Zoo Botanica
ISSN: 3007-2050 (E), 3007-2042 (P)

Research Article

Morphological characterization and evaluation of watermelon inbred lines

Nusrat Parveen, Sana Akbar, Wajeeha Khan, Muneeb Munawar, Muhammad Iqbal, Mehvish Tahir
Vegetable Research Institute, Ayub Agricultural Research Institute, Faisalabad, Punjab, Pakistan.

ABSTRACT

Watermelon can be considered a potential food snack by the health-conscious consumers. Due to its phytochemicals such as vitamin C and lycopene, and total phenolic content containing anti-cancer and antioxidant properties. It helps with healthy diets which leads to a significant decrease in chronic diseases, hypertension and cardiovascular diseases. Watermelon is one of the major vegetables cultivated in Sahiwal district. This study was aimed to assess the genetic variability of lines of this Institute. In 2017, Sixteen genotypes were collected from various regions of Faisalabad (Lodhra, Sahiwal, Jaranwala, Tandliawala, and Samundari), China and Turkey to evaluate them for quantitative and qualitative traits. These genotypes were selfed over six to seven consecutive years to ensure homozygosity. These inbred lines were further evaluated for quality and yield related traits. The accessions SBA (red flesh) (TSS: 12), 1HB (yellow flesh) (TSS: 11), Shannua (orange flesh) (TSS: 14), 6. No (red flesh) (TSS:13), 802 (yellow rind & red flesh) (TSS: 11) were identified promising for future breeding program based on Total Soluble Solids (TSS) and fruit shape. High genetic variability has been observed among lines for the quality traits including fruit shape, size and color. Statistical procedure including ANOVA, PCA and correlation have been used to study variability for different trait among inbred lines. Significant positive correlation has been present among quantitative traits i.e., leaf width, internode length, number of primary branches, vine length, fruit weight, days of harvesting and yield per plant. Principal component analysis identified two main clusters, suggesting a clear distinction based on morphological characters. Eigan values greater than zero indicate that the corresponding principal component contributed highly to variance of different characters. Correlation studies suggested that fruit weight is strongly correlated with yield per plant.

Keywords: *Citrullus lanatus*; genetic diversity; principal component analysis; inbred lines.

Correspondence
Nusrat Parveen
nusratvri@gmail.com

Article History
Received: January 11, 2025
Accepted: April 20, 2025
Published: April 30, 2025

INTRODUCTION

Watermelon (*Citrullus lanatus*), family *Cucurbitaceae*, is a vegetable mainly important for its large size sweet fruit (pepo) and seeds. Plant exhibits an annual herbaceous growth habit characterized by creeping vine. *Citrullus* is believed to be originated in Africa where wild types still grow (Assefa et al., 2020). *C. lanatus* has been cultivated in various regions across world where the long warm season is ideal for production. Third forth of world production is from Asia, with China the highest producing country of watermelon. In Pakistan, it is cultivated on an area of 4.9 thousand ha with an average production of 1.5 million tons. It is cultivated extensively in three provinces including Sindh, Punjab and Balochistan. Pakistan ranks 30th in world production in which 55.87%, 21.29% and 10.29% shares come from Punjab, Balochistan, Sindh respectively (FAO.STAT 2022). Watermelon has become the 5th most consumed fruit in the world. usually fruit is harvested manually, with skilled labors cutting the fruit from vine after the curly tendril dried out. it is composed of 90-

https://doi.org/10.55627/zoobotanica.003.01.1103

92% water, making it an excellent hydrating fruit, especially in hot climate. If stored correctly at temperature 10-15 °C and 90% humidity, remain fresh for two-three weeks' post-harvest (Maoto et al., 2019). Nutrient profile has vitamins A & C, and also contain important minerals like potassium and magnesium, essential for maintaining healthy skin and immune function. Lycopene, an antioxidant that is linked to reduced risks of cancer and heart disease is also present abundantly (Zamuz et al., 2021).

Domestication of *C. lanatus,* 4000 years ago, started in north-eastern Africa and Egypt. In 8th century, some of the elite material from Africa were introduced into Indian region (Paris et al., 2013). Area alongside China and India is considered as the secondary center of origin of genus *Citrullus* due to existence of abundant genetic diversity (Wehner, 2008). Crop was first introduced into America after 15th century (Zoltán et al., 2007). Some of the US cultivars, Mickey lee and Bush Sugar Baby is genetically related to Asian gene pool (Hwang et al., 2011).

Studies revealed narrow genetic diversity among cultivars (Kwon et al., 2010; Minsart et al., 2011; Levi et al., 2013). Breeding programs require sufficient genetic diversity to produce new varieties that meet demands for high productivity, quality and traits like color, shape and resistance to biotic and abiotic stresses. Watermelon exhibits significant genetic diversity due to the high degree of cross-pollination. It shows great diversity in the fruit quality traits like seed shape, fruit shape and size, skin color & pattern, flesh color and TSS content (Dutta et al., 2023). Some genotypes may excel in certain traits but short fall in others and their morphological characteristics can differ. The lack of locally developed watermelon varieties in Pakistan is a significant constraint for sustainable production. For development of local varieties/ hybrids assessment of genetic variation is required. Therefore, assessing genetic variation is essential to determine genetic relationships among cultivars and selections used in breeding programs. This study aimed to determine the genetic variation, correlation and PCA among various yield components in watermelon.

