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GENETIC VARIABILITY ASSESSMENT OF TOMATO GENOTYPES FOR MORPHOLOGICAL TRAITS UNDER ARID CONDITION OF QUETTA BALOCHISTAN

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ABSTRACT

The assessment of genetic variability of available tomato material is an efficient strategy for identifying elite breeding lines and developing improved varieties for local ecologies. This study aimed to evaluate ten tomato genotypes with diverse genetic backgrounds for nine morphological traits in a Randomized Complete Block Design (RCBD) with three replications. The mean squares from analysis of variance revealed appreciable variation for almost all morphological traits, except number of pickings. This indicated that studied tomato material exhibited considerable genetic variability, suggesting the potentiality of evaluated tomato genotypes for breeding and genetic improvement of tomato through cross-breeding. The mean value of genotypes showed wide range of variation for all measured traits, particularly for tomato fruit yield per plant. The correlation analysis indicated that all traits were positively and significantly interlinked with each other. However, tomato yield showed strongly positive association with plant height, number of fruits per cluster, fruit length and fruit girth, days to flowering and number of pickings which indicating that selection based on these traits would be reliable. Multivariate principal component analysis (PCA) accounted for 91.54% of total variation which is explained by first two principal components (PCs) with individual contribution of 74.05% and 17.49% respectively. Moreover, PCA facilitated in identifying the most divergence genotypes for selection and hybridization. Conclusively, two potential genotypes, namely O.E GSNOR-05 and Tom-VSF-05 performed superior for almost all studied traits as compared to local check variety i.e., Rio Grande, which is popularly grown for high productivity. Other important tomato genetic resources, including Tom-VSF-06 and Empty line might be useful in crossbreeding programs for varietal development or novel gene incorporation. Thus, this study would provide a benchmark for upcoming varietal development programs in Balochistan.

Keywords: Balochistan, Tomato genotypes, Morphological traits, Principal Component Analysis, Correlation Analysis

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INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) belongs to the Solanaceae family and is a very important vegetable on a global scale with a yield potential of up to 50 tonnes/ha (Mehmood et al., 2021). Tomato is commercially appealing because of its short growth cycle and high productivity, which leads to an increase in cultivated land (Khalid, 2013). Being an important item in the kitchen, tomato plays a vital role in human nutrition and help to maintain a healthy and balanced diet by containing abundance of minerals, vitamins, essential amino acids, carbohydrates, and dietary fiber (Ali et al., 2020). Tomatoes contain lycopene, a dominant antioxidant that may help to prevent cancer-causing compounds (Adenuga et al., 2013).

Due to its versatile usages, tomato can be eaten raw in salads, or cooked into a variety of dishes. Fresh tomatoes are processed into sauces and ketchup, which are primarily used for snacks, burgers, and sandwiches (Pennington & Hernandez, 2002). Canned and dried tomatoes are also economically significant food products which are widely used in traditional dishes, including pasta and pizza, etc (Amit et al., 2017).

Tomato is a major vegetable crop with significant acreage production, yield, commercial use, and consumption. The annual production of tomatoes all over the world, both processed as well as freshly consumed, is about 189.1 million metric tonnes engaging an area of 5.17 million acres, and it contributes 14% to global vegetable production with an average productivity is nearly 37 tonnes/ha (FAOSTAT, 2021). The topmost tomato producing countries are China, USA and India, accounting for 35%, 11%, and 8%, respectively in total global production (Tiwari et al., 2022). In Pakistan, it is grown by small farmers with the opportunity of higher profits under open field conditions as well as through tunnel farming. Pakistan holds the rank of 33rd in tomato production, with total country production estimated at around 569 thousand tons from 61 thousand hectares of cultivable land, with an average production of 9.5 tonnes/ha, far below the global competition (Farooq et al., 2020). Sindh is the leading tomato-producing province followed by Balochistan and Punjab with a share of 176, 144 and 130 thousand tonnes respectively (Economic Survey of Pakistan, 2021-22).

