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Genetic Dissection for Yield and Fruit Quality Traits in Tomato (*Lycopersicon esculentum* Mill.)

Sidratul Muntaha, Nur-Un-Nesa, and G. H. M. Sagor

ABSTRACT

The genetic variability for yield, its attributing, and fruit quality traits using 38 tomato genotypes was studied. High significant differences among the genotypes were found for all recorded traits. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits indicating the presence of environmental influences. Most of the traits expressed moderate to high heritability. Plant height, number of seed/fruit, chlorophyll content in top leaf, red fruit weight, number of fruit/plant, soluble solid content in exocarp and endocarp of red fruit, titratable acidity of red fruit juice, lycopene content, beta-carotene and yield/plant had high heritability along with high genetic advance as percentage of the mean. Yield/plant exhibited a significant positive correlation with number of fruit/plant, number of flower/bunch, red fruit girth, red fruit length and red fruit weight. Path analysis revealed soluble solid content in endocarp of red fruit, number of fruit/plant, plant height, number of bunch/plant, number of flower/bunch, number of seed/fruit, green fruit length, red fruit girth, red fruit length, red fruit weight, lycopene and beta-carotene content had direct positive effect on yield/plant. Principal component analysis depicted first eight PCs with Eigen-value higher than one contributing 76.74% of total variability. Thirty-eight genotypes grouped into seven clusters where cluster II contains maximum genotypes. Based on the mean performance, genotypes Tm-131 and WOP-10 for yield and ascorbic acid content; Puli-25, VI005584 and Tm-2 for total soluble solids; VI-063607 and VI-0337183 for lycopene and beta-carotene content may be considered as superior genotypes which can be used as potential genetic resources for the development of nutritionally rich high-yielding tomato variety.

Keywords: Genetic variability, heritability, tomato genotypes, yield and fruit quality traits.

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I. Introduction

Tomato (*Lycopersicon esculentum* Mill.) is a well-known plant that belongs to the family Solanaceae, which includes more than 3000 species. It is a widely consumed vegetable either fresh or industrially processed [1]. Tomato is a self-pollinated crop (2n=24). Its identical features make them valuable for both economic and research purposes. It is also used as model plant because of its diploid compact sequenced genome and large genetic and genomic resources [2]. Wild tomatoes, especially self-incompatible species, exhibit the highest genetic diversity [3]. Tomatoes are extensively consumed vegetables, having exceeded an annual production of 180 million tons over the last seven years [4]. In 2020, the world harvested 186.821 million metric tons of tomatoes on a 5,051,983 ha area, with an average yield of 37.1 metric tons per hectare [5]. Annual production of tomato in Bangladesh was 442 thousand metric tons in 2021-22 fiscal years [6]. It ranks next to potato and sweet potato in respect of vegetable production in the world [7]. In case of production, tomato holds the fourth position, while it ranks third in terms of cultivation area in Bangladesh [8].

After potatoes and before onions, tomato is one of the most consumed vegetables in the world and perhaps the most preferred garden crop. It is a rich source of macro and micronutrients [9], vitamins, and phytochemicals for dietary habits of humans [10]. Tomatoes are also rich in Vitamin A. It has high nutritive values of 3.6 g carbohydrate, 585 IU Vitamin A, 31 mg Vitamin C, Vitamin B, ascorbic acid and other minerals. In addition, 100 g of fresh fruits contributed between 4.5 and 7.7% of K, 0.8 to 1.8% of Ca, 2.3 and 4.4% of Mg, 3 to 6.6% of P, 3.1 to 6.9% of Fe, and 1.9 to 4.2% of Zn to meet daily needs [11]. Tomatoes are sold not only fresh but also processed into products like paste, juice, and sauce. They can aid in eliminating toxins from the body and act as a mild kidney stimulant. Short sightedness, night blindness, and other eye diseases prevention is possible from regular consumption of tomatoes [12]. Due to special nutritive value and antioxidant properties including presence of lycopene and flavonoids, they are together considered as 'Protective food' [13]. Tomato intake safeguards against oxysterols, aids kidney disease patients. Lycopene's protective impact on cholesterol products and health anomalies noted in older individuals [14]. The amount of lycopene in tomatoes varies depending on the variety and rises as the fruit ripens [15] and varies from 0.85 mg to 13.6 mg per 100 g of fresh tomato [16]. It is present almost exclusively in tomato and tomato-based products. Processed tomato products like ketchup, tomato juice, spaghetti sauce,

and pizza sauce contribute to over 80% of dietary lycopene intake [17]. The sweetness of tomato fruits is attributed to sugars, which play a crucial role in determining the primary aspect of fruit quality. A number of horticultural studies were conducted to evaluate the relationship between sugar content, measured as the soluble solids content and fruit yield [18].