MATERIALS AND METHODS

Study Area

The experiment was consisting of sixteen diverse genotypes, which were selected from different sources (Table 3) on the basis of yield and quality parameters. The collected material was selfed for six-seven consecutive years to achieve homozygosity. Two commercial cultivars- Sugar baby from AARI and Augusta from Syngenta Seed Company were also included in the study for standardization. The experiment was conducted in split plot design with two replications at field area of Vegetable Research Institute, Faisalabad. The experiment was carried out between December to April in the years 2023 and 2024 and evaluated for several quantitative and qualitative traits of watermelon under polycarbonate tunnel. This tunnel provides controlled temperature and humidity for plants and also provide protection from frost, rainfall and direct sun light. At the time of sowing temperature was maintained at 25-30° C as temp above 38-40 ° C decline germination rate during vegetative to flowering stage day temp was maintained at 25-35° and night temp was 18-22°C. At maturity temperature was around 35-40°C.The seeds were directly sown in polycarbonated tunnel in a plot size of 10 Kanal with P×P distance of 40cm & R×R distance of 5 ft. All recommended cultural practices were followed during vegetative & reproductive phases. Before sowing DAP and SOP was applied. At 5-6 leave stage plants were trained on net trellis. Before flowering recommended doses of nitrophos, SOP and CAN (Calcium ammonium nitrate) was applied. After 15 days during flowering phase again nitrophos, CAN and SOP was applied for better fruit development. The observation for traits like germination percentage, main vine length, internode length, stem diameter, leaf length, leaf width, number of primary branches, days to fruit harvest, fruit weight, fruit diameter, total soluble salts, rind color, fruit shape, flesh color, seed per fruit, seed length and seed width were recorded. Collected data were evaluated by R statistical environment for correlation & principal component (PCA) analyses. Statistics was used for ANOVA to separate the means for the fourteen quantitative characters (Steel et al., 1997).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant difference among the 16 genotypes for all characteristics listed in Table (1). Variations in quantitative traits (Table-2) were found to be significant across the genotypes. Qualitative traits such as leaf shape, fruit shape, rind color, flesh color and seed color are summarized in table 3. Genetic diversity based on qualitative traits is an important approach towards identification & improvement of crops. In the present study, observations on five qualitative traits were recorded for all 16 genotypes. Solmaz and sari performed morphological characterization of Turkish watermelon genetic resources and found excessive diversity among accessions (Solmaz and Sarı, 2008). First qualitative parameter was leaf type, Pentalobed leaf type was observed among all watermelon genotypes then fruit shapes were found to be Round in 11 genotypes, oval in 3 genotypes and oblong in 2 genotypes.

Table 1. Analysis of variance.

Source of variation	d.f	MVL	IL	SD	LL	LW	PB	FW	FD	S/F	SL	SW	Y/P
Replication	1	1.01	0.32	0.11	0.39	3.59	0.36	0.29	0.33	7098.1	0.05	0.07	7.38
Year	1	0.98	0.38	0.21	0.31	5.83	1.26	0.03	44.89	612.6	0.01	0.00	8249.41
Error (rep×year)	1	0.008	0.03	0.02	0.76	0.02	0.14	0.03	0.45	564.1	0.01	0.09	0.61
Treatment	15	0.78	22.69	0.99	45.36	18.62	1.40	2.78	36.96	19388.7	6.24	3.17	135.80
Year×Treatment	15	0.12	0.59	0.05	0.48	0.04	0.39	0.24	3.15	1346.5	0.06	0.05	107.67
Error(rep× year×trt)	30	0.09	0.40	0.04	0.51	4.63	0.79	0.17	2.76	3026.9	0.05	0.02	6.64

MVL=Main vine length (cm), IL= Internode length (cm), SD= Stem diameter (cm), LL= Leaf length (cm), LW= Leaf width (cm), PB= Primary branches , FW= Fruit weight (kg) , FD= Fruit diameter, S/F= Seed per fruit, SL= Seed length (mm), SW= Seed width (mm), Y/P= Yield per plant.

