Mamta Sharma and Satish Sharma

School of Biotechnology, Sher-e-Kashmir University of Agriculture Sciences and Technology, Chatha, Jammu, 180009
Email id:
*E-mail: supneethr77@gmail.com

***Abstract*—** *Assessment of genetic diversity in any crop species provides a basis for devising future strategies for crop improvement; conservation and sustainable use. An experiment consisting of 24 genotypes of Tomato was conducted during the year 2016 at the Research Farm and Molecular Biology Laboratory of School of Biotechnology, SKUAST-J, Chatha. The experiment was conducted in Randomised Block Design (RBD) with three replications in 2 rows of 5m length with spacing of 45 x 90 cm. The extent of genetic divergence /relatedness was estimated among 24 genotypes by using 11 traits viz. plant height (cm), number of branches, number of fruits per bunch, total soluble solids, flesh thickness (mm), number of locules, fruit width (cm), fruit length (cm), yield per plant (g), average fruit weight (g), number of fruits per plant. The maximum number of fruits/bunch was recorded in "Utkal Pragyan" (3.66) and the minimum number was recorded in "Swarna Sampada" (2.03). Maximum TSS(%) was recorded in DCT-1 (8.06%) and minimum TSS was recorded in "Dhanshri" (2.83%). Maximum number of fruits and yield/plant was recorded in "DCT-1" (115.33) and "Hisar Lalit" (2507.36g), respectively. The minimum number of fruits and yield/ plant was recorded in "NDT-4" (23.20) and "DCT-1" (861.40g), respectively.Mean data revealed high range for most of studied traits. Hierarchical cluster analysis allowed the assessment of similarity and clarified some of the relationships among tomato genotypes. UPGMA produced a dendrogram with two main clusters with further sub clusters. Of all the studied 24 genotypes Anand tomato and Hisar lalit were found to be most dissimilar based on UPGMA clustering. Hisar lalit was found to be most promising variety among all the genotypes for most of the traits under study, which can be used for further breeding and crop improvement programmes.*

***Keywords*—Genetic diversity analysis, Morphological traits, cluster analysis, ANOVA, genetic advance.**

I. INTRODUCTION

Tomato is one of the significant vegetable crops of special economic importance in the horticulture industry, originating in South America and its many varieties are now commonly grown in greenhouse in cooler climates (He *et al.*, 2003). It is the most popular garden vegetable belonging to the genus *Lycopersicon*, the resemblance between leaves and flowers of potato and tomato plants seems to certify this taxonomic grouping (Wang *et al.*, 2005 and Shidfar *et al*., 2011). Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Furthermore, if an improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and breeding value of the available germplasm (Singh *et al.*, 2002).

Tomato crop has wider adaptability, high yielding potential and multipurpose uses in fresh as well as processed food industries. 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.

Tomato fruit and its products are the main source of lycopene and other antioxidants in the human diet (Fraser *et al*., 2002) and recent epidemiological studies have shown that their consumption helps to prevent cardiovascular disease (Arab and Steck, 2000, Jarquín-Enríquez*et al*., 2013) and some types of cancer, such as prostate cancer (Barber and Barber, 2002, Shi *et al*., 2002).

The tomato plants show ample morphological variation. The plants may be in form of bushes (determinate) or vines up to six feet tall (indeterminate). The stem and leaves are pubescent having non glandular and glandular trichomes with unpleasant odour. The stem hair may develop into roots when in contact with soil. The leaves display spiral phyllotaxy i.e. one leaf at each node and are petiolate, compound, imparipinate. Tomato shoots show sympodial

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branching with apical meristems. Cultivated tomato is autogamous and style is enclosed by the staminal cone to assure self pollination.

Morphological characters have for a long time remained the means of studying genetic variations in plant species. It is a traditional approach used to quantify genetic differences, and is often used for genetic diversity analysis (Khadivi-Khub *et al.*, 2008; Nikoumanesh *et al.*, 2011). Since the quantitative characters are markedly influenced by the environment, a study under different locations and years is likely to bring out the genotype-environment interaction for precise estimation of genetic parameters and predicting the progress of selection. Moreover, knowledge about association of various characters and their relative contribution to yield is helpful for multiple trait selection. Thus, the present study was conducted with the aim to study the genetic diversity of tomato cultivars using morphological traits and development of phylogenetic tree by using bio informatics tools in order to generate a sound breeding plan for its improvement.