Balochistan is Pakistan's largest province in terms of an area of about 347,190 square kilometres (34.72 million hectares), of which 2,633.8 square kilometres (2.06 million hectares) are used for agriculture (Khan et al., 2021), but it has the smallest population than other provinces (Ahmed et al., 2020). Balochistan's agricultural economy is based primarily on livestock, fruit crops and vegetables (Rana et al., 2021). Most of the districts in Balochistan are facing food insecurity due to limited water resources and long spells of drought prevailing over the year, which is badly affecting the crops and vegetable yield and causing severe socioeconomic distress to local people (Ashraf & Routray, 2013). Drought stress is a major threat to tomato crops by reducing yield, quality, and economic return to the local farming community (Ashraf et al., 2021). Implementing efficient water management practices and developing drought-resistant varieties may help to improve tomato production in Balochistan, particularly in upland districts including Quetta, Pishin, and Zhob. Therefore, it is necessary to increase the productivity of tomatoes by screening and developing new improved varieties in order to provide quality seeds for local farming communities.

MATERIALS AND METHODS

The present research work was conducted at the Directorate of Agriculture Research Vegetable Seed Farm, Agriculture Research Institute (ARI) Sariab Quetta, Balochistan, during *Kharif* 2021. The global position system (GPS) location of research station is 30°07'02.2"N latitude, 66°58'42.8" E longitude and an altitude of 5,500 feet above sea level. A total of ten tomato genotypes were evaluated, out of which 06 advanced lines viz., Tom-VSF-01, Tom-VSF-02, Tom-VSF-03, Tom-VSF-04, Tom-VSF-05, Tom-VSF-06 were developed by the Vegetable Research Institute (VSF) and three lines namely Empty, O.E GSNOR-05, O.E GSNOR-14 obtained from Balochistan Agriculture College, Quetta which were developed through genetic engineering mechanism under the laboratory conditions. However, a popular variety, Rio Grande was also used as a check. The nursery was grown in plastic trays in the month of February and transplanted in field condition after 34 days. The experiment was laid out in Randomized Block Design (RCBD) with three replicates. Overall three irrigations were applied after transplantation, 1st irrigation was given after 15 days, 2nd was applied at flowering, and 3rd irrigation was applied at fruiting time and no further water was applied to whole experimentation. Net unit plot size for each genotype was kept at 6 x 6 m^2 with three rows, having plant-plant distance 25 cm and row-row distance was maintained at 60 cm. The data was recorded from ten randomly selected plants for nine morphological characters, such as days to flowering (DTF), Plant height (cm) (PH), days to first fruiting (DFF), number of pickings (NP), number of fruits per cluster (NFPC), number of fruits per plant (NFPP), fruit length (cm) (FL), fruit girth (cm) (FG) and tomato yield per plant (g) (TYP) following the standard descriptors (IPGRI, 1996). The collected replicated data was subjected to analyzed for Analysis of Variance (ANOVA) to find out the significant differences between tested genotypes using computer statistical program Statistix-8.1, following the procedure described by Gomez and Gomez (1983). Means were compared for Least Significant Differences (LSD) as suggested by Steel and Blaszczynski (1998). Multivariate analysis, including Correlation and Principal Component Analysis (PCA) were analyzed through computer software STATISTCA ver. 7.0 in order to identify the traits association and genotype divergence.

RESULTS AND DISCUSION

Variance analysis for morphological traits

In present study, analysis of variance showed the highly significant ($P < 0.01$) variation among tomato genotypes for traits including DFT, DFF, NFPC, NFPP and TYP, while significant ($P < 0.05$) differences were observed for traits such PH, FL and FG (Table 1). However, non-significant differences only noted for number of pickings (NP). This sufficient variability demonstrated by evaluated tomato genotypes is signifying the genetic potential of studied materials, which might be efficiently utilize in breeding programs for developing high yielding varieties. The knowledge of genetic variability assessment would assist plant breeders to expand the genetic base of adaptable cultivars to meet the global food security challenges. Almost all crop breeding programs continuously exploit genetic variability in order to create efficient varieties with desirable characteristics (Bhandari et al., 2017). Previous studied also confirmed substantial variability among tomato genotypes which is supporting our current findings (Ismaeel et a., 2019; Salim et al., 2020; Tembe et al., 2018). Moreover, coefficient of variation (CV) in percentage was found to be maximum (14.89) for number of pickings, while it was observed minimum (4.25%) for plant height (cm), indicating the precession of experimentation and reliability of data. The coefficient of variation (CV) is a crucial indicator that measures the precision and accuracy of a field experiments (Shechtman, 2013). Our results are in line with the earlier researchers' findings (Akhter & Najnine, 2022; Salim et al., 2020).

