

Phenotypic Evaluation of Sunflower (*Helianthus Annuus* L.) Landraces as a Tool for Conservation and Valorization of Plant Genetic Resources

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ABSTRACT

Sunflower yield stagnation driven by genetic erosion threatens edible oil security, necessitates the integration of adaptive genetic resources. This study conducted the phenotypic valorization of 114 Pakistan's indigenous sunflower landraces along with 3 checks to characterize genetic diversity, analyze yield-associated traits, and identify superior genotypes for sunflower improvement programs. The experiment was conducted in an augmented block design using six blocks at the Agriculture Research Farm, Hazara University, Mansehra. Data on 9 morpho-yield related traits were analyzed using Analysis of Variance (ANOVA), principal component analysis (PCA), cluster analysis, and correlation analysis. Highly significant differences ($p < 0.001$) were observed for treatments, and 'Checks vs. Varieties' highlights

considerable genetic variability in the germplasm. Adjusted means performance revealed that Atika-09 (1947.5 kg ha⁻¹), Atika-11 (2427.3 kg ha⁻¹), and Mehraj-10 (1502.4 kg ha⁻¹) showed superior performance across important yield and adaptive traits. PCA revealed that seed yield (PC1) and disease incidence (PC2) accounted for 49.29% of the variation among genotypes. Cluster analysis grouped the genotypes into two clusters, dividing them into 4 groups and 8 subgroups, with group A1 comprising superior lines for yield stability and resistance. Seed yield showed a strong positive correlation with plant height ($r = 0.54^{**}$), head diameter ($r = 0.36^{**}$), and harvest index ($r = 0.92^{**}$). The results demonstrate that phenotypic selection, supported by multivariate analysis, can effectively accelerate the development of resilient high-yielding sunflower hybrids for Pakistan's cropping systems. These findings provide a valuable genetic foundation for breeding programs targeting resilience and yield stability in sunflowers.

Keywords: Landraces, Valorization, Phenotypic evaluation, Genetic diversity, Yield, Sunflower (*Helianthus annuus* L.)

Introduction

The surge in global demand for vegetable oils, driven by population growth and shifting diets, is being destabilized by climate volatility, necessitating immediate attention to resilient and genetically diverse crops (Rauf *et al.*, 2017; Foley *et al.*, 2011; Tilman *et al.*, 2011). Pakistan exemplifies this pressing challenge, ranking among the world's leading edible oil-importing countries, with an annual expenditure of nearly USD 3.5 billion, which highlights critical gaps in national food security (FAO, 2022; GOP, 2023; Hussain *et al.*, 2023). Sunflower (*Helianthus annuus* L.) offers a strategic solution to this constraint, with its short duration, drought tolerance, and high-quality oil making it ideal for both crop rotations and rainfed systems to enhance national production (Saylak, 2022; Alberio *et al.*, 2015). Despite high genetic potential, sunflowers' national yield remains low at 1.0–1.5 t/ha due to excessive dependence on imported hybrids with a narrow genetic base and limited adaptation to local biotic and abiotic stresses (Rauf, 2008; Seiler *et al.*, 2017). This leads to a critical bottleneck on genetic diversity. Therefore, evaluating Pakistan's indigenous sunflower landraces is vital to identify pre-adapted high-yielding

genotypes for national crop improvement programs.

Landraces are genetically diverse populations with dynamic gene pools that evolve within specific agro-ecological conditions through natural and farmers' selection, resulting in a rich source of adaptive traits for local stress conditions (Casañas *et al.*, 2017). Their importance for crop improvement relies on valorization, a systematic process of describing the genetic material and determining its breeding value (Dwivedi *et al.*, 2016). This served as an essential link between the conservation of the gene bank and its practical use in developing improved cultivars. This unexplored genetic material is a vital national reservoir with a strong potential to carry novel alleles and useful trait combinations for resilience to regionally specific stresses such as terminal heat stress, local drought patterns, and prevalent diseases, which are usually absent in commercial hybrids with a narrow genetic base (Seiler *et al.*, 2017; Khan *et al.*, 2018; Radanović *et al.*, 2018; Dudheet *al.*, 2025).