For the identification and estimation of genetic diversity, morphological or agro-morphological traits are the major factors [19]. Wide genetic variability in germplasm is the primary requirement for crop improvement [20]. Heritability and genetic advance can be used to measure how much the environment affects a character's expression and how much improvement is achievable following selection [21]. For successful genetic research, it's crucial to have inheritable variation and significant genetic progress. High heritability and substantial advancement are necessary for effective selection in subsequent generations with diverse traits [22]. Phenotypic and genotypic coefficients show germplasm diversity. Multivariate analysis, like Principal Component Analysis (PCA), gauges genotypic diversity. It depicts character variation patterns among genotypes [23]. Correlation coefficients aid desired trait selection in breeding program. They measure relationships among plant characteristics. Path coefficient analysis adds insight by predicting interactions and effects on yield [24], [25]. Path analysis identifies elite genotypes by separating direct and indirect effects of dependent variables on independent ones.

Therefore, the present research work has been undertaken in order to determine the nature of association direct and indirect relationship between yield and yield contributing characters through the genetic analysis, correlation coefficient, path coefficient analysis, principal component analysis, and diversity analysis.

II. Materials and Methods

A. Plant Materials

This study was conducted with 38 tomato genotypes (Walter, Feridal (CARE), Bonset, CL170-0-2-2-0, Puli No-25, Derinia, Sunlight pole, Marmeud, ROBIN CVFS F1 RS ($^{\times}$46), Manik (BARI Tomato 1), TC0014-52-18-13-14-12-0, TC0131-41-12-35-38-0-0, TC0131-41-12-14-16-0-0, TC0130-41-52-3-56-0-0, TC242-14-15-47-23-41, TC233-9-10-4-1-28-8, TC0-02-11-47-8-21-22-12-0, TC0245-53-8-17-4-7-0, BARI Tomato-3, BINA Tomato-5, BINA Tomato-8, BINA Tomato-11, VI006136, VI005599, VI057583, VI005583, VI007282, VI005584, VI063607, VI037183, VI006422, Tm-2, Tm131, WOP-10, T2, T6, T8, TC0256) which were collected from Bangladesh Institute of Nuclear Agriculture (BINA) and the Field Laboratory of Genetics and Plant Breeding Department, Bangladesh Agricultural University, Mymensingh, Bangladesh.

B. Experimental Area, Environment and Experimentation

The field study was carried out at the Experimental Farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh during October 2018 to April 2019. Seeds were sown in 24th of October 2018 and 28 days old seedlings were transplanted in the main field in 22nd of November 2018. This experiment was performed with three replications following Randomized Complete Block Design (RCBD) and randomization was done in each experimental unit where 40 cm and 60 cm spacing were practiced between replications and rows, respectively. The experimental area's terrain was medium-high land that was in Agro-Ecological Zone 9 (Old Brahmaputra Flood Plain). The soil consistency was sandy loam and the soil pH ranged from 6.5 to 6.7. The experimental field was followed by congenial agronomic practices.

C. Data Collection

Nine qualitative traits (leaf surface, leaf arrangement, internode distance, succulence, pigmentation, hairiness, bushiness, fruit size and disease) were recorded according to the IPGRI (International Plant Genetic Resources Institute) tomato descriptor and twenty-one quantitative traits including morphological (plant height, number of bunch/plant, number of flower/bunch, number of fruit/bunch, number of seed/fruit, chlorophyll content in top leaf, green fruit girth, green fruit length, green fruit weight, red fruit girth, red fruit length, red fruit weight and Number of fruit/plant) and biochemical characters (soluble solid content in exocarp of red fruit, soluble solid content in endocarp of red fruit, ph of red fruit juice, titratable acidity in red fruit juice, ascorbic acid in red fruit exocarp, lycopene content and beta-carotene) were studied from three randomly selected plants from each replication.

D. Lycopene and Beta-Carotene Quantification

Quantification of lycopene and beta-carotene was conducted according to a method described by [26]. About 0.5 g tomato pulp was homogenized with 5 mL acetone-hexane (4:6) solution. All pigments were extracted. Optical density of the supernatant was measured at 663 nm, 645 nm, 505 nm, and 453 nm by spectrophotometer. The content of lycopene and beta-carotene content were estimated.

E. Total Soluble Solids (TSS), pH and Titratable Acidity

Total Soluble Solids (TSS) in red fruit exocarp and endocarp, pH and titratable acidity in red fruit juice were measured by following [27].

F. Ascorbic Acid Determination

About 0.1 g of red fruit extract was mixed with 1 mL of 10% trichloroacetic acid (TCA). After vortexing for 1-2 minutes, the mixture was cooled in an icebox for 5 minutes and centrifuged at 3000 g for 5 minutes. Supernatant (220 µL) was combined with 2 mL of distilled water and 200 µL of Folin reagent. After shaking and a 10-minute rest at room temperature, absorbance was measured at 760 nm using a spectrophotometer.