Table: 1 Analysis of variance (ANOVA) for nine morphological traits in ten tomato genotypes.

S.O.V	df	DTF	PH	DFF	NP	NFPC	NFPP	FL	FG	TYP
Replications	2	0.371	4.654	1.652	0.034	0.329	5.112	0.101	0.301	14063.8
Genotypes	9	14.19^{**}	16.46^{*}	38.89^{**}	0.385^{NS}	1.383^{**}	91.21^{**}	1.992^{*}	0.423^{*}	98759.6^{**}
Error	18	3.062	11.71	9.246	0.662	0.276	5.761	0.587	0.144	7483.1
CV (%)	–	10.61	4.52	13.38	14.89	9.60	8.31	13.69	9.01	7.95

** = Highly significant ($P < 0.01$), * = Significant ($P < 0.05$), ^{NS} = Non-significant, *CV* = Coefficient of variation *DTF* = Days to flowering, *PH* = Plant height (cm), *DFF* = Days to Fruiting, *NP* = Number of pickings, *NFPC* = Number of fruits per cluster, *NFPP*= Number of fruits per plant, *FL* = Fruit length (cm), *FG* = Fruit girth (cm), *TYP* = Tomato yield per plant (g)

Mean Variability

The descriptive statistics was computed for mean, range (minimum and maximum), grand mean, standard error, and least significant differences (Table 2). After nursery transplantation, the least days to flowering was taken by genotype Empty line (12.76), whereas the highest days for flowering was taken by local check variety Rio Grande (19.05 days). Similarly, mean value of tallest plant in height was recoded for O.E GSNOR-05 (79.34 cm) and shortest height (71.92 cm) was measured for genotype Empty line (Table 2). Likewise, Rio Grande has taken maximum days (27.7) for fruit setting, while Empty line was taken minimum days (16.26) to fruiting after nursery transplantation. The maximum number of pickings (6.00) were attempted for Tom-VSF-05, whereas least number (5.00) of pickings were equally attempted for Tom-VSF-04, Tom-VSF-06 and Empty line. The highest number of fruits per cluster was bear by genotype O.E GSNOR-05 (6.60), whereas minimum number of fruits per cluster (4.37) was totaled for Tom-VSF-04 (Table 2). The total number of fruits plant^{-1} was counted maximum (36.44) for O.E GSNOR-05, nearly followed by Tom-VSF-06 (33.93), while minimum number of fruits (21.1) was stand equally by two genotypes, Tom-VSF-05 and Empty line (Table 2). For two important morphological measurements, i.e., fruit length and fruit girth, was recorded highest for genotype O.E GSNOR-05, whereas Empty line was found to be lowest values for both these traits. The tomato yield plant^{-1} is a trait of high importance and was observed maximum (1441.7 g) for O.E GSNOR-05, closely followed by genotype Tom-VSF-05 (1292.3 g) and Rio Grande (1239.6 g), while fruit yield plant^{-1} weighed minimum (894.3 g) for genotype Empty line (Table 2). The remarkable range in mean values indicated that traits with high variance magnitudes are of greater importance in tomato selection and genetic improvement programs (Zannat et al., 2013). According to Kaur et al. (2017) conventional breeding procedures can improve morphological characters of tomato with low variation in rang values.

