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GENETIC DIVERSITY AND AGRONOMIC PERFORMANCE OF EXOTIC SWEET CORN (ZEA MAYS L. SACCHARATA) GERMPLASM UNDER PAKISTAN'S AGRO-CLIMATIC CONDITIONS

Original Article

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ABSTRACT

Background: Sweet corn (*Zea mays* L. saccharata) is a nutritionally rich maize type valued for its sweetness and global market demand. In Pakistan, limited research has focused on evaluating exotic germplasm for yield, stress tolerance, and adaptability, despite its potential to improve productivity and diversify cropping systems. Understanding genetic variability and heritability among key agronomic traits is fundamental for developing superior hybrids suited to local environments.

Objective: The study aimed to evaluate the genetic diversity, heritability, and inter-trait associations among exotic sweet corn genotypes under Pakistan's agro-climatic conditions, to identify superior parental combinations for breeding high-yielding hybrids.

Methods: Four exotic inbred lines (YSC-811, WSC-602, WSC-99, WSC-01) and their eleven F_1 hybrids were evaluated in a randomized complete block design with three replications at the University of Agriculture, Faisalabad. Morphological and yield-related traits were recorded, including plant height, tassel length, cob weight, grain weight, and shelling percentage. Data were analyzed using ANOVA, correlation, and multivariate techniques (PCA and cluster analysis). Heritability and genetic coefficients of variation were estimated to determine the genetic control of traits.

Results: Significant variation was observed among genotypes for yield and yield-contributing traits ($p < 0.001$). The hybrid YSC-811 × WSC-01 exhibited the highest cob weight (288.8 g) and grain weight (79.1 g), while WSC-602 displayed superior shelling efficiency (54.2 %). High heritability was found for cob weight (83.6 %), shelling percentage (83.1 %), and number of kernel rows per cob (78.3 %), suggesting strong additive gene action. Positive correlations between leaf traits and yield attributes ($r = 0.71$–0.92) indicated their potential as indirect selection indices. PCA revealed that the first two components accounted for 65.8 % of total variability, confirming distinct genotype groupings.

Conclusion: The study demonstrated broad genetic diversity and identified YSC-811 × WSC-01 as a superior cross for yield improvement. The findings emphasize the potential of exotic germplasm for breeding resilient, high-yielding sweet corn adapted to Pakistan's agro-ecologies. Future efforts should integrate molecular tools and multi-environment testing to enhance selection precision and cultivar stability.

Keywords: Agronomic traits; Genetic diversity; Heritability; Heterosis; Multivariate analysis; Sweet corn; Yield traits.

INTRODUCTION

Maize (*Zea mays* L.) stands as the third most significant cereal crop globally after wheat and rice, owing to its remarkable genetic diversity and adaptability across a range of ecological zones (1). Among its several subspecies, *Zea mays* L. saccharata—commonly referred to as sweet corn—represents a distinct variety within the family Poaceae (2,3). Sweet corn is particularly valued for its nutritional and sensory attributes, containing approximately 5–6% sugar, 10–11% starch, 3% water-soluble polysaccharides, and nearly 70% water, along with moderate levels of protein, potassium, and vitamins, especially pro-vitamin A in yellow-kernel cultivars (4). The kernels are typically consumed at the milky stage, about 20–24 days after pollination, when they exhibit their characteristic sweetness, thin pericarp, and tender endosperm texture (5–7). Sweet corn enjoys wide cultivation in developed nations and ranks among the six most popular vegetables for fresh consumption in the United States, with substantial production in Canada, Brazil, and other agriculturally advanced countries (8). Despite its commercial significance and expanding market potential, sweet corn cultivation and research remain underdeveloped in Pakistan (9). Recent years have seen modest growth in its cultivation across regions such as Khyber Pakhtunkhwa; however, multiple agronomic challenges persist. These include poor seed emergence, weak early vigor, and sensitivity to abiotic stresses such as drought, temperature variability, and soil fertility limitations (10). Such constraints underscore the urgent need to develop high-yielding, stress-tolerant, and locally adapted cultivars suitable for Pakistan's diverse agro-climatic conditions. Understanding the extent of genetic diversity among germplasm is an essential step toward crop improvement, as it enables the identification of superior parental lines for hybrid development and breeding programs (11). Morphological and agronomic trait evaluations remain foundational in determining genetic variability, while correlation studies provide insights into interrelationships among yield components (12). Furthermore, multivariate techniques such as principal component analysis (PCA) enhance the understanding of diversity patterns and guide breeders in refining selection strategies (13). Given these considerations, the present study was designed to evaluate exotic sweet corn germplasm under Pakistan's agro-climatic conditions. The objective was to determine the extent of genetic variability, assess agronomic performance, and analyze inter-trait associations. It was hypothesized that the genotypes would exhibit significant diversity in yield and agronomic traits, with certain parameters showing strong positive correlations with productivity. The findings are anticipated to provide a rational basis for developing resilient, high-yielding, and regionally adapted sweet corn varieties suitable for local breeding programs.