G. Statistical Analysis

Statistical analysis was done using the statistical software RStudio, version 4.0.3 Genotypic variance (GV), phenotypic variance (PV), heritability in a broad sense (h^2b), genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), genetic advance (GA), genetic advance as percentage of mean (GA%), Pearson correlation coefficient,

path coefficient, Principal Component Analysis (PCA) [28], Cluster analysis (Ward's method) were done using software.

III. Results and Discussion

A. Morphological Documentation

Thirty-eight tomato genotypes were documented morphologically. The modern tomato breeding programs have emphasized yield, resistance to biotic and abiotic stresses and quality attributes. In addition, morphological traits assess genetic variation and genotypes performance under specific conditions. The table showed that thirty-eight genotypes exhibited variation in terms of studied qualitative characters which can be utilized in tomato genotypes selection.

B. Genetic Parameters

Analysis of variance, genotypic variance (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (%), genetic advance (GA) and genetic advance as a percentage of mean (GA%) of the recorded traits were presented in Table I. Genotypes showed significant variation and non-significant variation was found for replication denoting the existence of wide genetic diversity among the selected genotypes provided sufficient scope for selection for these traits. Significant differences among the selected 40 tomato genotypes were estimated by [29] for all the selected traits except days to 50% flowering. Similar results were also observed by [30].

The PCV values were but not significantly higher than those of the GCV for all the traits suggesting the apparent variation was mainly due to genotypes. Low disparities between genotypic and phenotypic variance indicate better heredity and less environmental influence on the manifestation of any particular trait.

Additionally, number of flower/bunch, number of fruit/bunch, number of seed/fruit, chlorophyll content, green fruit length, green fruit weight, red fruit length, red fruit weight, soluble solid content in exocarp and endocarp of red fruit, titratable acidity, lycopene content, beta-carotene and yield/plant showed high GCV and PCV values. That means these traits can be improved through selection based on phenotypic performance. [31] deduced high GCV and PCV values for plant height, number of fruit cluster/plant, number of fruit/cluster, fruit weight, fruit/plant and fruit yield/plant. [32] also found higher GCV and PCV values for plant height, number of cluster/plant, number of fruit/cluster, fruit/plant, fruit weight and fruit yield. [33] also observed high GCV and PCV values for number of fruit/cluster, fruit length, number of seeds/fruit, total soluble solids and yield/plant.

Moreover, [34] found high GCV and PCV values for plant height, number of fruit cluster/plant, number of fruit/cluster, number of fruit/plant, total soluble solids, lycopene content and yield/plant. The value of GCV for soluble solid content in exocarp of red fruit was (22.19%) and PCV was (23%) which were similar to this study. Number of fruit/plant showed high GCV (38.99%) and PCV (39.12%); red fruit weight also showed high GCV (37.16%) and PCV (38.52%) that supported the findings of [33]. Number of bunch/plant, green fruit girth, red fruit girth and ascorbic acid content exhibited moderate GCV and PCV. Ascorbic acid content showed moderate GCV (15.94%) and PCV (17%). However, [30] observed GCV (15.21%) and PCV (15.72%) for this trait. pH contained the lowest GCV and PCV values that were agreed with [35]. The magnitude of genetic advance as a percentage of the mean categorized as high (>20%), moderate (10-20%), and low (<10%), as recommended by [22]. Lycopene and beta-carotene content showed the highest heritability (100%). GA% ranged from 1.69 % (pH of red fruit juice) to 202.78% (lycopene content). High heritability (>60%) with high genetic advance as a percent of mean (>20 %) were found in plant height, number of bunch/plant, number of flower/bunch, number of fruit/bunch, number of seed/fruit, chlorophyll content, green fruit girth, red fruit weight, number of fruit/plant, soluble solid content in exocarp and endocarp of red fruit, titratable acidity in red fruit juice, ascorbic acid content, lycopene content, beta-carotene and yield/plant indicating the presence of the effects of additive gene. [31], [32] showed high heritability and high genetic advance for plant height, number of fruit clusters/plant, number of fruit/cluster, number of fruit/plant, individual fruit weight, total soluble solid content, ascorbic acid and fruit yield. [36] also observed high heritability and high genetic advance as percentage of mean for total soluble solids, titratable acidity, ascorbic acid, and lycopene content; [30] found high heritability and genetic advance as percentage of mean for beta-carotene, ascorbic acid and lycopene content. Directional selection could be effective for desired genetic improvement. Furthermore, moderate heritability (30%-60%) was found for green fruit length and weight, pH, and red fruit girth. Red fruit length performed low heritability (<30%).

Among 21 variables, lycopene content, beta-carotene, red fruit weight, and yield/plant showed high heritability, low genetic advance along with high genetic advance as percentage of mean and these characters can be improved by inter-mating with superior genotypes of segregating populations which are developed through breeding.