II. MATERIAL AND METHODS

The experimental material for the study comprised of 24 genotypes of Tomato (*Solanum lycopersicum* L.), which were grown in a Randomized Block Design (RBD) with three replications in which 21 days old seedlings were transplanted in 2 rows of 5m length with plot spacing of 45 x 90 cm. All the agronomic and plant protection practices as applicable for commercial tomato crop were adopted. In each genotype, 5 plants were selected for various observations. The materials used in this study were taken from Indian Institute of Vegetable Sciences (IIVR), Varanasi. The details of tomato genotypes are shown in Table 1.

2.1 Methodology adopted

Recommended package practices were followed for raising a good crop. Observations were recorded for the various morphological, agronomical, yield and quality traits in order to study the magnitude of variability and level of genetic divergence in the material. Five plants per plot per replication were randomly selected and tagged for recording the characters. Mean values for all the characters were worked out. Eleven characters were studied for morphological characterization of tomato viz. Plant height (cm), Number of branches per plant, Number of fruits per bunch, Fruit length (cm), Fruit width (cm), Number of fruit per plant, Number of locules per fruit, Total soluble solids (^{0}Brix), Flesh thickness(cm), Yield per plant(g) and Average fruit weight (g).

2.2 Data analysis

The morphological data recorded during the investigation was subjected to the statistical analysis which included ANOVA, Genotypic and phenotypic coefficient of variation, Heritability and Genetic advance.

III. RESULTS AND DISCUSSION

24 genotypes of tomato was evaluated for morphological characters as per the standard procedure. The significant variation in tomato genotypes with respect to yield and quality characters may be due to the genetic makeup, status of water and oxygen during the growing period of these genotypes. The oxygen deficiency restricts root respiration and negatively affects water and nutrient uptake. This eventually reduces the yield and its quality. The description of the genotypes with respect to 11 characters is described in Table 2.

3.1 Analysis of variance (ANOVA)

Analysis of variance was carried on various morpho-physiological, phenological, yield components and quality traits for studying the variation. ANOVA showed highly significant variation among the genotypes for all the characters. The analysis of variance revealed significant mean square estimates for all the characters indicating sufficient diversity among the genotypes. The variation in the genotypes would be helpful in the development of superior varieties. The results are in agreement with the observations of Golani *et al*. (2007). The analysis of variance for the data recorded on various traits viz. plant height, number of branches, number of fruits per bunch, total soluble salts, pericarp thickness, fruit length, fruit width, number of locules, average fruit weight, number of fruits per plant and yield per plant are presented in the Table 3.

3.2 Genetic parameters for various morphological, phenological, yield components and quality traits in tomato genotypes

3.2.2 Phenotypic coefficient of Variation (PCV)

The phenotypic variance ranged from 14.61 to 46.57 and the lowest variance was recorded for fruit width (14.61) and maximum was recorded for number of fruits per plant (46.57) followed by flesh thickness (33.53) and average fruit weight (33.21) (Table 5). Phenotypic coefficient of variation (PCV) was more than genotypic coefficient of variation (GCV) for all studied 11 traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for Number of fruits/plant

(45.35, 46.57%), Average fruit weight (32.71, 33.21 %), flesh thickness (29.06, 33.53 %), Yield per plant (26.55, 29.14%) and Number of locules/ Fruit (22.68, 22.97 %), which suggested greater phenotypic and genotypic variability among the accessions and sensitiveness of the attributes for making further improvement by selection. Wide difference between GCV and PCV for Number of branches and Number of fruits/bunch implied its susceptibility to environmental fluctuation, whereas narrow difference between GCV and PCV for other traits suggested their relative resistance to environmental alteration. The PCV was higher than the respective GCV for all the characters denoting environmental factors influencing their expression to some degree or other. These results are in agreement with the observations of Henareh. (2015) who showed that high PCV and GCV was observed for plant height followed by average fruit weight estimated. In present study highest estimates of GCV and PCV were recorded for number of fruits per plant (45.35 and 46.57 per cent respectively) which is an important yield component.