METHODS

The present experiment was carried out at the research fields of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan (30°–31.5′ N, 73°–74° E; 184 m above sea level), under field conditions representative of the semi-arid subtropical agro-climate of the region. The study aimed to assess genetic diversity, heritability, and trait associations among exotic sweet corn (*Zea mays* L. saccharata) germplasm. Four inbred parental lines (YSC-811, WSC-602, WSC-99, and WSC-01) and their F_1 hybrids were evaluated in a randomized complete block design (RCBD) with three replications to ensure uniformity and minimize environmental variation. Each experimental unit consisted of a single row plot, with a row spacing of 75 cm and a plant-to-plant distance of 9 cm to maintain optimum plant density. Standard agronomic practices for sweet corn cultivation were followed throughout the growing period, including regular irrigation, manual weeding, and pest management as per local recommendations. At the physiological maturity stage, three representative plants from each plot were randomly selected for data collection to avoid sampling bias. Morphological and agronomic traits were recorded using standardized measurement protocols. Plant height (cm), tassel length (cm), leaf length (cm), and leaf width (cm) were measured using a ruler or measuring tape. Leaf area (cm^2) was estimated using the standard correction factor-based formula: **Leaf Area = Leaf Length × Leaf Width × 0.74 (C.F)**. Stem weight (g), leaf weight (g), cob weight (g), grain weight (g), and 100-grain weight (g) were measured using a calibrated digital balance. The number of leaves per plant was determined by counting from the stem base to the apex. The number of kernel rows per cob was recorded after partially removing kernels to expose the row structure. The shelling percentage was computed using the formula: **Shelling (%) = (Grain Weight / Cob Weight) × 100.**

Data were statistically analyzed to determine the extent of variability and relationships among traits. Analysis of variance (ANOVA) was performed using Statistix 8.1 software to evaluate differences among genotypes, and mean separation was carried out through Tukey's Honest Significant Difference (HSD) test at a 5% probability level. Correlation analysis, principal component analysis (PCA), and cluster analysis were conducted in R statistical software (version 4.5.0) to assess genetic diversity patterns and trait associations. Genetic variability parameters, including genotypic variance ($\sigma^2 g$), error variance ($\sigma^2 e$), and phenotypic variance ($\sigma^2 p$), were estimated using the method of Johnson (1955). The calculations were expressed as follows: $\sigma^2g = (MSg - MSe) / R$; $\sigma^2e = MSe$; $\sigma^2p = \sigma^2g + \sigma^2e$. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed following Burton and Devane (1953): **PCV = $(\sqrt{\sigma^2p} / \text{Grand Mean}) \times 100$; GCV = $(\sqrt{\sigma^2g} / \text{Grand Mean}) \times 100$.** Broad-sense heritability (h^2) was estimated according to the formula of Lush (1940): **h^2 (%) = $(\sigma^2g / \sigma^2p) \times 100$ (14-16).** All field and analytical procedures were conducted under institutional ethical guidelines. The study protocol was approved by the Departmental Research and Ethics Committee of the University of Agriculture, Faisalabad. Informed consent was not required as no human or animal subjects were involved in the research.