A major challenge in pre-breeding is phenotypic evaluation of large unexplored germplasm, where the need for reliable selection data opposes the constraints due to logistical and resource limitations (Bari *et al.*, 2012; Dozet *et al.*, 2016; Sinha *et al.*, 2020). This phase introduces a core methodological issue; while replicated experimental designs are an ideal approach for accurate estimates of genetic merit, they are prohibitively expensive and operationally complex for initial evaluation across hundreds of distinct genotypes, mainly due to limitations including field space, labor, seed availability, and time (Dudhe *et al.*, 2020; Seiler *et al.*, 2011; Sanders *et al.*, 1982; Williams *et al.*, 2011; Piepho *et al.*, 2016). Consequently, the initial evaluation shifts the objective from maximum precision of every genotype to applying a practical and statistically robust triage approach that highlights the best-performing genotypes for advanced replicated multi-environment trials in subsequent seasons (Burgueño *et al.*, 2018). The experimental approach and design used to address this challenge are therefore decisive, which determines the effectiveness, cost, and success of the valorization process, ensuring that important genetic resources are not accidentally thrown out due to poor experimental planning.

The convergence of low national yields and an underexplored gene pool define a critical knowledge gap that hinders systematic crop improvement. Although augmented design is suitable for preliminary screening, it primarily addresses the logistical issue of evaluating diverse genotypes with limited replication (Federer, 1956; Cyrilus *et al.*, 2014). A major limitation is the absence of a decoded phenotypic architecture of germplasm, which is a detailed map of key adaptive and yield-related traits that interact and vary under local field conditions (Yan and Tinker, 2006). The selection process lacks precision and becomes uncertain due to a lack of essential basic understanding, preventing breeders from identifying superior genotypes and well-balanced trait combinations, leading to an inefficient and unpredictable valorization of landraces (Radić *et al.*, 2020; Millet *et al.*, 2019). Therefore, this study aimed to develop a phenotypic overview of Pakistan's indigenous sunflower landraces, merging multi-trait data to reveal genetic potential and trait relationships. This model will function as a predictive tool, transitioning from basic germplasm documentation to strategic multi-trait selection, providing data-driven, smart pre-breeding, and the development of stress-resilient, high-yielding cultivars.

This study delivers two major contributions for national sunflower breeding: a predictive trait guide and a selected group of pre-evaluated elite lines. The guide derived from plant architecture analysis acts as a strategic selection guide that helps breeders select traits related to better adaptation and high yield. The operation of this tool depends on the second component, a selected set of high-performing superior genotypes assessed for stress resilience and yield. Together, these outcomes transform indigenous landraces from a conserved gene pool to active breeding platforms for developing improved cultivars. Providing both the decoded genetic information and elite breeding material, this work establishes a rapid pre-breeding platform for the development of high-yielding and resilient cultivars to Pakistan's diverse agro-ecological zones, directly supporting edible oil self-sufficiency, improved farmer income, and sustainable agriculture (Jannink *et al.*, 2010; Tester and Langridge, 2010).