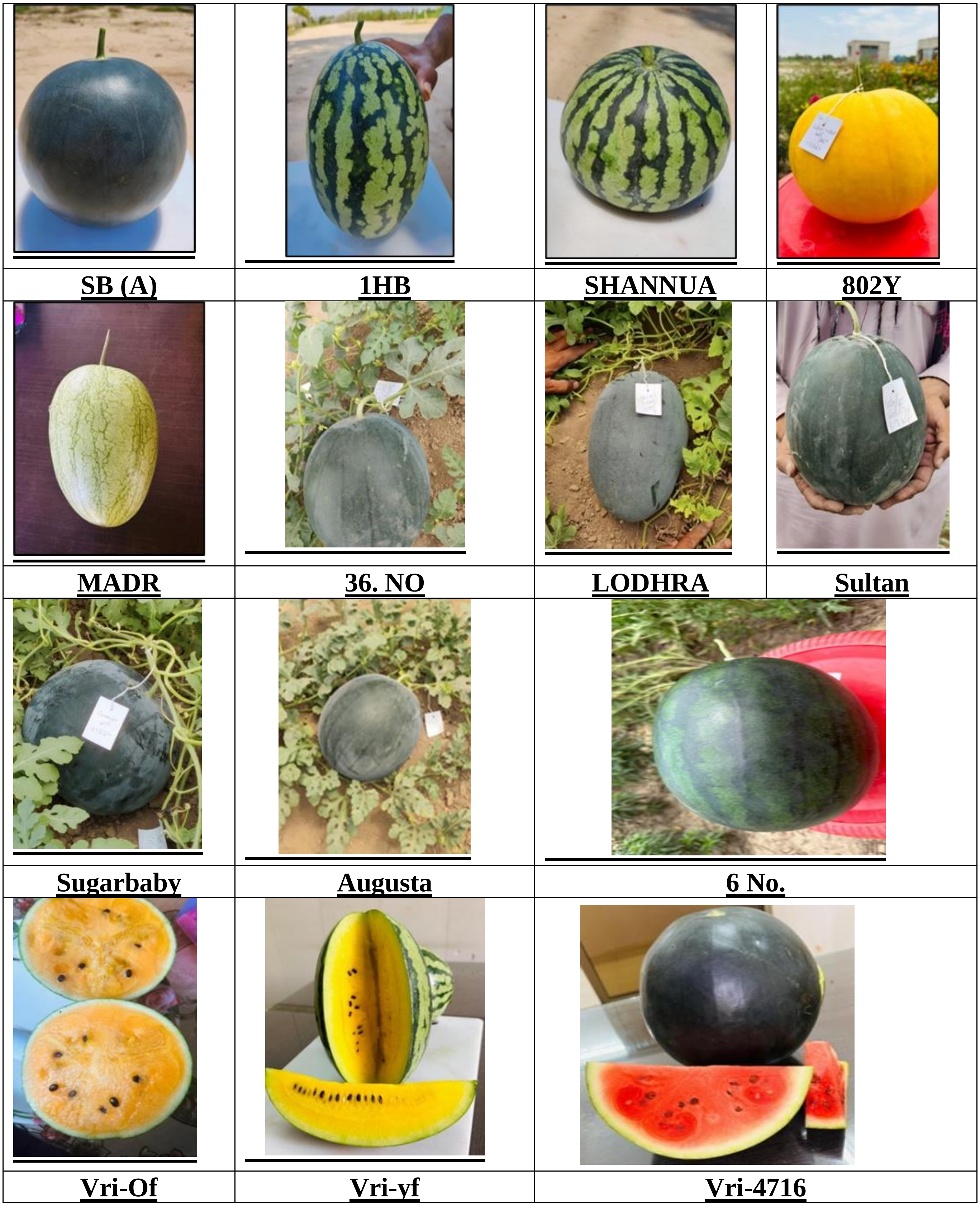
Table 2. Mean performance of 16 genotypes.

Genotype	MVL	IL	SD	LL	LW	PB	FW	FD	S/F	SL	SW	Y/P
802 Y	1.32±0.15	14.78±0.23	3.55±0.26	11.60±0.43	13.20±0.29	4.00±0.40	3.56±0.13	21.38±0.55	174.25±15.10	7.35±0.16	4.85±0.08	010.67±.41
SP	1.92±0.08	9.54±0.28	3.08±0.09	12.94±0.34	14.19±0.31	3.50±0.64	4.29±0.35	16.88±0.82	194.50±28.86	8.20±0.04	5.50±0.09	8.57±0.70
1HB	1.67±0.30	8.85±0.13	2.18±0.11	17.33±0.34	15.58±1.76	3.50±0.28	2.98±0.29	17.78±1.32	113.75±8.98	6.60±0.12	3.83±0.07	8.94±0.89
MADR	1.80±0.27	15.93±0.72	2.79±0.15	15.80±0.14	18.21±1.42	3.75±0.47	2.96±0.07	14.75±0.85	88.00±23.45	6.78±0.08	3.85±0.02	7.45±0.98
SHANUA	1.62±0.23	13.19±0.5	2.03±0.04	11.75±0.47	16.14±0.85	5.00±0.40	2.20±0.09	20.25±1.65	84.75±8.43	9.00±0.04	5.60±0.04	7.68±0.62
36 NO.	2.49±0.22	15.37±0.27	2.64±0.12	19.24±0.27	14.73±0.53	5.50±0.28	3.34±0.17	20.63±0.55	160.50±12.01	11.60±0.10	7.23±0.08	6.68±0.35
MEHYFEST	3.15±0.13	8.05±0.29	2.27±0.16	12.28±0.35	11.08±0.39	3.50±0.28	2.28±0.11	15.63±0.68	56.25±4.26	7.23±0.13	3.85±0.06	5.74±0.79
SB(A)	2.40±0.22	9.53±0.22	3.31±0.14	10.68±0.62	10.89±0.73	3.50±0.28	3.93±0.04	26.00±0.70	170.25±63.4	7.93±0.02	4.78±0.1	11.78±0.14
1 NO.	2.28±0.21	9.38±0.22	3.54±0.11	13.38±0.25	11.24±0.33	3.50±0.64	3.31±0.15	22.25±1.03	269.00±28.6	6.33±0.08	4.13±0.04	6.61±0.31
38 (B)	1.95±0.05	10.28±0.24	3.50±0.05	12.54±0.31	15.09±2.02	4.00±0.40	3.01±0.08	21.50±0.86	201.50±28.19	7.88±0.15	5.18±0.13	6.02±0.17
6 NO. (A)	2.25±0.06	13.53±022	3.32±0.09	18.17±0.31	16.77±0.67	4.50±0.28	4.15±0.11	23.38±0.89	145.00±34.09	8.75±0.13	5.35±0.14	12.45±0.35