3.2.2 Genotypic coefficient of Variation (GCV)

The genotypic coefficient of variance (GCV) ranged from 10.07 to 45.35. High GCV was observed in number of fruits per plant (45.35) and is followed by average fruit weight (32.71) and flesh thickness (29.06). Lowest GCV was recorded in fruit width (10.07) (Table 5).

3.2.3 Heritability

The heritability for the various phenotypic traits ranged from 42.60 per cent for number of fruits per bunch to 97.00 per cent for average fruit weight (Table 5). In the present study, the broad sense heritability estimates were high for all the parameters. Such high values of heritability for Average fruit weight, Number of fruits per plant, Yield per plant, Plant height and Total soluble solids clarified that they were least affected by environmental modification and selection based on phenotypic performance would be reliable. In traits with high heritability, genotypic variance is more than environmental variance and these characters could be considered and exploited for selection in earlier generations. Whereas, in the traits with low heritability, influence of environmental factors is strong for their expression and genotype selection based on these characters should be postponed to the later generations. The results are in close conformity with Golani *et al*. (2007) who observed high heritability for average fruits weight, fruit length, number of locules/fruit and fruit yield.

3.2.4 Genetic Advance

Genetic advance ranged from 0.60(minimum) to 75.01(maximum) for all the characters under study. High genetic advance was observed for yield per plant, number of fruits per plant, average fruit weight and plant height. The results are in close conformity with Golani *et al*., (2007). High heritability (94.80%) with low genetic advance (47.73%) was reported for number of fruits per plant (Table 5). These characters also exhibited high values of GCV which portrayed that these are controlled by additive gene effect and phenotypic selection for their improvement could be achieved by simple selection.

3.3 Diversity analysis in tomato genotypes based on Ward's linkage

Distance between all pairs of 24 genotypes was calculated using Squard Euclidean Distance method and genotypes were clustered based on Ward's method (1963). All the 24 genotypes were grouped into two main clusters with sub clusters (Figure 1). The results showed that the cluster A had two sub clusters; i.e. sub cluster A_1 and sub cluster A_2. Sub cluster A_1 had 8 genotypes (BT-136, SEL-12, NDT-9, ANGHA-1, ANGHA, NDT-1, Anand Tomato-3, NDT-4) followed by cluster Sub cluster A_2 which again had 8 genotypes (ANGHA (L-E415), Dhanshri, Punjab Ratta, PANT-T-5, Hisar Anmol, AZAD-T-2, PT-11 and NDTUR-73). Cluster B had further two sub clusters; i.e. Sub cluster B_1 and B_2. Sub cluster B_1 had 4 genotypes (DCT-1, CO-3, Swarna Sampada and ANGHA (L-E415)).Sub cluster B_2 had 4 genotypes (Utkal Pragyan, Hisar Lalit, Kashi Hemant and FEB-2). Anand Tomato-3 and Hisar Lalit were found to be highly dissimilar among 24 genotypes. The results of this study are in agreement with the results of Henareh (2015) which can be exploited for breeding new tomato varieties for the development of hybrid genotypes.

IV. CONCLUSION

The study revealed considerable phenotypical (and presumably genetic) diversity among tomato genotypes. The cluster analysis grouped the genotypes into two main clusters with further sub clusters. Highest dissimilarity was found between Anand Tomato-3 and Hisar Lalit among 24 genotypes. Hisar Lalit showed large fruit size with reference to Single fruit weight, Flesh thickness, Fruit length and Fruit width and Yield per plant. The range of the mean values defines the genetic potential of different genotypes for various characters studied. The results showed that there was significant genetic distance between the genotypes for some of the characters like yield and its attributing traits. These results indicate that if the genotypes having larger value for range of variability for various characters, there will be better chance to improve the exiting cultivars by different breeding procedures. It can be used in selection or hybridization programme for the respective characters. Phenotypic coefficient of variation (PCV) was more than

genotypic coefficient of variation (GCV) for all studied 11 traits which suggested greater phenotypic and genotypic variability among genotypes and sensitiveness of the attributes for making further improvement by selection. High values of heritability for average fruit weight, fruit length, number of locules/ fruit and fruit clarified that they were least affected by environmental modification and selection based on phenotypic performance would be reliable. Considerable genetic diversity among the cultivated 24 tomato genotypes was observed at morphological levels, which is of importance for germplasm classification, management, and further utilization.