C. Mean Performance

The highest plant height was found in VI005599, V1007282 and V1005584 genotypes. This trait ranged from 41.34 cm to 138.29 cm. [37] also reported similar range for plant height (41 cm to 137 cm) during the evaluation of tomato genotypes. Maximum number of bunch/plant was found in BINA Tomato-11. The trait varied significantly among the genotypes and ranged from 16 to 7 with mean value 11.61. [38] found range 15 to 8.6 and [39] remarked mean value 10.15 for this trait. The genotype walter and WOP-10 produced the highest number of flower/bunch (12 and 11.67 respectively), whereas the highest number of fruit/bunch (7.67) found in the V1005584. Number of fruit/bunch ranged from 7.67 to 2.33. Similar finding was reported by [40] who noted number of fruit/cluster ranged from 6.7 to 2.5. [38] found mean range 9.8 to 5.2 for number of fruit/cluster. The mean value for number of fruit/bunch was 4.69 which agreed with [39].

TABLE I: GENETIC PARAMETERS OF DIFFERENT TRAITS OF 38 TOMATO GENOTYPES

Sl.	Characters	MS	GV	PV	GCV	PCV	Heritability (%)	GA	GA%
1	PH	1416.01***	469.83	476.35	36.83	37.08	98.63	44.34	75.35
2	BP	16.01***	4.77	6.47	18.8	21.91	73.61	3.85	33.23
3	FlB	9.35***	2.56	4.23	19.05	24.5	60.46	2.56	30.52
4	FB	6.33***	1.78	2.78	28.41	35.51	64	2.2	46.81
5	SF	4463.4***	1479.8	1503.78	63.57	64.08	98.41	78.61	129.9
6	Chl	522.54***	171.33	179.89	27.17	27.84	95.24	26.31	54.63
7	GG	5.03***	1.57	1.89	12.43	13.65	82.9	2.35	23.3
8	GL	3.2 ***	0.77	1.66	20.31	29.89	46.22	1.23	28.46
9	GW	87.14***	18.27	50.6	22.81	37.96	36.11	5.29	28.24
10	RG	9.47 ***	2.24	4.99	13.82	20.65	44.79	2.06	19.05
11	RL	0.85**	0.15	0.54	14.16	26.84	27.85	0.42	15.4
12	RW	236.92***	77.06	82.8	37.16	38.52	93.07	17.44	73.85
13	FP	3995.7***	1328.97	1337.74	38.99	39.12	99.34	74.85	80.05
14	SEx	3.55**	1.16	1.24	22.19	23	93.08	2.14	44.1
15	SEn	7.59***	2.5	2.59	30.05	30.59	96.53	3.2	60.82
16	pH	0.02***	0.004	0.01	1.48	2.68	30.7	0.07	1.69
17	TA	0.08***	0.03	0.03	23.5	23.54	99.64	0.34	48.34
18	AA	0.04***	0.01	0.02	15.94	17	87.82	0.23	30.78
19	Lyc	0.006***	0.002	0.002	98.44	98.44	100	0.09	202.78
20	□C	0.002***	0.001	0.001	59.45	59.45	100	0.05	122.46
21	YP	6.21***	2.06	2.09	64.22	64.76	98.34	2.93	131.2

Here, ** and *** indicate significant at 1% and 0.1% level of probability respectively. (MS= Mean Square).

[38] found mean range 9.8 to 5.2 for number of fruit/cluster. The mean value for number of fruit/bunch was 4.69 which agreed with [39]. Genotype V1037183 showed maximum and WP 10 showed minimum number of seed/fruit (169 and zero respectively). The mean values showed a wide range of variation among the genotypes for chlorophyll content that also aligned with [30]. BINA Tomato-11 had the highest value for this trait. Number of fruit/plant ranged from 168 to 37.33. [41] noted this range from 171 to 19.02. Genotype TC0131-41-12-35-38-0-0, BINA Tomato-8, V1005584 and Walter showed highest green fruit girth; BINA Tomato-8, CL170-0-2-2-0, TC0131-41-12-35-38-0-0 and T2 had larger green fruit length; highest green fruit weight was found in genotype T8; highest red fruit girth and weight was observed in TC233-9-10-4-1-28-8; genotype ROBIN CVFS F1 RS (^{x}46) showed highest red fruit length. Maximum number of fruit/plant was found in WOP-10.