311 (A)	2.18±0.11	11.53±0.24	3.15±0.06	17.09±0.36	15.29±0.24	3.50±0.28	2.14±0.06	21.50±1.55	83.00±20.15	7.38±0.06	4.38±0.12	4.28±0.12
LODHRA	2.33±0.08	12.05±0.08	3.39±0.04	15.30±0.23	14.68±0.54	4.00±0.40	4.28±0.30	23.00±1.22	111.00±8.88	7.70±0.04	4.90±0.10	8.56±0.60
SULTAN	2.01±0.15	11.17±0.28	2.96±0.02	23.18±0.29	12.38±0.27	4.00±0.40	3.86±0.26	19.63±0.55	197.75±9.49	8.20±0.12	5.43±0.16	7.72±0.53
SUGAR BABY	2.44±0.11	11.22±0.27	3.31±0.05	14.18±0.31	13.18±0.38	3.50±0.28	4.75±0.48	17.13±0.31	289.50±10.28	7.78±0.25	4.90±0.10	11.50±0.51
AGUSTA	2.58±0.25	11.45±0.51	3.28±0.10	13.25±0.32	12.05±0.38	4.00±0.40	4.52±0.15	19.25±0.47	244.50±23.14	6.83±0.11	3.98±0.04	10.16±1.15
CV (rep×year)	4.19	1.71	5.59	5.86	1.03	9.49	5.47	3.37	14.71	1.59	6.18	4.07
CV(rep× year×geno)	14.03	5.47	7.37	4.81	15.34	22.61	11.97	8.30	34.07	3.08	3.43	13.38

Table 3. Different Qualitative traits of watermelon genotypes.

Genotype/Variety	Source	Leaf shape	Fruit shape	Rind color	Flesh color	Seed color
802 y	Local market	Pentalobed	Round	Yellow	Red	Dark brown
SP	Local market	Pentalobed	Round	Dark Green	Red	Blackish brown
1HB	Turkey	Pentalobed	Oval	Light & dark green stripes	Yellow	Brown with black spots
MADR	Turkey	Pentalobed	Oblong	Light green	Bright Yellow	Dark brown
SHANUA	China	Pentalobed	Round	Light & dark green stripes	Orange	Orange brown
36 NO.	Local	Pentalobed	Round	Black	Red	Black
MEHFYST	Turkey	Pentalobed	Oblong	Light & dark green stripes	Yellow	Light brown
SB (A)	Local market	Pentalobed	Round	Black	Red	Light brown
1 NO.	Local market	Pentalobed	Round	Dark green	Red	Light brown
38 (B)	Local market	Pentalobed	Round	Dark green	Red	Orange brown
6 NO. (A)	Local market	Pentalobed	Oval	Dark green	Bright Red	Reddish brown
311 (A)	Local market	Pentalobed	Oval	Dark green	Red	Light brown
LODHRA	Farmer field	Pentalobed	Round	Dark green	Red	Dark brown
SULTAN	Local market	Pentalobed	Round	Dark green	Red	Light brown
SUGAR BABY	VRI-OPV	Pentalobed	Round	Black	Red	Dark brown
AGUSTA	Syngenta seed company	Pentalobed	Round	Black	Red	Black



SB (A)
1HB
SHANNUA
802Y
MADR
36. NO
LODHRA
Sultan
Sugarbaby
Augusta
6 No.
Vri-Of
Vri-yf
Vri-4716

Figure 1. Variability in flesh & rind color of tested genotypes

Rind color intensity varies from black, light green, dark green and yellow (Figure 1). 802-y is a unique watermelon line showing yellow colored ovary and rind with red flesh. It could be a useful parent to develop yellow rind varieties and hybrids of watermelon. Some genotypes showed light and dark streaks on rind of fruit. A total of 12 genotypes showed red color flesh, 3 with yellow colored flesh and one with orange colored flesh color. Yellow colored flesh is dominant over red & orange (Figure 1) Seed color varies from black, light brown, dark brown, reddish & orange brown. Choudhary, and Gichimu also characterized the watermelon genotypes for different morphological traits (Choudhary et al., 2012) (Gichimu et al., 2009).

Correlation

Correlation coeffients of measure characters in first year of experimentation is given in the table (4). Correlation analysis depicted that leaf width,internodel length, seed length, and seed width are positively correlated with leaf length. While total soluble salts (TSS) is negatively correlated with leaf length. More leaf length results in less sweet watremelon. Leaf width has strong and positive correlation with internode length and primary branches. It also showed positive association with seed length & seed width. Leaf width showed strong negative correlation with main vine length and no. of seeds per fruit. Negative correlation of leaf width with fruit weight, fruit diameter and stem diameter was also observed. Internode length is positively associated with primary branches, seed length & seed width while negative correlation with main vine length. Primary branches are strongly correlated with seed length & seed width, while negatively correlated fruit weight, stem diameter and main vine length. Fruit weight is positively correlated with yield per plant, stem diameter, seed per fruit, days of harvesting and fruit diameter (Figure 2). The above results are supported by the research work of other researchers. (Mohosina et al., 2020) (Bhagyalekshmi et al., 2020) (Singh et al., 2022) Fruit weight is negatively correlated with TSS which shows as the fruit gains size sugar contents are reduced. Yield per plant is positively correlated with fruit diameter, days of harvesting and TSS. Stem diameter showed neagtive correlation with the seed width. No of seeds per fruits depends upon the diameter of the fruit. Seed length is strongly and positively correlated with seed width.