REFERENCES

[1] Arab, L. and Steck, S. (2000). Lycopene and cardiovascular disease.*American Journal of Clinical Nutrition*, **71** (Suppl.): 1691S-1695S.

[2] Barber, N.J. and Barber, J. (2002). Lycopene and prostate cancer.*Prostate Cancer and Prostatic Disease*, **5**: 6-12.

[3] Fraser, P., Romer, S., Shipton, C., Mills, P., Kiano, J., Misawa, N., Drake, R., Schuch, W. and Bramley, P. (2002). Evaluation of transgenic tomato plants expressing an additional phytoene synthase in a fruit-specific manner.*Proceedings of the National Academy of Sciences of the United States of America*,**99**(2): 1092-1097.

[4] Golani, I.J., Mehta, D.R., Purohit, V.L., Pandya, H.M. and Kanzariya, *M.V.* 2007.Genetic variability, correlation andpath coefficient studies in tomato.*Indian Journal of Agriculture and Research*, **41** (2):146 – 149.

[5] Henareh, M. 2015. Genetic Variation in Superior Tomato Genotypes Collected from North West of Iran. *International Journal of Scientific Research in Environmental Sciences*,**3**(6): 0219-0225.

[6] He, C., Poysa, V. and Yu, K. 2003. Development and characterization of simple sequence repeat (SSR) markers and their use in determining relationships among *Lycopersicon esculentum* cultivars. *Theoretical and Applied Genetics*, **106**: 363-373.

[7] Jarquin-Enriquez, L., Mercado-Silva, E.M., Maldonado, J.L. and Lopez-Baltazar, J. 2013. Lycopene content and color index of tomatoes are affected by the greenhouse cover. *Scientia Horticulturae*, **155**: 43-48.

[8] Khadivi-Khub, A., Zamani, Z. and Bouzari, N. 2008. Evaluation of genetic diversity in some Iranian and foreign sweet cherry cultivars by using RAPD molecular markers and morphological traits.*Horticulture Environment Biotechnology*.**49**: 188-196.

[9] Singh, J. K., Singh, J. P., Jain, S. K., Aradhana, J. and Joshi, A. 2002. Studies on genetic variability and its importance in tomato (*Lycopesicum esculentum* Mill.).*Progressive Horticulture*, **34**: 77-79.

[10] Shi, J., Le Maguer, M. and Bryan, M. (2002). Lycopene from tomatoes. In: Shi, J., Ghazza, Le Maguer, M. (Eds.), Funtional Foods. *Biochemical and Processing Aspects*, vol. 2. CRC Press, Ottawa, Canada, pp. 135-166.

[11] Shidfar, F., Froghifar, N., Vafa, M., Ajab, A.R., Hosseini, S., Shidfar, S. andGohari, M. 2011. The effects of tomato consumption on serum glucose, apolipoprotein B, apolipoprotein A-I,homocysteine and blood pressure in type 2 diabetic patients.*International Journal of Food Sciences and Nutrition*, **62**(3), 289-94.

[12] Wang, X.F., Knoblauch, R. and Leist, N. 2005.Varietal discrimination of tomato (*Lycopersicon esculentum* L.) by ultrathin-layer isoelectric focusing of seed protein. *Seed Science and Technology*, **28**: 521–526.

[13] Ward, J. H. 1963. Hierarchical grouping to optimize an objective function.*Journal of the American Statistical Association*, **58**: 236-244.

[14] Nikoumanesh, K., Ebadi, A., Zeinalabedini, M. and Gogorcena, Y. 2011. Morphological and molecular variability in some Iranian almond genotypes and related Prunus species and their potentials for rootstock breeding.*Scientia Horticulturae*, **129**: 108-118.

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Table.1: Genotypes of Tomato used in study

S.No	GENOTYPE	S.No	GENOTYPE
1.	UTKAL PRAGYAN	13.	HISAR ANMOL
2.	HISAR LALIT	14.	AZAD-T-2
3.	KASHI HEMANT	15.	PT-11
4.	FEB-2	16.	NDTUR-73
5.	DCT-1	17.	BT-136
6.	CO-3	18.	SEL-12
7.	ARKA ABHAY	19.	NDT-9
8.	SWARNA SAMPADA	20.	ANGHA-1
9.	ANGHA(L-E415)	21.	ANGHA
10.	DHANSHRI	22.	NDT-1
11.	PUNJAB RATTA	23.	ANAND TOMATO-3
12.	PANT –T-5	24.	NDT-4