Material and Methods

The current experiment was conducted at Agriculture Research Farm, Hazara

University, Mansehra, during the 2025 crop season, using an augmented design layout, consisting of 114 landraces divided into 6 blocks, each block containing 19 new landraces and 3 check entries (Hysun-33, Hysun-38, and VIP-123) randomized in each block. Each experimental plot consisted of a single row of 5 m length, with row-to-row spacing of 60 cm and plant-to-plant spacing of 30 cm. The plot size for each block is 66 m², resulting in a total experimental area of 396 m². Data were collected on days to 50% flowering (DFF), plant height (PH)-cm, stem diameter (SD)-cm, head diameter (HD)-cm, 1000-seed weight (SW)-g, seed yield (SY)-kg ha⁻¹, harvest index (HI)-%, oil content (OC)-%, and disease incidence (DI)-%. Data were analyzed using analysis of variance (ANOVA) under an augmented design in R software, with estimation of adjusted mean performances, standard error (SE), critical difference (CD), and coefficient of variation (CV) as suggested by Federer (1956). Principal Component Analysis (PCA) was conducted using PAST version 4.03 to evaluate the multivariate structure of trait variation. The first two principal components (PC1 and PC2) were plotted to visualize diversity among genotypes, as described by Venujayakanth *et al.* (2017). Genetic relationships were analyzed using cluster analysis as described by Ward (1963) using PAST version 4.03 software. Furthermore, the relationship between yield and yield-related traits was assessed through Pearson's correlation analysis using Past version 4.03, as described by Singh and Chaudhary (1997).

Results and Discussions

Analysis of Variance

Analysis of variance revealed highly significant differences among the 117 indigenous landraces, including checks across all nine morpho-yield traits (Table 1). High significant differences ($p < 0.001$) were observed for treatments in days to 50% flowering (DFF), plant height (PH), stem diameter (SD), head diameter (HD), 1000-seed weight (SW), seed yield (SY), harvest index (HI), oil content (OC), and disease incidence (DI), highlights considerable genetic variability in the germplasm for targeted breeding. Similarly, Sonawane *et al.* (2025) reported highly significant variation across all traits in their study of genetic variability in a sunflower breeding program. In contrast, Arshad *et al.* (2019) observed non-significant differences for some traits in hybrid sets of a crop.

The distinction between standard checks and new lines was prominent. Highly significant differences ($p < 0.001$) in 'Checks vs. Varieties' for traits including DFF, HD, SY, HI, OC, and DI indicate landraces perform distinctly by underlining their genetic uniqueness and potential from the checks, like the observation of Singh *et al.* (2019), who observed considerable variation in sunflower germplasm for yield traits. Blocks showed non-significant differences for most traits, supporting the effectiveness of the experimental design, minimizing field variation, and increasing the accuracy of genotype evaluation. Low error variance in SD, HD, and OC demonstrates high precision and stable trait expression, whereas SY had higher error variance, indicating its responsiveness to micro-environmental factors. A similar observation was reported by Sonawane *et al.* (2025), where yield components showed higher environmental variance than morphological traits.

Mean Performance of Landraces and Checks for Morphological and Yield Traits

Mean performance revealed several landraces outperformed the commercial checks, reflecting breeding potential within this germplasm (Table 2). Atika-09, Atika-11, and Mehraj-10 showed superior performance across important yield and adaptive traits. Seed yields of Atika-11 ($2427.3 \text{ kg ha}^{-1}$), Mehraj-05 ($2477.4 \text{ kg ha}^{-1}$), and Mehraj-07 ($2420.3 \text{ kg ha}^{-1}$) matched or higher than the best check, Hysun-33 ($2501.1 \text{ kg ha}^{-1}$), showing competitive performance in the evaluation. An earlier study by Kulkarni *et al.* (2015) has reported similar patterns of variation for yield in sunflower. Several genotypes exhibited early to medium flowering (70–79 days), compared with the checks (82–87 days), offering potential for escape from late-season stress, like the findings of Ali *et al.* (2023). Plant height (203–253 cm) in elite lines was generally taller than in checks, reflecting vigorous growth and enhanced biomass partitioning, similarly reported by Nishat (2020). Aamehria-17 (96.6 g) and Mehraj-10 (92.0 g) closely matched or exceeded Hysun-38 (94.98 g), while maintaining good stem diameter and head size, as observed by Radić *et al.* (2013). Atika-11 (49.6%) and Mehraj-05 (50.4%) showed a high harvest index to checks (45–50%), highlighting efficient formation of seed yield, consistent with the findings of Chakraborty *et al.* (2022). Disease incidence (DI) was low in many selected lines

(4.5–10.2%), equal to or lower than the checks (5.1–5.3), indicating inherent disease resistance, like the findings of Seiler *et al.* (2017).