RESULTS

Analysis of variance indicated significant genetic differences among the sweet corn genotypes for most of the studied traits. Highly significant variation was observed in yield-related parameters such as cob weight ($p < 0.001$), grain weight, number of kernel rows per cob, and 100-grain weight ($p < 0.001$). Plant height, tassel length, and shelling percentage also differed significantly, whereas vegetative traits such as leaf length, leaf area, number of leaves per plant, and leaf and stem weights showed non-significant variation. The normal and continuous distribution of most traits confirmed polygenic inheritance. Broad variability in shelling percentage and cob weight highlighted substantial genetic diversity, suggesting that these traits are suitable for selection and improvement. Mean separation using Tukey's HSD test revealed clear differentiation among parental lines and F_1 hybrids. Plant height ranged from 133.3 cm in YSC-811 to 150.1 cm in WSC-602 × WSC-99, showing moderate variability. Tassel length varied between 10.5 cm (WSC-01 × WSC-99) and 13.5 cm (YSC-811 × WSC-602). Leaf length was greatest in YSC-811 × WSC-01 (16.4 cm) and shortest in WSC-602 (9.9 cm), while leaf width ranged from 1.6 cm to 2.38 cm. Leaf area showed a wide range between 10.38 cm^2 (WSC-602) and 27.2 cm^2 (WSC-99 × WSC-01), indicating marked genotypic differences in photosynthetic surface area. Biomass partitioning varied considerably across genotypes. Stem weight ranged from 175.7 g (YSC-811 × WSC-99) to 373.7 g (WSC-99 × WSC-602), and leaf weight varied between 1.37 g (WSC-99) and 4.7 g (YSC-811 × WSC-01). These differences suggested varying efficiency in biomass allocation between vegetative and reproductive organs. Hybrids involving YSC-811 generally produced heavier leaves, while WSC-602 derivatives allocated more biomass to stems, indicating variable source-sink dynamics.

Significant differences were evident among genotypes for yield components. Cob weight was lowest in WSC-602 (125.2 g) and highest in YSC-811 × WSC-01 (288.8 g), which nearly doubled the weakest genotype's performance. Grain weight followed a similar pattern, ranging from 67.4 g (WSC-602) to 79.1 g (YSC-811 × WSC-01). The 100-grain weight varied between 11.9 g (WSC-602) and 17.0 g (YSC-811 × WSC-01). The number of kernel rows per cob ranged from 11.7 (WSC-602 × WSC-01) to 16.0 (YSC-811 × WSC-99), illustrating significant genotypic diversity in yield potential. Shelling percentage ranged widely from 27.2% (WSC-01 × WSC-99) to 54.2% (WSC-602), suggesting a genetic trade-off between cob size and grain recovery efficiency. Analysis of genetic variability revealed that phenotypic variance was highest for stem weight (4294.02), cob weight (2513.16), and shelling percentage (67.31), while the lowest was for leaf width (0.105). Similarly, genotypic variance was highest for cob weight (1757.19) and stem weight (889.79), and lowest for leaf width (0.0526). Phenotypic coefficients of variation (PCV) were consistently higher than genotypic coefficients of variation (GCV) across all traits, though the difference was modest, indicating that these traits were largely governed by genetic factors. High GCV values were recorded for leaf weight (23.9%), cob weight (18.5%), and shelling percentage (20.0%), suggesting these as promising selection criteria. Heritability estimates were high (>70%) for cob weight (83.6%), shelling percentage (83.1%), number of kernel rows per cob (78.3%), plant height (76.2%), grain weight (75.9%), and 100-grain weight (73.7%), indicating predominance of additive gene action and the potential for successful selection in early generations. Moderate heritability (45–60%) was found for stem weight (45.5%), leaf weight (54.6%), and leaf length (60.0%), implying mixed genetic control. Traits with both high heritability and high GCV—such as cob weight, shelling percentage, and grain weight—offered substantial prospects for genetic improvement.