Table.2: Mean values of morphological traits

Genotype	Plant hei (cm)	No. of branche	No. of fruits/bu	Total s salts (b	Flesh thic (mm)	No. of lo	Fruit le (cm)	Fruit wi (cm)	Average weight (g	No. of fruits/pl	Yield/pl (g)
UTKAL PRAGY	57.55	6.43	3.66	6.20	4.08	2.18	4.88	3.91	36.26	34.00	1233.40
HISAR LALIT	59.50	6.99	2.48	3.20	4.31	2.66	5.63	4.66	54.10	46.23	2507.36
KASHI HEMAN	52.19	5.44	2.40	5.40	3.00	2.50	4.13	4.42	28.66	38.33	1092.00
FEB-2	55.00	5.32	2.61	5.20	2.00	3.50	3.52	3.50	31.80	32.66	1039.20
DCT-1	52.15	6.33	3.10	8.06	1.21	2.33	2.90	2.85	7.43	115.33	861.40
CO-3	48.29	6.20	2.66	4.83	1.83	4.33	3.63	4.45	46.00	28.33	1304.33
ARKA ABHAY	60.12	7.33	2.42	5.86	3.10	3.50	3.71	4.78	44.50	46.00	2049.33
SWARNA SAMPADA	47.97	4.53	2.03	6.00	2.10	4.66	4.03	4.36	40.83	28.33	1157.66
ANGHA(L-E415	43.43	7.09	2.51	6.36	2.75	4.00	3.90	4.53	46.00	41.00	1883.00
DHANSHRI	58.23	6.99	2.10	2.83	4.31	3.00	4.48	4.98	47.33	25.00	1182.66
PUNJAB RATT	82.02	9.20	2.72	5.86	1.91	4.16	3.62	3.76	32.30	52.00	1676.80
PANT –T-5	66.72	8.44	2.55	4.66	2.66	3.33	3.69	4.03	45.56	41.00	1873.06
HISAR ANMOL	79.55	9.00	2.51	4.20	3.13	3.13	3.76	4.50	35.56	31.66	1123.63
AZAD-T-2	52.34	5.99	2.50	5.73	2.41	3.16	3.36	4.23	27.80	36.00	995.66
PT-11	74.80	8.00	3.44	5.43	3.03	3.16	3.51	4.36	33.50	65.66	2198.96
NDTUR-73	65.63	5.75	3.32	6.13	2.83	2.66	3.44	3.87	33.26	46.00	1530.10
BT-136	57.45	6.22	2.42	5.03	3.41	3.66	4.29	4.60	47.80	37.00	1764.76
SEL-12	45.00	6.66	3.00	5.80	2.46	3.83	3.51	4.11	31.86	43.00	1373.63
NDT-9	43.31	5.44	2.35	3.56	2.33	4.66	4.55	4.76	55.05	25.66	1415.40
ANGHA-1	51.40	8.33	2.95	4.76	2.76	5.50	3.35	4.48	38.36	38.66	1480.76
ANGHA	50.02	7.23	2.87	5.80	2.66	5.33	3.55	4.57	41.26	33.66	1389.30
NDT-1	55.28	7.96	2.91	6.26	2.61	3.83	3.57	4.34	36.86	48.33	1745.83
ANAND TOMA	35.10	6.66	3.00	7.00	1.50	3.33	3.83	3.33	54.00	25.66	1394.66
NDT-4	41.24	9.66	3.33	5.30	1.66	3.33	3.98	4.45	80.00	23.00	1834.33
Mean	55.59	6.96	2.74	5.39	2.67	3.57	3.86	4.24	40.67	40.94	1504.47
C.V.	8.20	15.51	14.75	7.62	16.72	16.38	10.30	10.58	5.71	10.60	11.99
S.E.	2.63	0.62	0.23	0.23	0.25	0.33	0.23	0.25	1.34	2.50	104.18
C.D. 5%	7.50	1.77	0.66	0.67	0.73	0.96	0.65	0.73	3.82	7.13	296.57
C.D. 1%	10.01	2.37	0.88	0.90	0.98	1.28	0.87	0.98	5.10	9.52	395.90

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Table.3: Analysis of Variance (ANOVA) for morphological traits in tomato genotypes