Genotype Puli No-25 contained highest soluble solids in red tomato fruit. Mean value of soluble solid content in exocarp and endocarp of red fruit were 4.84% and 5.26% respectively. [42] reported red tomato fruit contain 3.55% sugar in the exocarp and 2.79% in the locule. [35] noted mean value 4.83% for soluble solids in red tomato. [31] observed total soluble solid content in ripe fruit ranged from 5.60% to 3.50%. According to [43], total soluble solids ranged from 7.17% to 3% and as per [44], 6.17% to 3.42% was recorded. Elevated levels of total soluble solids are the primary quality factor for both nutritional value and processing applications [45]. Genotype T6 had maximum pH but minimum titratable acidity. Fruit pH fluctuated from 4.17 to 3.83 with 3.988 mean whereas [46] reported, fruit pH from 4.59 to 3.36 with 4.08 mean. The highest ascorbic acid examined in genotype V1006422 and WOP-10. In this study, ascorbic acid ranged from 1.05 to 0.51 mg/g. Maximum lycopene and beta-carotene content were found in genotype Puli No-25. Fruit yield/plant ranged from 6.34 to 0.63 kg/plant where fruit yield (kg/plant) 0.18 to 5.63 was stated by [41].

The results insinuate that genotype Tm-131, WOP-10 are superior for yield and ascorbic acid content; Puli-25, VI005584 and Tm-2 for total soluble solids; VI-063607, VI-0337183 for lycopene and beta-carotene content have the potential to serve as genetic resources for creating a tomato variety that is both high-yielding and rich in nutrition.

D. Character Association

Correlation studies between characters exhibited an important role in deciding on the most efficient breeding procedures shown in Table II (A, B). The genotypic correlations showed greater strength than phenotypic correlations indicating a robust inherent connection among different traits and the presence of environmental effects. These findings aligned with [30].

Yield/plant had positively and highly significant correlation with number of fruit/plant (rg=1***, rp=1***) and number of flower/bunch at both genotypic and phenotypic level. [47] found similar results. Besides, [48], [49] also mentioned that yield/plant showed positive significant association with number of fruit/plant. Again, yield/plant showed strong positive interrelation with red fruit girth and weight that supported the findings of [49]. Phenotypically red fruit length had significant positive link with yield/plant and red fruit weight. [47] stated that fruit length had significantly and positively correlated with fruit weight and yield/plant as well as [50], [51] reported that fruit length had significant positive link with yield/plant genotypically and phenotypically. On the other hand, yield/plant strongly associated negatively with chlorophyll content at both level and phenotypically with lycopene. In addition, plant height showed non-significant positive correlation with yield/plant which agreed with the findings of [30], [50].

Plant height exhibited highly significant positive interrelation with number of fruit/bunch at both level. Number of flower/bunch appeared significant positive link with number of fruit/bunch and number of fruit/plant at both level indicating any plant will have more fruit if it had more flower.

TABLE II (A): GENOTYPIC CORRELATION COEFFICIENT OF YIELD AND FRUIT QUALITY TRAITS IN 38 TOMATO GENOTYPES

Traits	Corr.	FB	Chl	GG	GL	GW	RG	RL	RW	FP
PH	rg	0.4**	0.11	0.2	-0.1	-0.1	-0.2	-0.3	-0.1	0.2
BP	rg	-0.03	0.13	0.1	0.1	0.3	0.3*	-0.01	0.1	-0.2
FlB	rg	0.4*	-0.4**	0.4*	0.1	0.4**	0.1	-0.2	0.1	0.4*
FB	rg	1	-0.4*	0.3*	0.1	0.4*	0.3*	-0.1	0.2	0.2
SF	rg		-0.02	0.1	-0.003	0.1	0.1	-0.1	0.04	0.1
Chl	rg		1	-0.1	0.14	-0.12	-0.5***	-0.2	-0.3	-0.4*
GG	rg			1	0.6***	0.9***	0.1	-0.3	0.04	0.2
GL	rg				1	0.5***	0.2	0.2	0.4***	-0.1
GW	rg					1	0.4***	0.1	0.2	-0.1
RG	rg						1	0.4***	0.9***	-0.03
RL	rg							1	0.1	-0.02
RW	rg								1	0.1
FP	rg									1