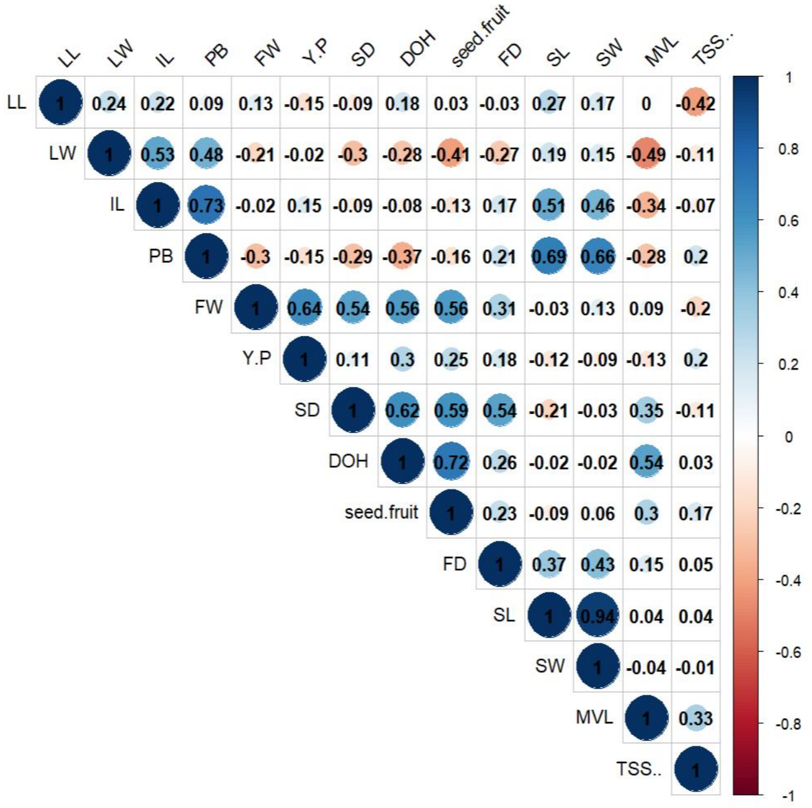
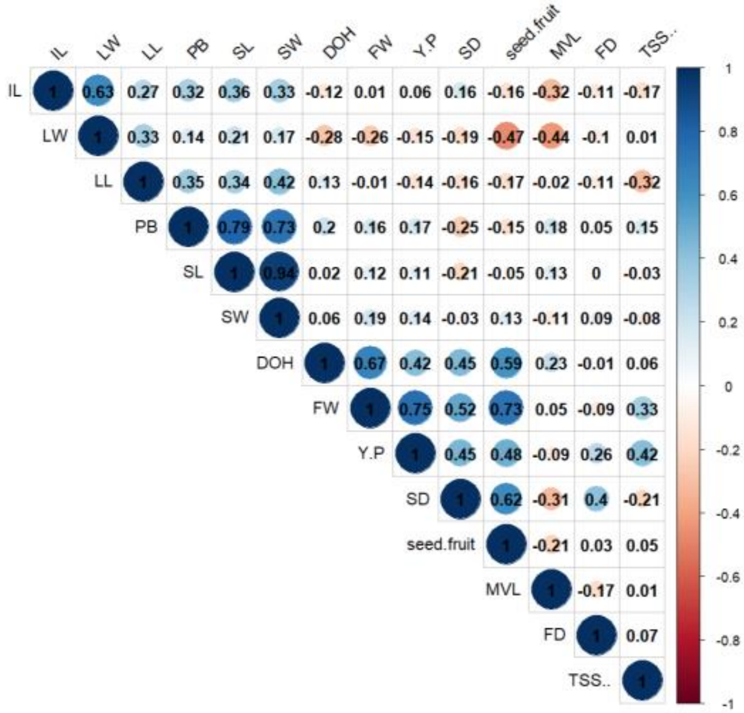


Figure 2. First year genotypic correlation coefficient among all traits of watermelon, IL: Internodal length; LW: Leaf width; LL: Leaf length; PB: Primary branches; SL: seed length; SW: stem width; DOH: days of harvesting; FW: fruit width; YP: yield per plant; SD: stem diameter; MVL: main vine length; FD: fruit diameter; TSS: total soluble sugar; SF: seed per fruit.

In second year of experimentation, we observed strong positive correlation of leaf length, leaf width, seed length & seed width with internode length and negative correlation with main vine length. Leaf width exhibited a strong negative correlation with main vine length and no. of seed/fruit (Figure 3). Seed length was strongly and positively correlated with seed width as observed in first year of experimentation. Fruit weight is positively correlated with yield per plant, stem diameter and TSS. Mulyani and Waluyo also performed a correlation analysis between yield component traits and the yield of watermelon genotypes and found similar associations for one or more (Mulyani and Waluyo, 2020; Singh et al., 2022). The results of correlation analysis depicted that the traits leaf width, internode length, number of primary branches, vine length, fruit weight, seed length, seed width, days of harvesting, no of seeds/fruit and yield per plant are the major yield attributing characters. So, more emphasis should be given to the above characters while improving these genotypes.