	DF	Plant Height (cm)	No. of branches	No. of fruits/ bunch	Total soluble salts (brix)	Flesh thickness (mm)	No. of locules	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits/plant	Yield /plant (g)
Treatment	23	9443.27**	121.29**	12.17**	94.30**	46.23**	53.274**	22.99**	17.26**	12344.45**	24225.11**	11765066.78**
Replication	2	63.02	1.85	0.27	0.08	0.45	1.46	0.23	0.05	2.12	70.11	109133.20
Error	46	958.22	53.81	7.55	7.78	9.193	15.78	7.30	9.29	248.94	866.55	1497909.25

*P≤0.01% level of significance ** P≤0.05% level of significance

Table.4: Descriptive statistics for morphological traits in tomato genotypes

Traits	Mean±SD	Standard error	Maximum	Minimum	Range	Variance
Plant height (cm)	55.59±12.14	1.43	82.02	35.10	35.10-82.02	147.38
No. of branches	6.96±1.57	0.18	9.66	4.53	4.53-9.66	2.49
No. of fruits/bunch	2.74±0.53	0.06	3.66	2.03	2.03-3.66	0.28
Total soluble solids (brix)	5.39±1.19	0.14	8.60	2.83	2.83-8.60	1.43
Flesh thickness (mm)	2.67±0.88	0.10	4.31	1.21	1.21-4.31	0.78
No. of locules	3.57±0.99	0.11	5.5	2.18	2.18-5.5	0.99
Fruit length (cm)	3.86±0.65	0.07	5.63	2.90	2.90-5.63	0.43
Fruit width (cm)	4.24±0.61	0.07	4.98	2.85	2.85-4.98	0.37
Average fruit weight (g)	40.67±13.31	1.56	80	7.43	7.43-80	177.40
No. of fruits/plant	40.94±18.82	2.21	122	21	21-122	354.39
Yield/plant (g)	1504.47±433.98	51.14	2507.36	861.40	861.40-2507.36	188339.56

Table.5: Genetic parameters for various morphological, phenological, yield components and quality traits in tomato genotypes

Trait	GCV (%)	PCV (%)	ECV (%)	Heritability (h^2)	GA (@ 5%)	GA (@ 1%)
Plant height (cm)	20.50	22.08	8.20	86.20	21.79	27.93
No. of branches/ Plant	16.78	22.85	15.51	53.90	1.76	2.26
No. of fruits/bunch	12.70	19.47	14.75	42.60	0.46	0.60
Total soluble salts (^{0}brix)	21.20	22.53	7.62	88.60	2.21	2.84
Flesh thickness (mm)	29.06	33.53	16.72	75.10	1.38	1.77
No. of locules/Fruit	22.68	27.97	16.38	65.70	1.35	1.73
Fruit length (cm)	13.68	17.13	10.30	63.80	0.87	1.11
Fruit width (cm)	10.07	14.61	10.58	47.50	0.60	0.77
Average fruit weight (g)	32.71	33.21	5.72	97.00	27.00	34.60
No. of fruits/plant	45.35	46.57	10.60	94.80	37.24	47.73
Yield/plant (g)	26.55	29.14	11.99	83.06	75.01	96.13

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Table.6: Distribution of 24 tomato genotypes into two main clusters

Cluster	Sub clusters	Total entries	Genotypes
A	A_1	8	BT-136, SEL-12,NDT-9,ANGHA-1,ANGHA,NDT-1,ANAND TOMATO-3 NDT-4
	A_2	8	ANGHA(L-E415), DHANSHRI, PUNJAB RATTA, PANT-T-5, HISAR ANMOL, AZAD-T-2, PT-11, NDTUR-73
B	B_1	4	UTKAL PRAGYAN, HISAR LALIT, KASHI HEMANT, FEB-2
	B_2	4	DCT-1, CO-3, ARKA ABHAY, SWARNA SAMPADA