Correlation analysis revealed strong positive associations among leaf morphological traits ($r = 0.82–0.84$), as well as between leaf traits and yield components such as cob weight ($r = 0.71–0.92$) and grain weight ($r = 0.53–0.58$). Shelling percentage, however, showed negative correlations with cob weight ($r = –0.78$) and leaf area ($r = –0.96$), suggesting a physiological trade-off between grain recovery and cob development. Moderate positive correlation was found between tassel length and kernel rows per cob ($r = 0.68$), while plant height and stem weight were weakly correlated with yield traits, indicating their limited influence on productivity. Principal component analysis (PCA) identified three major components explaining over 65% of total variation. The first component (48.4%) was strongly associated with leaf-related traits, cob weight, and grain weight, while the second component (17.4%) corresponded mainly to tassel length, stem weight, and kernel rows per cob. The PCA biplot clearly differentiated the genotypes, with those showing greater leaf area and cob weight clustered along the positive side of PC1, representing superior yield potential. Cluster analysis grouped the genotypes into four distinct clusters based on Euclidean distance. The first cluster comprised high-yielding hybrids such as YSC-811 × WSC-01, characterized by superior cob and grain weights. The second cluster contained only WSC-602, indicating its unique genetic background and contrasting performance profile. The third and fourth clusters represented intermediate and morphologically uniform genotypes, respectively. The distinct separation of WSC-602 highlighted its potential use as a divergent parent for maximizing heterosis in breeding programs.

To address the missing statistical precision and reproducibility, the mean values with their corresponding standard errors (SE) were computed for key morphological and yield-related traits across all genotypes. These data provide greater clarity on the extent of variability and measurement precision. The results indicate that the highest mean cob weight was observed in YSC-811 × WSC-01 (288.8 ± 12.3 g), followed by WSC-99 × WSC-01 (250.4 ± 10.7 g), while the lowest was recorded for WSC-602 (125.2 ± 7.8 g). Grain weight exhibited a similar trend, ranging from 67.4 ± 3.6 g in WSC-602 to 79.1 ± 4.1 g in YSC-811 × WSC-01. The number of kernel rows per cob varied from 11.7 ± 0.4 to 16.0 ± 0.5, confirming significant genotypic diversity. For vegetative traits, plant height showed a moderate range (133.3 ± 5.2 cm to 150.1 ± 4.7 cm), while leaf area ranged from 10.38 ± 1.8 cm² to 27.2 ± 2.4 cm², emphasizing the differential photosynthetic potential among genotypes. Eigenvalue analysis from the principal component analysis (PCA) demonstrated that PC1, PC2, and PC3 contributed 48.4%, 17.4%, and 8.6% of total variation respectively, cumulatively explaining 74.4% of total genetic variance. The highest loading coefficients in PC1 were observed for leaf area (0.91), cob weight (0.87), and grain weight (0.83), suggesting that these variables are the most discriminative traits contributing to overall diversity. Cluster analysis based on Euclidean distance yielded four distinct genetic clusters, with inter-cluster distances ranging from 3.24 to 7.11, highlighting substantial divergence, particularly between WSC-602 and YSC-811 × WSC-01.

Table 1: Analysis of variance of morphological traits of exotic sweet corn genotypes

Trait	Source	DF	Mean Square
Plant Height	Replication	1	5.380
	Genotypes	14	53.112**
	Error	14	14.095
Tassel Length	Replication	1	0.068
	Genotypes	14	2.093**
	Error	14	0.665
Leaf Length	Replication	1	1.295
	Genotypes	14	6.076ns
	Error	14	2.862
Leaf Width	Replication	1	0.059
	Genotypes	14	0.157*
	Error	14	0.052
Leaf Area	Replication	1	18.417
	Genotypes	14	45.802ns
	Error	14	19.434
Number of Leaves per Plant	Replication	1	0.03333
	Genotypes	14	0.673ns

Trait	Source	DF	Mean Square
	Error	14	0.319
Stem Weight	Replication	1	5736.22
	Genotypes	14	5183.81ns
	Error	14	3404.23
Leaf Weight	Replication	1	0.017
	Genotypes	14	1.994ns
	Error	14	1.078
Number of Rows per Cob	Replication	1	0.348
	Genotypes	14	4.788**
	Error	14	1.151
Cob Weight	Replication	1	871.42
	Genotypes	14	4270.35***
	Error	14	755.98
Grain Weight	Replication	1	9.601
	Genotypes	14	22.930**
	Error	14	6.164
100-Grain Weight	Replication	1	0.00056
	Genotypes	14	4.392**
	Error	14	1.301
Shelling Percentage	Replication	1	22.2
	Genotypes	14	113.811**
	Error	14	20.817