	IL	LW	LL	PB	SL	SW	DOH	FW	Y.P	SD	seed.fruit	MVL	FD	TSS..
IL	1	0.63	0.27	0.32	0.36	0.33	-0.12	0.01	0.06	0.16	-0.16	-0.32	-0.11	-0.17
LW		1	0.33	0.14	0.21	0.17	-0.28	-0.26	-0.15	-0.19	-0.47	-0.44	-0.1	0.01
LL			1	0.35	0.34	0.42	0.13	-0.01	-0.14	-0.16	-0.17	-0.02	-0.11	-0.32
PB				1	0.79	0.73	0.2	0.16	0.17	-0.25	-0.15	0.18	0.05	0.15
SL					1	0.94	0.02	0.12	0.11	-0.21	-0.05	0.13	0	-0.03
SW						1	0.06	0.19	0.14	-0.03	0.13	-0.11	0.09	-0.08
DOH							1	0.67	0.42	0.45	0.59	0.23	-0.01	0.06
FW								1	0.75	0.52	0.73	0.05	-0.09	0.33
Y.P									1	0.45	0.48	-0.09	0.26	0.42
SD										1	0.62	-0.31	0.4	-0.21
seed.fruit											1	-0.21	0.03	0.05
MVL												1	-0.17	0.01
FD													1	0.07
TSS..														1

Figure 3. second year genotypic correlation coefficient among all traits of watermelon, IL: Internodal length; LW: Leaf width; LL: Leaf length; PB: Primary branches; SL: seed length; SW: stem width; DOH: days of harvesting; FW: fruit width; YP: yield per plant; SD: stem diameter; MVL: main vine length; FD: fruit diameter; TSS: total soluble sugar; SF: Seed per fruit.

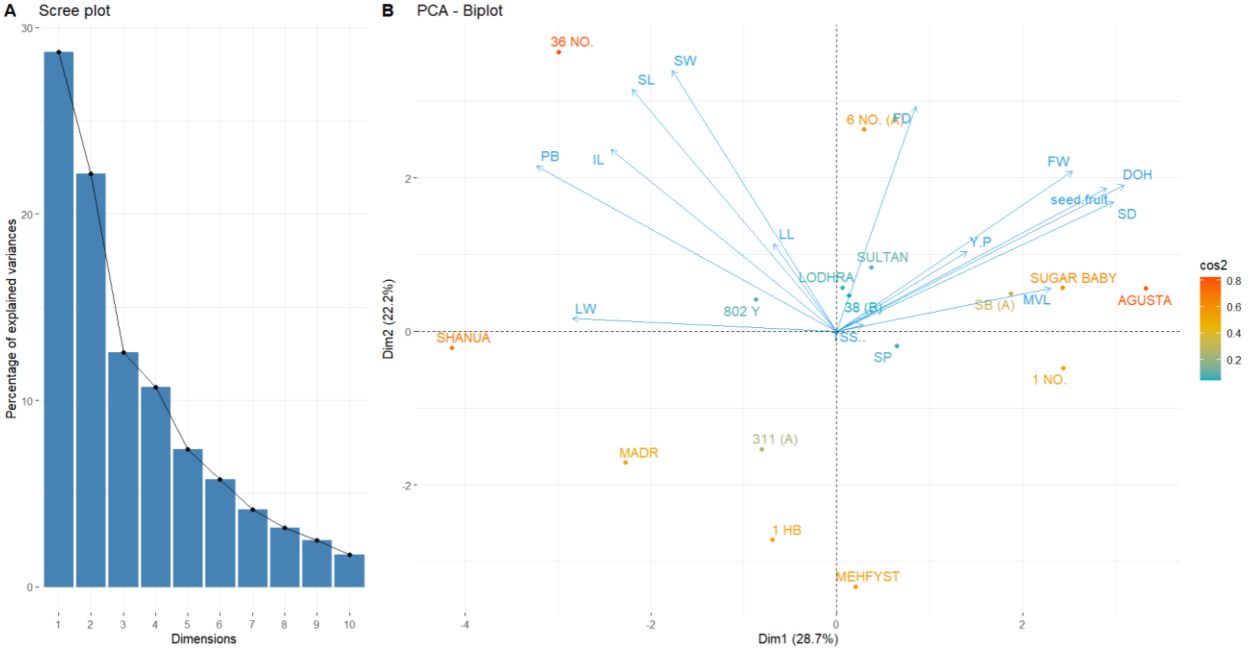


Figure 4. Biplot for all traits; IL: Internodal length; LW: Leaf width; LL: Leaf length; PB: Primary branches; SL: seed length; SW: stem width; DOH: days of harvesting; FW: fruit width; YP: yield per plant; SD: stem diameter; MVL: main vine length; FD: fruit diameter; TSS: total soluble sugar; SF: Seed per fruit.

Table 4. Principal component analysis of watermelon genotypes based on agro-morphological traits (1st year)

Eigen value	Variance %	Cumulative Variance %
4.01	28.70	28.70
3.10	22.15	50.85
1.75	12.54	63.40
1.49	10.70	74.11
1.03	7.38	81.49
0.80	5.75	87.24
0.57	4.13	91.38
0.44	3.15	94.53
0.34	2.49	97.02
0.23	1.69	98.72
0.09	0.70	99.43
0.05	0.38	99.81
0.02	0.17	99.98
0.00	0.01	100.00