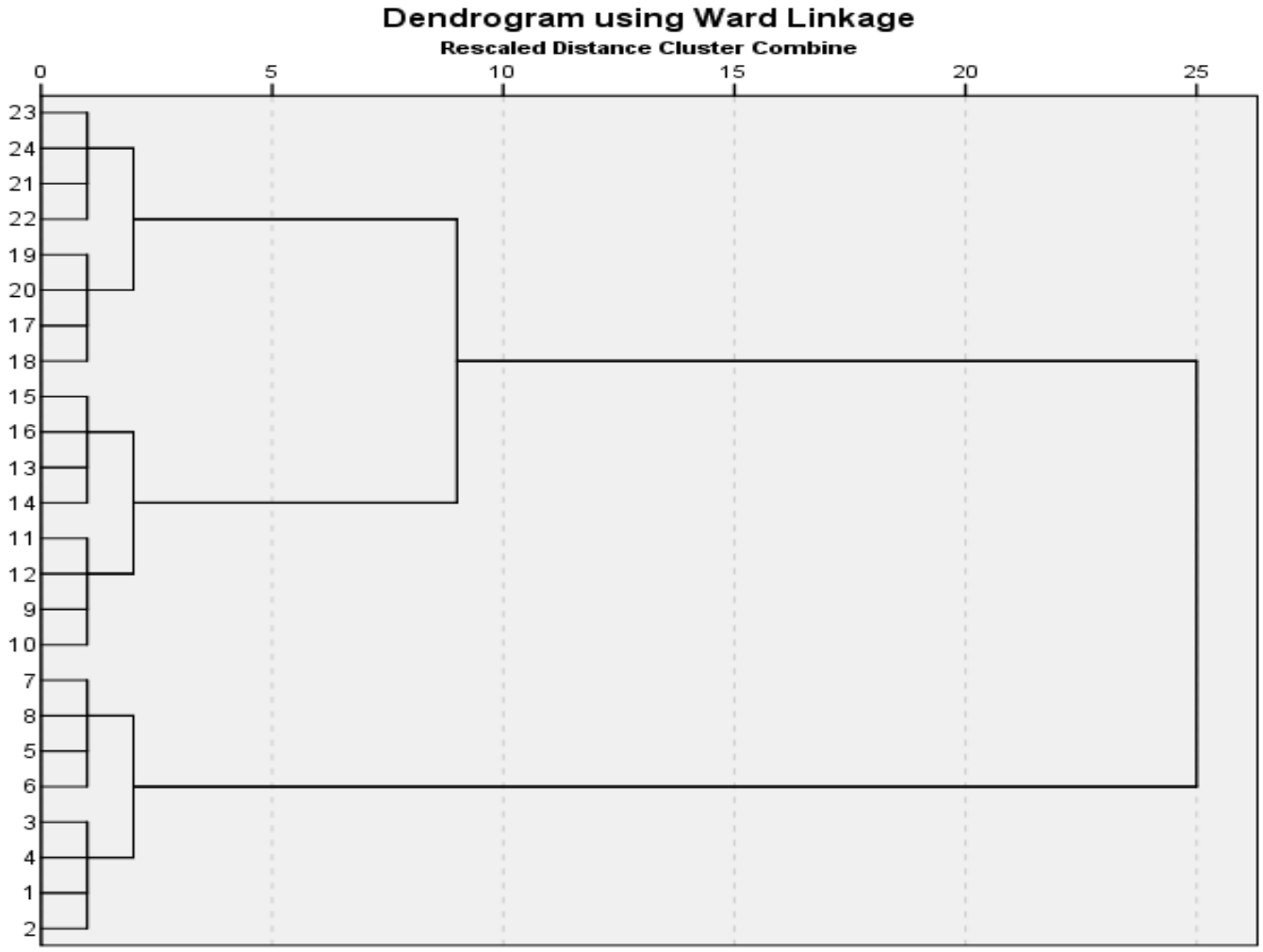

Fig.1: Dendrogram showing Genetic diversity in Tomato genotypes based on morphological markers using Ward linkage.

1-Utkal Pragyan, 2- Hisar Lalit, 3- Kashi Hemant, 4- FEB-2, 5- DCT-1, 6-CO-3, 7- Arka Abhay, 8-Swarna Sampada, 9- ANGHA (L-E415), 10- Dhanshri, 11- Punjab Ratta, 12-PANT-T-5, 13- Hisar Anmol, 14- AZAD-T-2, 15- PT-11, 16- NDTUR-73, 17- BT-136, 18- SEL-12, 19- NDT-9, 20- ANGHA-1,21- ANGHA, 22-NDT-1, 23- Anand Tomato-3, 24- NDT-4