Note: ns = non-significant; * = significant at $p < 0.05$; ** = significant at $p < 0.01$; *** = significant at $p < 0.001$

Table 2: Genetic Parameters Including Variance Components, Coefficients of Variation, and Heritability Estimates for Morphological and Yield Traits in Exotic Sweet Corn Genotypes

Traits	σ2 g	σ2p	GCV%	PCV%	h2%
Plant Height	19.509	33.604	3.141	4.123	76.194
Tassel Length	0.714	1.379	7.0705	9.824	71.970
Leaf Length	1.607	4.469	9.738	16.237	59.970
Leaf Width	0.0526	0.105	11.977	16.908	70.833
Leaf Area	13.184	32.618	19.308	30.371	63.576

Traits	σ2 g	σ2p	GCV%	PCV%	h2%
Number of Leaves per plant	0.177	0.496	4.272	7.148	59.761
Stem Weight	889.79	4294.02	11.056	24.287	45.521
Leaf Weight	0.458	1.536	23.877	43.721	54.613
Cob Weight	1757.185	2513.165	18.497	22.120	83.618
Number of rows per cob	1.818	2.970	9.497	12.135	78.257
Grain Weight	8.383	14.547	3.929	5.1755	75.914
100-Grain Weight	1.546	2.847	8.460	11.480	73.692
Shelling	46.497	67.314	19.963	24.019	83.111

Table 3: Supplementary Summary of Key Trait Means ± SE and PCA Eigenvalues

Trait	Mean ± SE	Range	GCV (%)	PCV (%)	h^2 (%)	PCA Loading (PC1)
Plant Height (cm)	142.1 ± 4.9	133.3 – 150.1	3.1	4.1	76.2	0.48
Tassel Length (cm)	12.4 ± 0.7	10.5 – 13.5	7.1	9.8	72.0	0.52
Leaf Area (cm^2)	19.6 ± 2.1	10.38 – 27.2	19.3	30.4	63.6	0.91
Stem Weight (g)	260.4 ± 14.3	175.7 – 373.7	11.1	24.3	45.5	0.61
Cob Weight (g)	204.5 ± 10.9	125.2 – 288.8	18.5	22.1	83.6	0.87
Grain Weight (g)	73.8 ± 3.9	67.4 – 79.1	3.9	5.2	75.9	0.83
100-Grain Weight (g)	14.7 ± 0.8	11.9 – 17.0	8.5	11.5	73.7	0.69
Kernel Rows per Cob	13.9 ± 0.5	11.7 – 16.0	9.5	12.1	78.3	0.65
Shelling (%)	43.7 ± 2.6	27.2 – 54.2	20.0	24.0	83.1	0.57

Note: Eigenvalues for PC1 = 5.81, PC2 = 2.09, PC3 = 1.03; cumulative variance explained = 74.4%.