Principal Component Analysis

Principal component analysis (PCA) was carried out to explore patterns of variation among 117 sunflower genotypes, following the procedure adopted by Venujayakanth *et al.* (2017). Five principal components (PCs) were extracted with eigenvalues greater than 0.9, collectively explaining 82.20% of phenotypic variation (Table 4). PC1 (eigenvalue = 3.34; 37.13% variance) was strongly influenced by seed yield (SY; 0.999), highlighting its role in genetic diversity. PC2 (1.09; 12.16%) was strongly associated with disease incidence (DI; 0.834) and negatively with plant height (PH; -0.545), indicating differences in vigor and resilience. PC3 (eigenvalue = 1.06; 11.75% variance) captured differences in plant height (PH; 0.823) and DI (0.529), representing differences in plant architecture and response to disease. PC4 (eigenvalue = 0.99; 10.99% variance), largely influenced by 1000-seed weight (SW; 0.978), reflecting the role of seed size in differentiating genotypes. PC5 (0.91; 10.17%) was strongly associated with days to 50% flowering (DFF; 0.993), emphasizing its importance for maturity synchronization. Traits such as head diameter, stem diameter, harvest index, and oil content contributed moderately to PCs, influencing overall genetic diversity.

PCA scores identified superior genotypes for each component (Table 5). In PC1, Atika-09 (3.57), Mehraj-05 (3.45), Hysun 33 (3.03), and Aamehria-16 (2.86) scored highest, excelling in seed yield and productivity traits. PC2 highlighted Mehraj-05 (1.37), Hysun 33 (1.83), and Mehraj-09 (1.53) as superior for plant vigor and disease resilience. In PC3, Mehraj-10 (1.57), Aamehria-15 (1.99), and Atika-03 (0.97) for combining strong vegetative growth with reproductive potential. PC4 identified SKS-12 (1.73), Hysun 38 (1.00), and Hysun 33 (0.81) for their heavier seeds, which contributed to yield stability. In contrast, PC5 highlighted Atika-12 (1.85), Hysun 38 (1.87), and SKS-12 (1.24) for their early and synchronized flowering. Genotypes such as Atika-09, Mehraj-05, Hysun 33, Aamehria-16, and Hysun 38 consistently scored high across multiple PCs, making them elite lines for hybrid breeding.

The biplot was generated based on PC1 (37.13%) vs. PC2 (12.16%) scores of

117 genotypes for 9 morpho-yield traits, only the top 20 high performing genotypes were mentioned (Figure 1), as described by Riaz et al. (2020). 1000-seed weight (SW), followed by oil content (OC), seed yield (SY), and harvest index (HI), have more discriminating ability in identifying genotypes with desirable characteristics due to their longer vector length. A moderate contribution to overall variation was observed for days to 50% flowering (DFF), disease incidence (DI), plant height (PH), stem diameter (SD), and head diameter (HD). SW, DI, and HD fall in the same quadrant, i.e., A, while SY, HI, and DFF fall in Quadrant B, PH and SD in Quadrant C, and OC in Quadrant D, reflecting contrasting trait associations within the germplasm. Correspondingly, Quadrant A consisted of Aamehria-16, Hysun 38, Aamehria-12, Aamehria-15, Atika-03, and Atika-09, representing genotypes with larger seed size and strong plant architecture. Quadrant B grouped Mehraj-09, Mehraj-05, VIP-123, Hysun 33, Aamehria-08, Atika-11, and Mehraj-07, showing higher yield potential and efficient biomass partitioning. Quadrant C included Aamehria-17, Mehraj-10, Aamehria-18, and Atika-17, indicating tall and vigorous plant growth, whereas Quadrant D included Atika-15, Mehraj-08, SKS-12, Atika-01, Atika-04, and Atika-12, associated with oil-rich but relatively low-yielding genotypes.