TABLE II (B): GENOTYPIC CORRELATION COEFFICIENT OF YIELD AND FRUIT QUALITY TRAITS IN 38 TOMATO GENOTYPES

Traits	Corr.	SEx	SEn	pH	TA	AA	Lyc	βC	YP
PH	rg	0.1	0.01	-0.2	-0.1	-0.2	-0.2	-0.1	0.1
BP	rg	0.2	0.1	-0.1	0.1	0.3	0.1	-0.2	-0.1
FlB	rg	-0.01	-0.04	0.2	-0.2	0.1	-0.1	-0.01	0.8***
FB	rg	-0.1	-0.16	-0.3*	-0.01	0.02	-0.2	-0.1	0.1
SF	rg	-0.1	0.1	-0.05	0.1	0.03	0.3	0.4**	-0.1
Chl	rg	0.2	0.3	0.3	-0.1	0.1	0.2	-0.1	-0.8***
GG	rg	0.1	0.2	-0.03	0.1	-0.4*	0.1	0.3	0.2
GL	rg	-0.3*	-0.3	0.2	-0.1	-0.3	-0.2	-0.1	0.2
GW	rg	0.001	0.05	0.2	-0.3	0.01	0.1	0.1	0.2
RG	rg	-0.5***	-0.5***	-0.4***	-0.2	0.3	-0.3	-0.2	0.4***
RL	rg	-0.1	0.01	0.3*	0.01	-0.01	-0.002	0.03	0.1
RW	rg	-0.4*	-0.3	-0.4**	-0.1	0.04	-0.2	-0.2	0.6***
FP	rg	-0.1	-0.2	-0.2	0.02	-0.05	-0.2	-0.02	1***
SEx	rg	1	0.9***	0.3	0.3	0.01	0.7***	0.5***	-0.2
SEn	rg		1	0.3	0.3	0.05	0.8***	0.5***	-0.2
pH	rg			1	-0.6***	0.1	0.2	0.2	-0.1
TA	rg				1	-0.1	0.2	0.3	0.1
Lyc	rg						1	0.8***	-0.3

Here, *, ** and *** indicate significant at 5%, 1% and 0.1% level of probability respectively. (Corr.= Correlation)

Furthermore, highly positive significant association was found between soluble solid content in exocarp and endocarp of red fruit. Soluble solid content in exocarp and endocarp of red fruit exhibited non-significant negative correlation with yield/plant which agreed with [52]. [53] also deduced that non-significant positive association between yield/plant and soluble solid content. On the contrary, soluble solid content in exocarp and endocarp of red fruit had highly significant positive correlation with lycopene and beta-carotene content as well as phenotypically positive relationship with titratable acidity. Moreover, soluble solid content in exocarp and endocarp of red fruit had non-significant positive link with pH and ascorbic acid. According to this results, soluble solid content in exocarp and endocarp of red fruit (total soluble solids) can be designated as an indicator of biochemical characters in tomato fruit.

Consequently, the number of fruit/plant, the number of flower/bunch, red fruit girth, length, and weight are crucial components of yield. Therefore, these parameters can be utilized to enhance yield. On the other hand, for the purpose of augmenting both nutritional value and yield in tomato selection, soluble solids content can be employed in conjunction with the aforementioned morphological characteristics.

E. Path Coefficient Analysis

Path Analysis has been presented in Table III. Path coefficient analysis dissects correlations into direct and indirect effects, revealing importance and underlying forces of causal factors [54], [55]. In this study, yield/plant was regarded as effect (dependent variable) and the rest of the characters as independent variables. The phenotypic and genotypic correlation coefficients between yield and other traits have been partitioned into direct and indirect effects by path coefficient analysis [56]. Higher positive direct effect was found in soluble solid content in red fruit endocarp followed by number of fruit/plant but lycopene and beta-carotene showed very poor positive direct effect on yield/plant. According to some previous studies, number of fruit/plant had direct positive effect on yield/plant [52]; individual fruit weight (0.719) and plant height (0.435) had direct positive effect on yield [37]; number of fruit/plant exerted very high direct effect upon yield/plant [56] that supported the present findings. On the contrary, number of fruit/bunch (-0.41), chlorophyll content (-0.27), green fruit girth (-0.08), green fruit weight (-0.15), soluble solid content in endocarp of red fruit (-1), pH of red fruit juice (-0.05), titratable acidity (-0.19) and ascorbic acid (-0.14) showed direct negative effect on yield/plant. In the present study, ascorbic acid content had direct negative effect on yield/plant that was also reported by [52].

F. Principal Component Analysis

Principal component analysis showed eight major components with Eigen-value more than one which cumulatively explained 76.74% of the total variation among the 38 tomato genotypes (Table IV). The first two

components PC1 and PC2 with a proportion of 20.108% and 13.313% respectively contributed more to the total variation. [35] found first two components PC1 (25.1%) and PC2 (16.3%) when first five components responsible for 75.1% of total variation. [55] were working with 36 tomato genotypes and reported that the first two principal components PC1 & PC2 contributed 37.14% and 13.79% respectively to the total variation while six PCs were responsible for 80% of total variation.

The PC1 had highest loadings for red fruit girth and weight that contributed positively as well as soluble solid content in exocarp and endocarp of red fruit and lycopene content contributed most negatively. As a result, the first principal component differentiated those genotypes that had less soluble solid content in exocarp and endocarp of red fruit, lycopene and more red fruit girth and weight. The PC2 had highest loadings for green fruit girth and weight as well as beta-carotene content showed higher value in PC2 among all PCs. The PC3 contributed 10.08% variability to the total variation where number of bunch/plant and number of fruit/plant had the highest loadings and lycopene content was higher in PC3. The PC4 illustrated 8.95% variability while plant height, number of fruit/bunch and green fruit girth contributed more in PC4. Therefore, PC4 could be referred to as vegetative axis.