Correlation of morphological traits

Correlation analysis of nine morphological traits indicated the strong and positive association between yield and yielding components of studied tomato genotypes. Since, correlation of days to flowering (DTF) was found highly significant ($P < 0.01$) with PH, DFF, NP NFPC, while significant ($P < 0.05$) with all other traits in including NFPP, FL and FG (Table 3). This indicated that an increase in flower duration would positively contribute in enhancement of other yield traits like plant height, fruiting period, pickings and fruit per cluster. However, tomato yield depicted strong positive relation with plant height (PH), number of fruits per cluster (NFPC), fruit length (FL) and fruit girth (FG), whereas significant ($P <$

0.05) association in positive direction demonstrated with days to flowering (DTF) and number of pickings (NFPP), which is signpost of closed relation between these traits. However, non-significant association of tomato yield plant^{-1} (TYP) was observed with days to first fruiting, and number of fruits per plant (Table 3). This indicated that more quantity of fruits in tomato leads to the reduction in size as well as yield.

Some other important and strong correlation was found between plant height and number of fruits per cluster, also in between fruit length and fruit girth and their inter-correlation with number of pickings, and number of fruits per cluster (Table 3).

Table: 2 Mean performances of ten tomato genotypes for nine morphological traits.

Genotypes	**DTF**	**PH**	**DFF**	**NP**	**NFPC**	**NFPP**	**FL**	**FG**	**TYP**
Tom-VSF-01	17.30	75.50	24.40	5.67	5.60	31.10	5.57	4.44	1091.4
Tom-VSF-02	16.70	75.05	22.06	5.67	5.50	30.30	5.54	4.21	1062.3
Tom-VSF-03	16.00	74.90	20.43	5.34	5.27	27.36	5.10	4.04	1002.7
Tom-VSF-04	13.30	73.90	19.90	5.00	4.37	26.30	5.04	3.83	898.7
Tom-VSF-05	17.06	79.11	19.70	6.00	6.20	21.10	6.71	4.66	1292.3
Tom-VSF-06	15.40	74.04	25.53	5.00	5.43	33.93	5.12	3.96	1008.8
Empty line	12.76	71.92	16.26	5.00	4.37	21.10	4.40	3.70	894.3
O.E GSNOR-05	18.83	79.34	25.63	5.67	6.60	36.44	7.06	4.73	1441.7
O.E GSNOR-14	18.50	75.30	25.60	5.67	5.10	32.41	5.31	3.90	950.6
Rio Grande	19.05	77.45	27.70	5.67	6.00	32.41	6.14	4.60	1239.6
Grand mean	16.49	75.64	22.72	5.47	5.47	28.89	5.59	4.21	1088.2
Minimum	12.76	71.92	16.26	5.00	4.37	21.10	4.40	3.70	894.3
Maximum	19.05	79.34	27.70	6.00	6.60	36.44	7.06	4.73	1441.7
S.E ±	1.428	2.793	2.482	0.661	0.422	2.64	0.625	0.309	70.631
LSD @ 0.5	3.01	5.86	5.21	NS	0.91	3.45	1.32	0.65	148.39

LSD = Least significant differences; S.E = Standard Error; *DTF* = Days to flowering, *PH* = Plant height (cm), *DFF* = Days to Fruiting, *NP* = Number of pickings, *NFPC* = Number of fruits per cluster, *NFPP*= Number of fruits per plant, *FL* = Fruit length (cm), *FG* = Fruit girth (cm), *TYP* = Tomato yield per plant (g)

Table 3: Correlation of nine morphological and yield related traits of tomato.

Traits	**DTF**	**PH**	**DFF**	**NP**	**NFPC**	**NFPP**	**FL**	**FG**	**TYP**
DTF	1								
PH	0.78**	1							
DFF	0.79**	0.46 ^{NS}	1						
NP	0.81**	0.81**	0.35 ^{NS}	1					
NFPC	0.82**	0.92**	0.57 ^{NS}	0.75*	1				
NFPP	0.63*	0.29 ^{NS}	0.89**	0.13 ^{NS}	0.45 ^{NS}	1			
FL	0.74*	0.99**	0.45 ^{NS}	0.77**	0.92**	0.32 ^{NS}	1		
FG	0.75*	0.93**	0.46 ^{NS}	0.79**	0.94**	0.29 ^{NS}	0.94**	1	
TYP	0.71*	0.94**	0.43 ^{NS}	0.69*	0.95**	0.33 ^{NS}	0.97**	0.95**	1

** = Highly significant ($P < 0.01$), * = Significant ($P < 0.05$), ^{NS} = Non-significant; Days to flowering, PH = Plant height (cm), DFF = Days to Fruiting, NP = Number of pickings, NFPC = Number of fruits per cluster, NFPP= Number of fruits per plant, FL = Fruit length (cm), FG = Fruit girth (cm), TYP = Tomato yield per plant (g).