Cluster Analysis

The dendrogram was generated based on a similarity-dissimilarity matrix and grouped 117 sunflower genotypes into two distinct clusters (Figure 2), as described by Ward (1963). Cluster I represents elite, high-yielding genotypes, comprising 53 genotypes divided into Group A (19) and Group B (34). Its sub-groups, A1 (9 genotypes) and A2 (10 genotypes), hold most top lines from the selection index. Key genotypes in A1 include Atika-09, Atika-01, and Aamehria-18, while A2 includes Hysun-38, Hysun-33, VIP-123, and superior landraces such as Atika-11, Mehraj-07, and Aamehria-16. Landraces closely associated with high-yielding checks show that group A represents the high-yielding genotypes characterized by ideal plant height, head diameter, and harvest index. Group B within Cluster I includes top-performing lines such as Atika-12 and Atika-17 from B1, which form a genetically distinct but phenotypically similar elite subset, suitable for selecting complementary parents to combine diversity with high yield. The divergent Cluster II consists of 64 genotypes

with a phenotypic pattern different from the elite ideotype. It is subdivided into group A (20 genotypes) and group B (44 genotypes). None of the top 20 high-yielding genotypes is included, highlighting their distinct separation from high-yield phenotypes. Genotypes in A1 and A2 (e.g., AM-17, Atika-19), B1 and B2 (e.g., SKS-09, AM-01) generally exhibited lower mean values for key yield-related traits. This cluster consists of landraces adapted to specific stresses or exhibiting alternative flowering and maturity patterns, providing a secondary pool of genetic variation for introducing traits such as disease resistance or drought tolerance, rather than for immediate selection for yield improvement.

Correlation Analysis

Pearson correlation analysis revealed significant associations among morpho-yield traits in 114 indigenous sunflower landraces and checks (Figure 3). Seed Yield showed a strong positive association with plant height ($r = 0.54^{**}$), head diameter ($r = 0.36^{**}$), and harvest index ($r = 0.92^{**}$), similarly observed by Rani *et al.* (2016), who observed that taller plants with bigger heads and higher biomass partitioning contribute to higher yields. Plant height is positively associated with head diameter ($r = 0.57^{**}$) and harvest index ($r = 0.55^{**}$), highlighting its importance in overall plant vigor and yield, as reported by Sharma and Kaila (2025), and dissimilar to the findings of Memon *et al.* (2014). Disease incidence (DI) strong negative association with PH ($r = -0.58^{**}$), HD ($r = -0.38^{**}$), SY ($r = -0.45^{**}$), and HI ($r = -0.47^{**}$), indicating that vigorous, high-yielding plants are less prone to diseases, similarly observed by Leite *et al.* (2006). Oil content (OC) has moderate negative correlations with SY ($r = -0.30^{**}$) and HI ($r = -0.36^{**}$), suggesting a potential trade-off between yield and oil concentration, while largely independent of morphological traits, similar to the findings of Dan *et al.* (2012). Days to 50% flowering were weakly associated with most yield and quality traits, except for slight negative correlations with PH ($r = -0.20^{*}$) and HD ($r = -0.23^{*}$), showing that flowering time does not strongly influence yield-related traits, similarly reported by Pandya *et al.* (2016). Stem diameter exhibited a weak association with most traits, implying a limited role in determining yield or disease resistance, similar to the findings of Sharma and Kaila (2025).