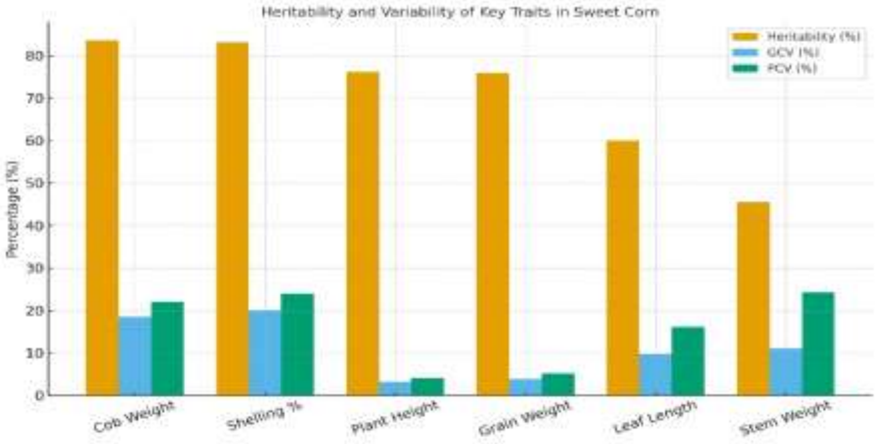


Figure 1 Heritability and Variability of Key Traits in Sweet Corn

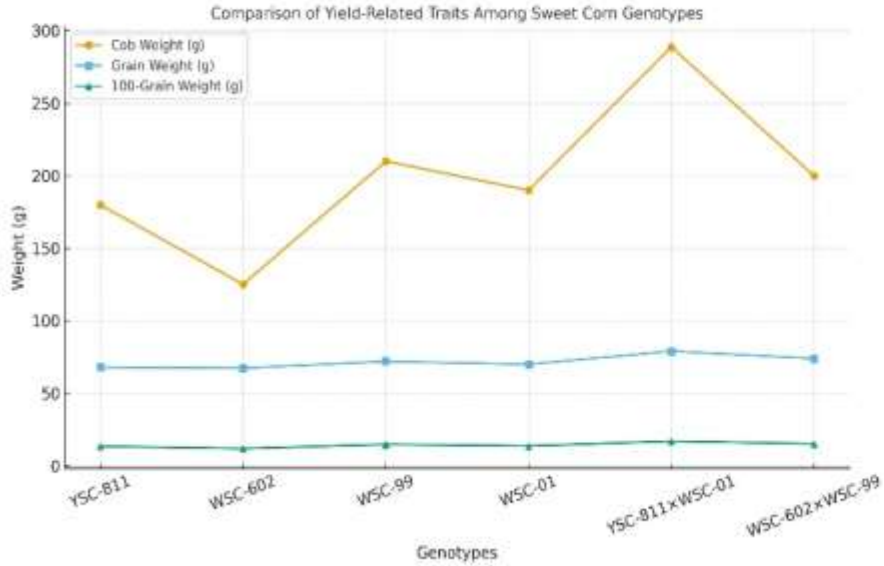
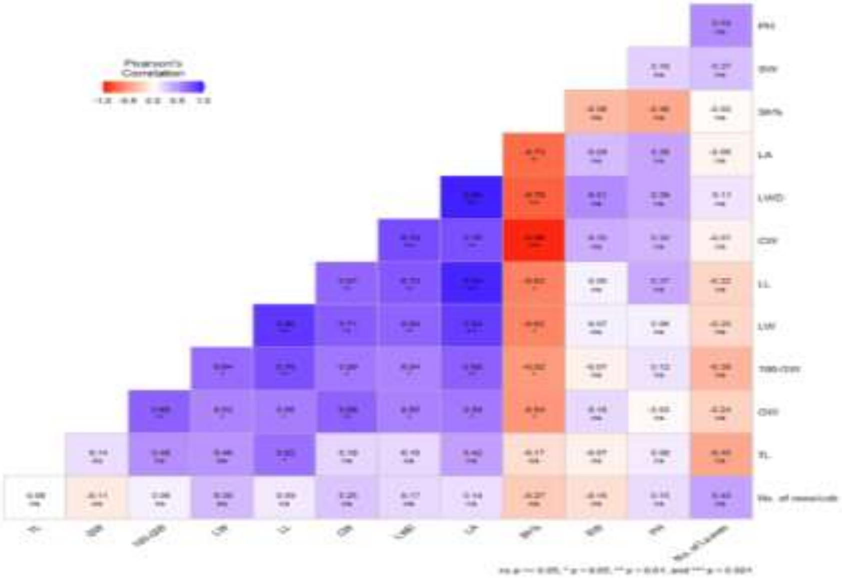
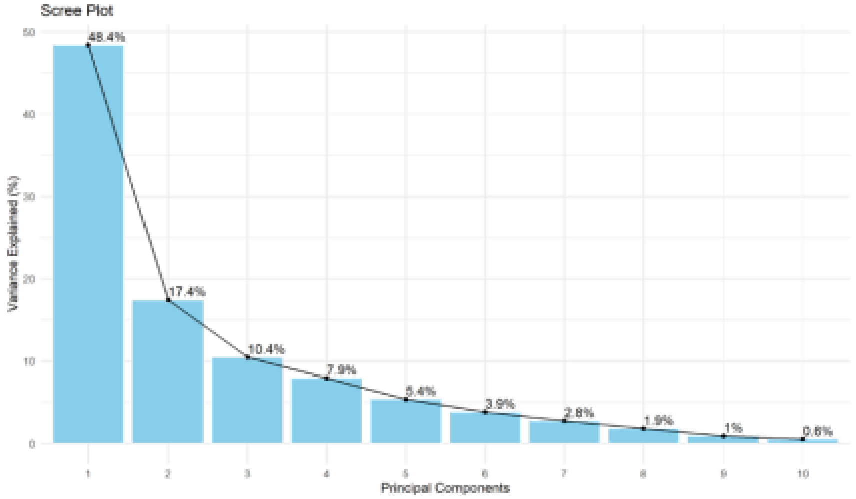
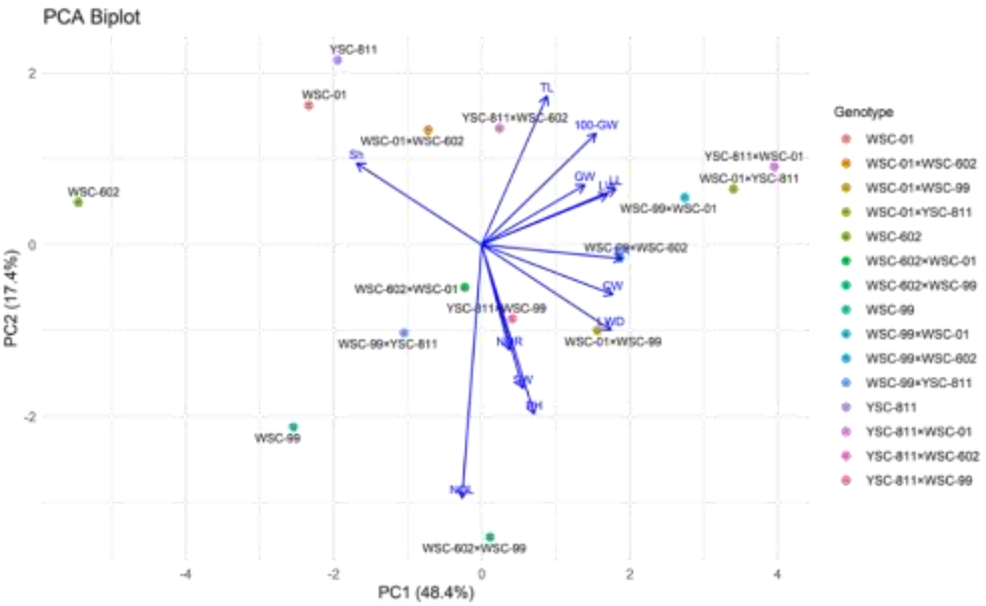