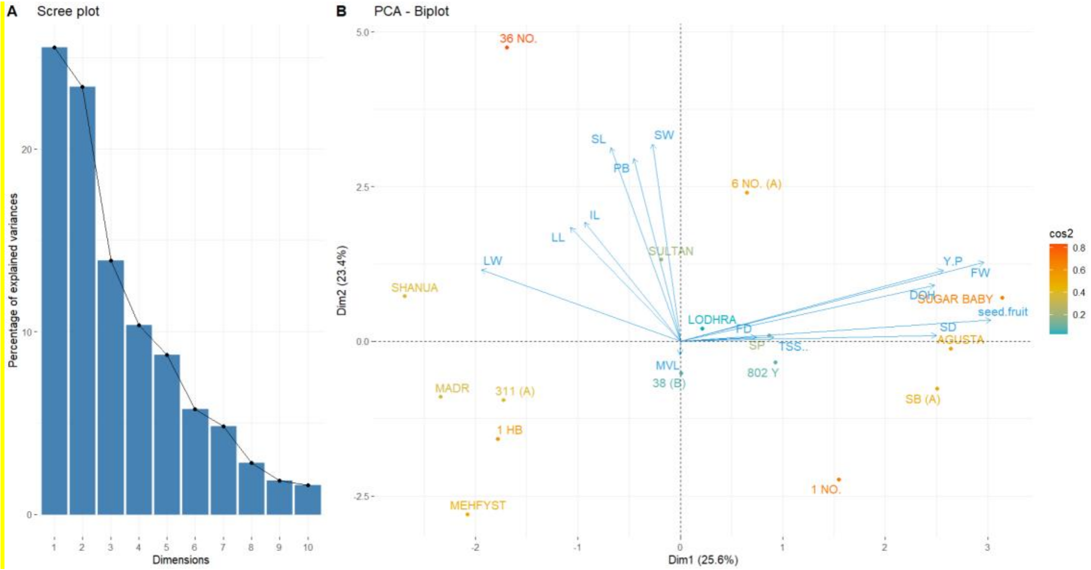


Figure 5. Biplot for all traits; IL: Internodal length; LW: Leaf width; LL: Leaf length; PB: Primary branches; SL: seed length; SW: stem width; DOH: days of harvesting; FW: fruit width; YP: yield per plant; SD: stem diameter; MVL: main vine length; FD: fruit diameter; TSS: total soluble sugar; SF: Seed per fruit.

Table 5. Principal component analysis of watermelon genotypes based on agro-morphological traits (2nd year).

Eigen value	Variance %	Cumulative variance %
3.58	25.57	25.57
3.28	23.40	48.97
1.94	13.87	62.84
1.45	10.35	73.19
1.22	8.73	81.92
0.80	5.74	87.65
0.67	4.81	92.47
0.39	2.82	95.29
0.26	1.83	97.11
0.22	1.58	98.70
0.12	0.88	99.58

0.06	0.40	99.98
0.00	0.02	100.00
0.00	0.00	100.00

Principle Component Analysis of Variables

Path analysis was carried out to find out direct and indirect effects of sixteen genotypes (Figure 4) PCA is a statistical technique that reduces the dimensionality of a dataset by transforming it into a set of principle components (PCs). The Biplot shows the relationships between variables and observations in the principle component. In (figure 2), the first main component (Dim1) is accounting for 28.7% of the variance and the second main component (Dim2) captures additional variance 22.2% that is perpendicular to the first component. Each vector indicates the direction and contribution of a parameter to the two principle components. The direction of each vector shows how much each parameter is related to the principle component. Vectors pointing in the same general direction are positively correlated, which tend to vary together in the data. Conversely, vectors pointing in opposite directions are negatively correlated, indicating an inverse relationship between parameters. Length of each vector represents the strength of that parameter. Longer vector indicates that parameter has a stronger contribution to the variation. Shorter vectors mean the parameter has less influence on the dataset. To further improve these genotypes selection can be made regarding measured parameters falling in clusters. For example, yield per plant can be improved by selecting the related traits like fruit weight, fruit diameter, stem diameter and seed/fruit. The findings also support previous research by soltani, sahin, adjoumani on the importance of morphological characteristics in assessing genetic diversity and selection within watermelon genotypes (Adjoumani et al., 2016; Şahin 2024; Soltani et al., 2016). Moreover, Genotypes that lie close to a vector are more strongly associated with that parameter, while those in opposite direction are less associated. The results of PCA were conducted with fourteen parameters of sixteen genotypes presented in figure 4 & figure 5. The table shows the main components and their percentage of variation. Eigan values show the variance among traits. Eigan values greater than zero indicate that the corresponding principle component contributes meaningfully to the data's variance.

CONCLUSION

The study demonstrated genetic variability among sixteen genotypes collected from diverse regions of Pakistan and other countries. This variability indicates the potential for genetic improvement through selection and hybridization. The use of statistical analyses helped to effectively identify promising lines for future breeding. Overall, the finding provides a foundational basis for developing high-yielding, quality rich, and locally adapted watermelon cultivars.

AUTHOR'S CONTRIBUTION

Nusrat Parveen: conceptualization and supervision; Sana Akbar: Data collection, methodology and initial draft preparation; Wajeeha khan: Data collection, manuscript editing and finalization; Muneeb Munawar: Data curation and statistical analysis; Dr Muhammad Iqbal: supervision and methodology; Mehvish Tahir: methodology and data collection.

FUNDING

This research was funded by Punjab Agriculture Research Board (PARB) under the project no. 20-426.

AVAILABILITY OF DATA AND MATERIAL

All data is given in the manuscript.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

CONSENT FOR PUBLICATION

All authors agreed to publication of manuscript in its present form.

CONFLICT OF INTERESTS

The authors declared no conflict of interest.

ACKNOWLEDGEMENT

We acknowledge our organization for providing research support.