Conclusion

This study demonstrates the substantial genetic diversity of Pakistan's indigenous sunflower landraces, serving as an important genetic resource for enhancing yield, disease resilience, and agro-climatic adaptability. The systematic assessment of 114 landraces resulted in the selection of elite genotypes, i.e., Atika-09, Atika-11, Mehraj-10, Mehraj-05, Mehraj-07, and Aamehria-16, which were characterized by their early to late maturity, high yield potential, robust plant architecture, and inherent disease resistance. These superior landraces provide valuable parental resources for hybrid development, supporting the strategic use of locally adapted germplasm to drive sustainable breeding progress and reduce dependence on edible oil imports. This study bridges the gap between conservation with practical breeding by establishing a valuable resource for breeding of high-yielding, resilient, and sustainable oilseed crops in Pakistan.

Author Contribution

Atika Liaquat and Shoaib Khan: Data collection and compiling. Muhammad Mehraj Riasat: Supervised the project, original draft, Technical guidance. Ubaid Ullah, Jannat Ul Bareen, Naeem Malik, Muhammad Hadi, Saqib Waqar Ahmed: Formal analysis, Review and editing the draft, all authors contributed to the review and editing of the manuscript.

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Table 1. Augmented block design ANOVA for various traits of 117 genotypes of Sunflower (*Helianthus annuus L.*).

SOV	Treatments	Checks	Blocks	Entries	Checks vs Landraces	Error
Degree of freedom	113	2	5	116	1	10
Days to 50% flowering	34.48***	50.24***	0.76	50.53***	22.76***	0.70
Plant height	155.26***	330.69***	0.12	331.54***	1.33	3.43
Stem diameter	5.17**	54.49***	0.19	8.28***	0.11	0.03
Head diameter	278.68***	664.63***	6.85**	126.20***	56.74***	0.04
1000-seed weight	691.11***	773.71***	0.54	855.17***	7.70*	0.45
Seed yield	139.00***	138.65***	3.27	88.29***	71.34***	3017.58
Harvest index	1239.75***	682.09***	7.15**	451.14***	108.89***	0.06
Oil content	53.83***	111.95***	2.13	40.25***	8.32*	0.05
Disease incidence	540.00***	0.09	0.20	849.80***	19.24**	1.83

* p<0.05, ** p<0.01, *** p<0.001

Table 2. Mean performance of top 20 genotypes in comparison with checks of sunflower (*Helianthus annuus L.*) under an augmented design.

Genotypes	DFF	PH	SD	HD	SW	SY	HI	OC	DI
		(cm)	(cm)	(cm)	(g)	(kg/ha)	(%)	(%)	(%)
Atika-09	72.33	239.42	2.36	26.14	90.61	1974.55	44.61	41.21	5.17
Atika-11	72.33	217.02	2.26	20.34	83.01	2427.30	49.61	42.21	5.17

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Mehraj-10	70.33	219.32	3.16	20.61	92.01	1502.44	40.41	40.71	4.50
Atika-12	73.33	253.02	2.66	23.94	61.61	1219.68	29.61	46.21	5.17
Mehraj-07	78.33	221.32	2.66	19.61	76.51	2420.30	44.41	42.71	4.50
Mehraj-05	81.33	232.92	2.26	20.41	85.91	2477.44	50.41	40.71	4.50
Atika-17	75.33	243.42	2.76	23.34	73.71	1297.63	34.61	43.21	5.17
Aamehria-17	77.33	244.28	2.56	25.68	96.61	1272.94	38.27	39.88	5.17
Aamehria-15	79.33	226.28	3.06	20.88	94.41	1572.94	45.27	39.88	10.17
Aamehria-18	72.33	226.88	2.26	21.38	81.51	1940.80	42.27	41.88	25.17
Atika-03	78.33	233.02	2.76	23.34	90.71	1713.01	44.61	41.21	50.17
Aamehria-12	75.33	223.88	2.76	21.88	92.31	1690.25	40.27	39.88	20.17
Aamehria-16	79.33	225.68	1.96	22.88	92.21	2090.25	45.27	40.88	15.17
SKS-12	87.33	221.05	3.16	19.24	81.28	1911.92	39.51	42.18	10.50
Mehraj-08	78.33	226.52	2.46	19.61	78.21	1730.77	40.41	42.71	4.50
Atika-04	79.33	233.22	2.46	22.74	68.41	1673.01	34.61	44.21	10.17
Aamehria-08	75.33	203.48	2.26	22.08	78.91	1797.94	42.27	42.88	20.17
Mehraj-09	80.33	218.72	2.06	20.61	88.21	2200.52	46.41	40.71	9.50
Atika-15	74.33	241.62	2.06	18.94	81.61	1541.58	36.61	42.21	5.17
Atika-01	80.33	220.22	2.56	20.94	68.51	2005.32	37.61	44.21	20.17
Hysun 38	87.00	209.72	2.98	25.05	94.98	2058.08	45.05	42.07	5.17
Hysun 33	84.83	190.03	2.03	26.13	87.72	2501.12	47.98	41.12	5.33
Vip 123	82.17	216.50	2.05	21.95	79.83	2030.63	50.08	40.15	5.00