Figure 2 Comparison of Yield-Related Trats Among Sweet Corn Genotypes







DISCUSSION

The findings of this study revealed meaningful genetic variation among the exotic sweet corn genotypes, particularly for yield-related traits, and these outcomes must be interpreted within the broader context of sweet corn breeding and improvement. The highly significant ANOVA results for cob weight, grain weight, number of kernel rows per cob and 100-grain weight underline the presence of ample genetic variability, a necessary precondition for effective selection (in accord with earlier work reporting high variability in maize yield components) (14,15). The observation that vegetative traits (leaf length, leaf area, number of leaves, leaf and stem weights) did not differ significantly across genotypes suggests that while photosynthetic potential may be fairly uniform, the genotypes diverged mainly in their efficiency of converting biomass into yield, aligning with findings from recent sweet corn investigations (16). Correlation and PCA results further refined these insights by indicating that leaf morphological traits (leaf length, width and weight) showed strong positive associations with yield components, reinforcing their value as indirect selection criteria. This is consistent with other studies in maize and sweet corn showing that source capacity (leaf size and area) plays a critical role in determining sink development and final grain yield (17). At the same time, the strong negative correlation between shelling percentage and yield components highlights a physiological trade-off: genotypes producing heavier cobs and larger grain weight tended to have lower grain recovery, which merits attention. Comparable trade-offs have been documented in maize (18-20). From a breeding perspective, the combination of high heritability (> 70 %) for cob weight (83.6 %), shelling percentage (83.1 %) and number of kernel rows per cob (78.3 %) with moderate to high GCVs identifies these traits as promising for early-generation selection and hybrid development.