The PC5 contained highest coefficients for pH in red fruit juice, titratable acidity, green fruit length and weight with 8.10% variability to the total variation. The contribution of PC6 towards variability was 6.3% to the total variance and had highest loadings for titratable acidity, ascorbic acid, pH, number of flower/bunch and number of seed/fruit. That suggests PC5 and PC6 are useful for nutrient rich genotype selection. Seventh PC showed highest loadings for number of bunch/plant, number of flower/bunch, red fruit weight and yield/plant. The PC8 had highest loadings for number of seed/fruit, chlorophyll content and number of fruit/plant along with 4.23% variability. Therefore, PC3, PC7 and PC8 could be collectively denominated as reproductive axis.

G. Genetic Diversity Analysis

Dendrogram analysis was prepared by following Ward's method where 38 genotypes were grouped into seven clusters viz. I, II, III, IV, V, VI and VII for all the recorded traits (Fig. 1). For 36 tomato genotypes, six clusters were found by cluster analysis. Among seven clusters, cluster II had maximum number of genotypes (11) and cluster IV contained minimum genotypes (1). However, cluster I, III, V, VI and VII included 7, 6, 5, 6 and 2 genotypes, respectively. Regarding plant height, cluster VII showed the highest value (94.17 cm), and cluster V showed the lowest value (41.73 cm). Number of bunch/plant appeared variation in the clusters, highest value (14) was found in cluster IV and lowest (10.27) in cluster V. Cluster IV showed the highest value (9) and cluster VI showed the lowest value (7.06) for number of flower/bunch. In case of number of fruit/bunch, cluster VII appeared the highest mean value (6.17) and cluster VI had the lowest value (3.28). Cluster V showed the highest value (96) and cluster II showed the lowest mean value (33.73) for number of seed/fruit. Cluster mean value of chlorophyll content was highest in cluster VI (70.01) and lowest in cluster II (42.36).

The results showed that cluster IV comprised of maximum number of traits which exhibited highest mean value followed by cluster I as well as suggesting that cluster IV and I contained nutritional rich and yield contributing genetic resources respectively.

IV. Conclusion

The result of this study represented wide diversity among the characters. Simple selection can improve these traits. Moreover, cluster IV and I may be considered as parents in regard to nutritional value and yield contribution in plant breeding program.

TABLE III: Partitioning Genotypic Correlation into Direct (BOLD) and Indirect Effects of 20 Traits on Yield/Plant

Char.	PH	BP	FlB	FB	SF	Chl	GG	GL	GW	RG	RL
PH	**0.14**	0.01	-0.03	-0.16	-0.02	-0.03	-0.02	-0.02	0.02	-0.04	-0.08
BP	0.01	**0.1**	0	0.01	-0.03	-0.04	-0.01	0.02	-0.04	0.06	0
FlB	-0.03	0	**0.17**	-0.15	0.01	0.11	-0.03	0.03	-0.06	0.02	-0.05
FB	0.05	0	0.06	**-0.41**	-0.01	0.1	-0.03	0.04	-0.05	0.06	-0.03
SF	-0.03	-0.02	0.01	0.03	**0.11**	0	-0.01	0	-0.01	0.02	-0.03
Chl	0.01	0.01	-0.07	0.15	0	**-0.27**	0.01	0.04	0.02	-0.09	-0.06
GG	0.03	0.01	0.06	-0.13	0.01	0.03	**-0.1**	0.16	-0.13	0.02	-0.08
GL	-0.01	0.01	0.02	-0.05	0	-0.04	-0.05	**0.28**	-0.07	0.04	0.07
GW	-0.02	0.03	0.07	-0.15	0.01	0.03	-0.08	0.13	**-0.15**	0.08	0.03
RG	-0.03	0.03	0.02	-0.13	0.01	0.14	-0.01	0.06	-0.06	**0.18**	0.12
RL	-0.04	0	-0.04	0.04	-0.01	0.06	0.03	0.07	-0.02	0.08	**0.27**
RW	-0.01	0.03	0.01	-0.09	0	0.08	0	0.12	-0.04	0.17	0.18
FP	0.03	-0.02	0.06	-0.09	0.01	0.1	-0.02	-0.02	0.01	-0.01	-0.05
SEx	0.01	0.02	0	0.06	-0.01	-0.06	-0.01	-0.09	0	-0.1	-0.13
SEn	0	0.01	-0.01	0.07	0.01	-0.07	-0.01	-0.08	-0.01	-0.09	-0.12
pH	-0.03	-0.01	0.04	0.14	-0.01	-0.07	0	0.07	-0.03	-0.08	0.08
TA	-0.01	0.01	-0.03	0	0.01	0.02	-0.01	-0.02	0.04	-0.04	-0.08
AA	-0.03	0.03	0.02	-0.01	0	-0.02	0.03	-0.08	0	0.05	-0.01
Lyc	-0.02	0.01	-0.01	0.08	0.03	-0.04	-0.01	-0.06	-0.02	-0.05	-0.12
βC	-0.02	-0.02	0	0.02	0.04	0.02	-0.02	-0.03	-0.02	-0.04	-0.12

Here, residual effect = 0.0062, ***P< 0.01. Char. indicates characters and Gcorr. Y means genotypic correlation with yield/plant.