DDF (Days to 50% flowering), PH (Plant height), SD (Stem diameter), HD (Head diameter), SW (1000-Seed weight), SY (Seed yield), HI (Harvest index), OC (Oil content), DI (Disease incidence)

Table 3. Standard error (SE), Critical difference (CD), and coefficient of variation (CV) for 117 genotypes of sunflower (*Helianthus annuus L.*).

Trait	DFF	PH	SD	HD	SW	SY	HI	OC	DI
SE (Landraces)	0.95	2.09	0.20	0.23	0.75	62.10	0.27	0.25	1.53
SE (Checks)	0.34	0.76	0.07	0.08	0.27	22.43	0.10	0.09	0.55
CD (Check vs landraces)	2.01	4.46	0.43	0.50	1.61	132.20	0.57	0.53	3.26
CV (%)	1.04	0.93	7.56	1.04	0.86	4.29	0.69	0.53	4.24

DFF (Days to 50% flowering), PH (Plant height), SD (Stem diameter), HD (Head diameter), SW (1000-Seed weight), SY (Seed yield), HI (Harvest index), OC (Oil content), DI (Disease incidence)

Table 4. Summary of principal component analysis of 117 genotypes of sunflower (*Helianthus annuus L.*).

Component	PC1	PC2	PC3	PC4	PC5
Eigenvalue	3.34	1.09	1.06	0.99	0.91
% Variance	37.13	12.16	11.75	10.99	10.17
Cum. Eigenvalue	3.34	4.43	5.49	6.48	7.39
Cumulative %	37.13	49.29	61.04	72.03	82.20
Traits	Eigen vectors				
Days to 50% Flowering	0.00	0.02	-0.03	0.00	0.99
Plant Height	0.03	-0.55	0.82	-0.14	0.04
Stem Diameter	0.00	0.00	0.00	0.00	0.00
Head Diameter	0.00	-0.04	0.05	0.01	-0.10
1000-Seed Weight	0.00	0.05	0.20	0.98	0.01
Seed Yield	1.00	0.04	-0.01	0.00	0.00
Harvest Index	0.01	-0.02	0.01	0.04	0.02
Oil Content	0.00	0.01	0.01	-0.01	0.03
Disease Incidence	-0.03	0.83	0.53	-0.15	0.00

Table 5. Principal component scores of the top 20 performing genotypes and checks of sunflower (*Helianthus annuus L.*).