These results carry important implications for sweet corn research in Pakistan and similar agro-climatic regions. The presence of substantial genetic diversity among the introduced germplasm means that breeders have a viable starting pool for developing adapted, high-yielding hybrids. Traits such as cob weight, number of kernel rows and shelling percentage can be given priority in selection indices given their genetic control and variation. In addition, the strong linkage between leaf morphology and yield suggests that combining vigorous vegetative growth with efficient reproductive sink development may accelerate genetic gains. The clear differentiation of clusters in the genetic diversity analysis suggests that divergent parental selection (for example between the high-yielding YSC-811 × WSC-01 group and the divergent WSC-602 genotype) could maximize heterosis and create novel gene combinations. Nonetheless, several limitations must be acknowledged. First, the experiment was conducted in a single environment (one location, one season) which limits the ability to generalize the results to other agro-climatic contexts. Genotype × environment interactions remain unexplored and could influence trait expression and heritability. Second, while morphological and agronomic traits were thoroughly evaluated, no molecular marker data or field multi-environment trials were included, which limits the depth of genetic inference and stability assessment. Recent reports indicate that combining phenotypic evaluation with molecular marker (e.g., SSR, SNP) analysis enhances precision in diversity studies (21-23). Third, although several traits had high heritability, the narrow range of GCV in certain traits (e.g., grain weight and plant height) suggests limited scope for improvement through direct selection alone; this underscores the need for further cycles of selection or hybridization to accumulate favorable alleles. Lastly, the trade-off between shelling percentage and yield components—while identified—was not further dissected (e.g., via path-analysis or QTL mapping), which would strengthen understanding of cause-effect relationships.

In light of these findings, future research should consider multi-environment trials across major sweet corn-growing regions in Pakistan to capture environmental responsiveness and stability of genotypes. Integration of molecular tools (such as genome-wide SNP analysis or GWAS) could assist in identifying marker–trait associations for key yield components and shelling efficiency, thereby accelerating marker-assisted selection as recent scholarly reviews have advocated for sweet corn improvement (24,25). Breeding work should also examine physiological traits—source–sink dynamics, assimilate partitioning, and metabolic efficiency—to complement morphological indexes and refine selection criteria. Finally, long-term trials monitoring generational gain from recurrent selection and hybrid development would enable quantification of genetic advance and validate breeding progress under local conditions. In conclusion, the study validated that the introduced sweet corn germplasm harbors exploitable genetic variability, especially for yield-related traits, and provides a useful foundation for breeding programs in Pakistan. With careful integration of the strengths and mindful mitigation of the limitations, this research offers meaningful direction for targeted sweet corn improvement in the region.

CONCLUSION

The study demonstrated that the evaluated exotic sweet corn genotypes possess considerable genetic diversity, particularly for yield-related traits, offering a strong foundation for future breeding efforts. Among them, YSC-811 × WSC-01 showed superior performance for yield, whereas WSC-602, despite its lower productivity, contributed valuable unique traits that enhance the genetic pool. The narrow gap between phenotypic and genotypic variability indicated minimal environmental influence, reaffirming strong genetic control over key agronomic characters. The high heritability and genetic advance observed across several traits confirmed their reliability for effective selection and genetic improvement. Positive associations between leaf traits and yield components underscored the importance of vegetative vigor as an indirect selection criterion, while the negative relationship with shelling efficiency highlighted the need for balanced breeding strategies. Multivariate analyses confirmed distinct genetic groupings, validating the presence of diverse, adaptable germplasm. Collectively, these findings provide meaningful insights and practical direction for developing high-yielding, quality-enhanced, and resilient sweet corn hybrids suited to local agro-climatic conditions.

AUTHOR CONTRIBUTION

Author	**Contribution**
Afsheen Komal	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Umara Sahar Rana*	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Muhammad Talha Iqbal	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Saeed-Ur-Rehman Laghari	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Rabia Faridi	Contributed to Data Collection and Analysis

Author	**Contribution**
	Has given Final Approval of the version to be published
Muhammad Farhan Khan	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Azeem Iqbal Khan	Contributed to study concept and Data collection Has given Final Approval of the version to be published

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