The ultimate goal of a tomato breeder is to increase fruit yield, but the yield is a resultant product of many component traits that interact directly or indirectly in final productivity (Sherpa et al., 2014; El-Mansy et al., 2015). Fruit yield is a complex trait, and its direct improvement is difficult (Kumar et al., 2013). Thus, positive correlation of fresh fruit yield and its components is indispensable for the simultaneous selection of multiple agronomic traits (Kumar & Dudi, 2011). The yield increment in tomato is largely affected by the number of fruit per plant, fruits per cluster, fruit weight and fruit demission (Kumar et al., 2013). Previous, similar type of studies also indicated strong correlation of tomato yield with yielding components like maturity duration, number of locules per fruit and pericarp thickness (Al-Aysh et al., 2012), and plant height, number of flower plant^{-1}, primary branches plant^{-1}, number of fruits per plant, days to harvest and fruit weight were significantly and positively correlated with tomato yield (Mishra et al., 2023; Regassa et al., 2012).

Principal Component Analysis (PCA)

Multivariate approach was applied to identify the most divergent tomato genotypes which participated significantly in overall variation. The scree plot determined two essential components having eigenvalue > 1 (Figure 1). However, these first two PCs extracted 91.54 % of cumulative variation with individual participation of PC1 and PC2 viz., 74.05% and 17.49% respectively (Table 4). Other seven principal components contributed minimally with no significant impact on overall variability were excluded from further analysis. The PCA biplot relevant to loading factors indicated that traits with longest vector length mostly falls negative side of plot (Figure 2A). On the other hand, score plot for genomic divergence showed that four genotypes away from the origin of plot such as Tom-VSF-06, Empty line, Tom-VSF-05 and O.E GSNOR-05 were identified as most diverse genotypes (Figure 2B). Previously, Henareh et al. (2015) assessed the genetic diversity of Turkey and Iran tomato landraces based on morphological character and noted 71.6% variation for first three principal components and yield was the major trait, suggested for selection criteria to identify potential genotypes. In a similar study on genetic diversity estimation among tomato accessions based on agro-morphological traits revealed five important principal components with total 74% of variation mainly contributed by first two PCs (Hussain et al., 2018). Our results are in accordance with former researchers who conducted similar studies on tomato from different parts of world and identified potentially diverse lines using principal component analysis technique (Alam et al., 2020; Sinha et al., 2021; Williams & Anbuselvam, 2023).