REFERENCES

Adjoumani K, Kouonon LC, Koffi G, Bony B, Brou KF, Akaffou DS, Sié R. 2016. Analysis on genetic variability and heritability of fruit characters in Citrullus lanatus (Thunb.) Matsumura and Nakai (Cucurbitaceae) cultivars. Journal of Animal and Plant Sciences,28:4340-4355.

Assefa AD, et al. 2020. Fruit Morphology, Citrulline, and Arginine Levels in Diverse Watermelon (Citrullus lanatus) Germplasm Collections. Plants (Basel), 9:1054

Bhagyalekshmi T, Gasti V, Evoor S, Gopali J, Mastiholi A, Kamble CS. 2020. Studies on correlation and path-coefficient analysis for yield and its contributing characters in watermelon [Citrullus lanatus (Thunb.) Mansf.]. Journal of Pharmacognosy and Phytochemistry 9:1909-1912.

Choudhary B, Pandey S, Singh PK. 2012. Morphological diversity analysis among watermelon (Citrullus lanatus (Thunb) Mansf.) genotypes. Progressive Horticulture, 44:321-326.

Dutta SK, Nimmakayala P, Reddy UK. 2023. Watermelon: Advances in Genetics of Fruit Qualitative Traits. Pages 1-13 in Kole C, ed. Compendium of Crop Genome Designing for Nutraceuticals. Singapore: Springer Nature Singapore.

Food and Agriculture Organization. (2023). Watermelon production in Pakistan *2022*. FAOSTAT.

Gichimu BM, Owuor BO, Mwai GN, Dida MM. 2009. Morphological characterization of some wild and cultivated watermelon (Citrullus sp.) accessions in Kenya.

Hwang J, Kang J, Son B, Kim K and Park Y (2011) Genetic diversity in watermelon cultivars and related species based on AFLP and EST-ISSRs. Notulae Botanicae Horti Agrobotanici 39: 285–292

Kwon YS, Oh YH, Yi SI, Kim HY, An JM, Yang SG, Ok SH and Shin JS (2010) Informative SSR markers for commercial variety discrimination in watermelon (Citrullus lanatus). Genes and Genomics 32: 115–122.

Levi A, Jarret R, Kousik S, Wechter WP, Nimmakayala P, Reddy U (2017) Genetic resources of watermelon. In: Grumet R, Katzir N and Garcia-Mas J (eds.) Genetics and Genomics of Cucurbitaceae, Plant Genetics and Genomics: Crops and Models. Cham, Switzerland: Springer International Publishing AG, pp. 87–110.

Minsart LA, Zoro IA, Dje Y, Baudoin JP, Jacquemart AL and Bertin P (2011) Set up of simple sequence repeat markers and first investigation of the genetic diversity of West African watermelon (Citrullus lanatus ssp. vulgaris Oleaginous type). Genetic Resources and Crop Evolution 58: 805–814.

Maoto MM, Beswa D, Jideani AIO. 2019. Watermelon as a potential fruit snack. International Journal of Food Properties 22:355-370.

Mohosina F, Mehedi M, Mahmud E, Hassan M, Noor M, Rahman M, Chowdhury A. 2020. Genetic diversity of commercially cultivated watermelon (Citrullus lanatus) hybrids in Bangladesh.

Mulyani PT, Waluyo B. 2020. Correlation Analysis Between Yield Component Traits and Yield of Watermelon Genotypes (Citrullus lanatus): Analisis Korelasi antara Karakter Komponen Hasil dengan Hasil pada Beberapa Genotipe Semangka (Citrullus lanatus). AGROSAINSTEK: Jurnal Ilmu dan Teknologi Pertanian 4:41-48

Paris HS, Daunay MC and Janick J (2013) Medieval iconography of watermelons in Mediterranean Europe. Annals of Botany 112: 867–879

Şahin N. 2024. Morphological characterization of some local watermelon (Citrullus lanatus L.) genotypes of Turkey. International Journal of Life Sciences and Biotechnology 7:28-36.

Singh U, Kumar S, K A, Yadav K, K C, K S. 2022. Genetic variability and correlation studies in various genotypes of watermelon [Citrullus lanatus (Thunb.) Mansf.]. Journal of Agriculture and Ecology:65-78.

Solmaz I, Sarı N. 2008. Characterization of watermelon (Citrullus lanatus) accessions collected from Turkey for morphological traits. Genetic Resources and Crop Evolution 56:173-188.

Soltani F, Ebadi M, Mostoufi Y, Azizzadeh SM. 2016. Evaluation of phenotypic variation of Iranian watermelon (Citrullussp.) accessions by morphological markers. Acta Horticulturae:129-132.

Steel RG, Torrie JH, Dickey DA. 1997. Principles and procedures of statistics: a biometrical approach

Wehner TC (2008) Watermelon. In: Prohens J and Nuez F (eds.). Handbook of Plant Breeding; Vegetables I: Asteraceae, Brassicaceae, Chenopodiaceae, and Cucurbitaceae. New York: Springer Science Business LLC, pp. 381–418

Zamuz S, Munekata PES, Gullón B, Rocchetti G, Montesano D, Lorenzo JM. 2021. Citrullus lanatus as source of bioactive components: An up-to-date review. Trends in Food Science & Technology 111:208-222.

Zoltán T, Gyulai G, Szabó Z, Horváth L and Heszky L (2007) Watermelon (Citrullus lanatus) production in Hungary from the Middle Ages (13th century). Hungarian Agricultural Research 4: 14–19.