TABLE IV: PRINCIPAL COMPONENTS OF 38 TOMATO GENOTYPES FOR DIFFERENT YIELD AND FRUIT QUALITY TRAITS

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PH	0.002	0.09	-0.19	0.40	-0.13	-0.10	0.29	-0.03
BP	0.08	-0.03	0.37	0.09	-0.07	-0.19	0.35	-0.04
FlB	0.08	-0.27	-0.06	0.07	0.05	-0.41	-0.30	0.08
FB	0.15	-0.18	-0.06	0.30	-0.16	-0.22	-0.16	-0.20
SF	-0.06	-0.21	-0.02	-0.18	-0.02	0.30	-0.23	0.49
Chl	-0.14	0.25	0.22	0.07	0.17	0.02	0.11	0.35
GG	0.00	-0.32	0.01	0.43	0.24	0.10	-0.02	-0.01
GL	0.17	-0.09	0.08	0.23	0.39	0.24	0.00	0.16
GW	0.08	-0.30	0.15	0.21	0.36	-0.08	-0.03	-0.06
RG	0.33	-0.23	0.14	-0.18	0.00	0.05	0.11	-0.11
RL	0.22	0.03	-0.03	-0.31	0.24	0.12	0.26	-0.29
RW	0.32	-0.19	0.08	-0.12	-0.03	0.16	0.36	0.02
FP	0.07	-0.18	-0.42	0.11	-0.21	-0.13	0.14	0.34
SEx	-0.35	-0.09	0.16	0.10	-0.07	-0.16	0.26	-0.08
SEn	-0.34	-0.12	0.21	0.08	-0.05	-0.08	0.26	0.01
pH	-0.13	0.02	-0.05	-0.18	0.48	-0.30	0.05	0.05
TA	-0.11	-0.04	0.12	0.14	-0.36	0.37	-0.03	-0.16
AA	0.05	0.02	0.21	-0.23	-0.15	-0.42	0.01	0.34
Lyc	-0.30	-0.19	0.22	-0.05	0.00	0.10	0.11	0.15
βC	-0.27	-0.28	0.00	-0.02	0.01	0.25	-0.03	0.03
YP	0.26	-0.25	-0.16	-0.04	-0.16	0.00	0.36	0.29
Eigen values	5.03	3.33	2.52	2.24	2.03	1.58	1.40	1.07
%Variance	20.11	13.31	10.08	8.95	8.10	6.30	5.59	4.30
Cumulative (%) variance	20.11	33.42	43.50	52.46	60.56	66.86	72.45	76.74

Here, PC indicates Principal Component.

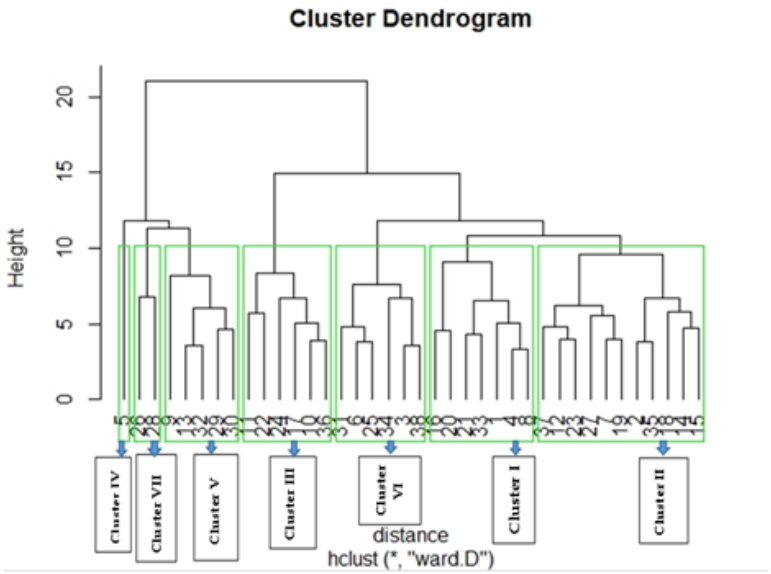

Fig. 1. Dendrogram based on summarized data on differentiation among 38 genotypes according to Ward's method.

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