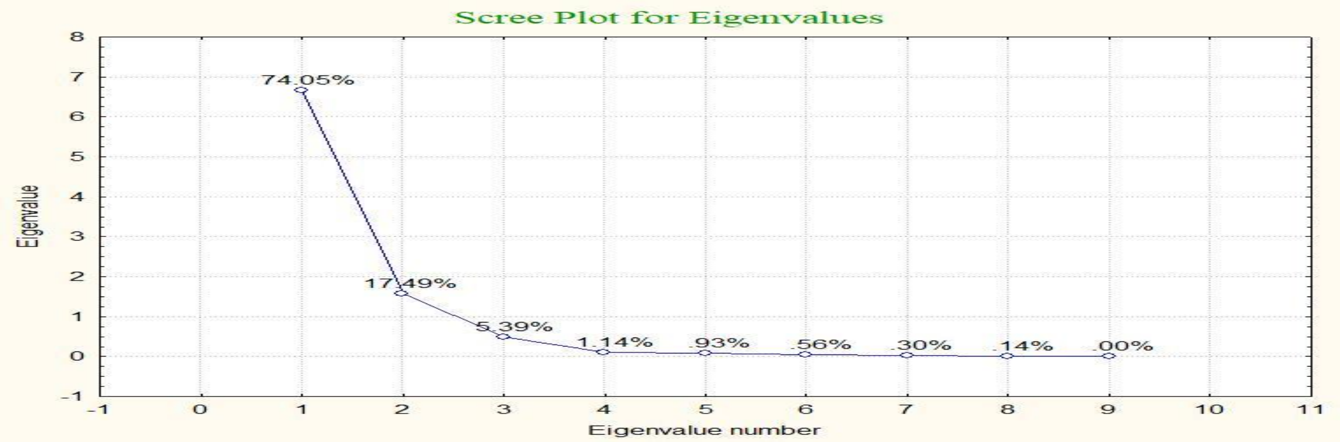

Figure 1: Scree plot showing nine reserved principal components for ten tomato genotypes.

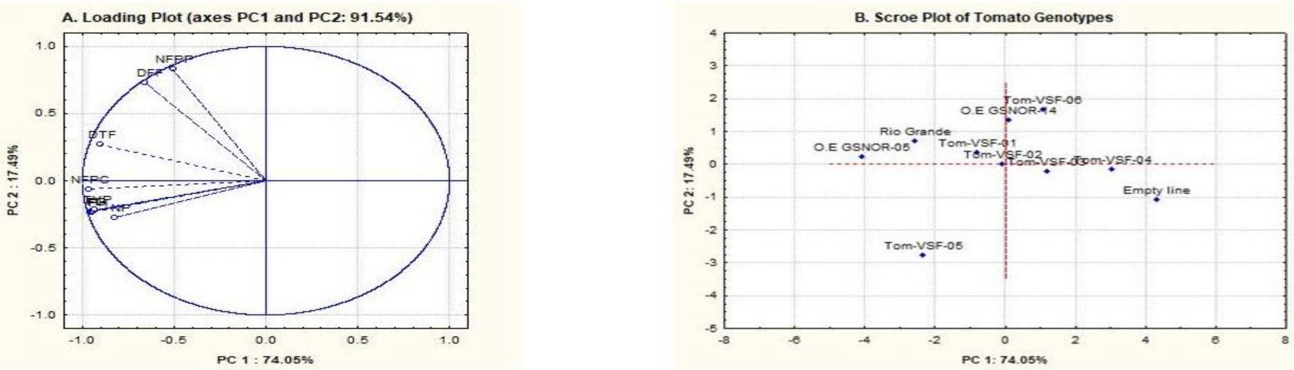

Figure 2: PCA biplot (loading factor (A) and score plot (B) displaying the contribution of essential traits and diverse tomato genotypes.

Table 4: First two principal components determined maximum variation for nine morphological traits.

Traits	PC 1	PC 2
Days to flowering	-0.901	0.266
Plant height	-0.950	-0.236
Days to first fruiting	-0.655	0.728
Number of pickings	-0.821	-0.274
Number of fruits per cluster	-0.966	-0.063
Number of fruits per plant	-0.506	0.831
Fruit length	-0.948	-0.226
Fruit girth	-0.943	-0.226
Tomato yield per plant	-0.932	-0.215
Eigenvalues	6.67	1.57
Proportion of variance (%)	74.05	17.49
Cumulative variance (%)	74.05	91.54

CONCLUSION

Estimation of genetic variability is prerequisite for the identification and selection of desired genotypes. In present study, we evaluated ten tomato genotypes for nine morphological attributes in order to select genetically diverse genotypes with higher yield potential. Considerable variation was observed for all most all morphological traits, which suggesting effectiveness of studied materials for the improvement of tomato and development of new varieties. Multivariate approach including principal component analysis and correlation analysis signposted highly diverse genotypes and essential traits which are interlinked with tomato yield such as number of fruits per cluster and fruit dimension. Overall, two genotypes, namely O.E GSNOR-05 and Tom-VSF-05 performed superior for almost all studied traits as compared to local check variety Rio Grande. Thus, the genetic potential of these lines must be utilized for upcoming breeding programs for the development of new improved local tomato varieties under the arid regions of Balochistan.

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