Genotype	PC1	PC2	PC3	PC4	PC5
Atika-09	3.57	0.08	-0.14	-1.21	0.29
Atika-11	3.13	0.98	-0.39	-0.36	-0.49
Mehraj-10	2.25	-1.08	1.57	-1.10	-0.33
Atika-12	1.04	-2.03	-2.12	-0.86	1.85
Mehraj-07	2.51	0.26	-0.01	0.70	0.27
Mehraj-05	3.45	1.37	0.32	0.96	-0.11
Atika-17	1.69	-1.43	-0.52	-0.54	1.00
Aamehria-17	2.72	-0.45	0.87	-0.88	0.53
Aamehria-15	2.55	-0.28	1.99	0.21	0.16
Aamehria-18	2.31	0.38	-0.40	-0.83	-0.32
Atika-03	2.28	0.10	0.97	-0.39	0.71
Aamehria-12	2.35	-0.20	1.33	-0.60	-0.26
Aamehria-16	2.86	1.49	-0.11	-0.09	0.05
SKS-12	1.53	-0.35	1.31	1.73	1.24
Mehraj-08	1.77	0.08	-0.28	0.29	0.33
Atika-04	1.38	-0.62	-1.23	0.19	1.24
Aamehria-08	1.71	0.50	-0.62	-0.45	0.12
Mehraj-09	2.74	1.53	0.13	0.47	-0.30
Atika-15	1.73	0.28	-0.79	-0.55	-0.23
Atika-01	1.32	-0.17	-0.84	0.61	1.02
Hysun 38	2.56	0.30	1.27	1.00	1.87
Hysun 33	3.03	1.83	-0.07	0.81	0.52
Vip 123	2.99	1.35	0.05	0.93	-0.44

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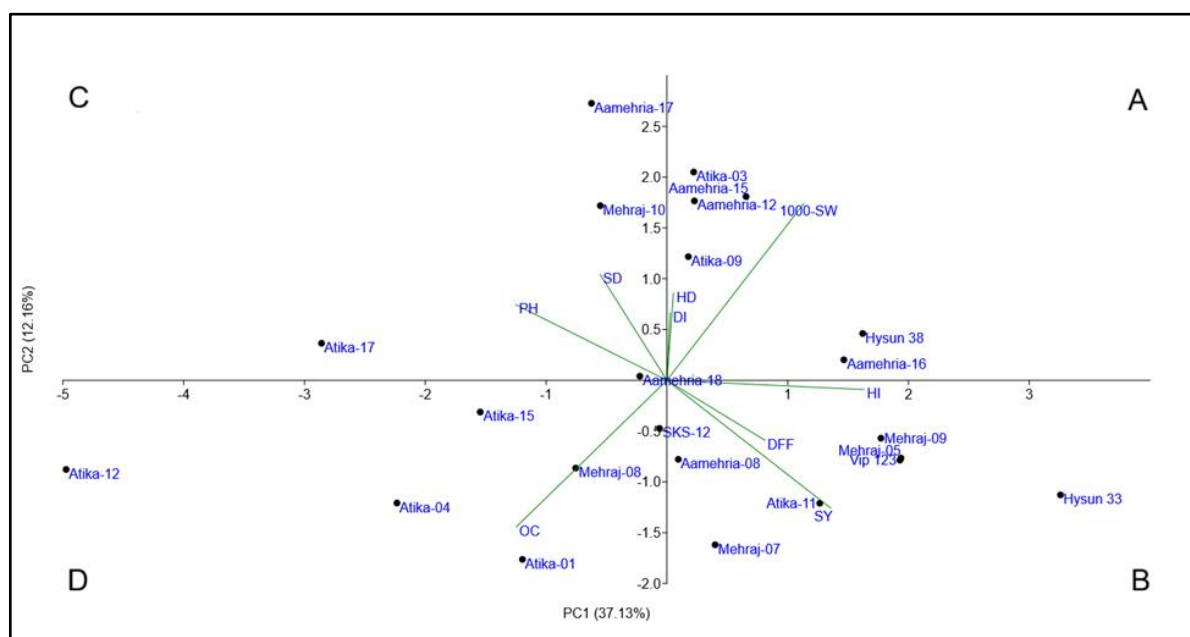


Figure 1. Biplot of the 117 genotypes of sunflower (*Helianthus annuus L.*) based on PC1 and PC2 scores.

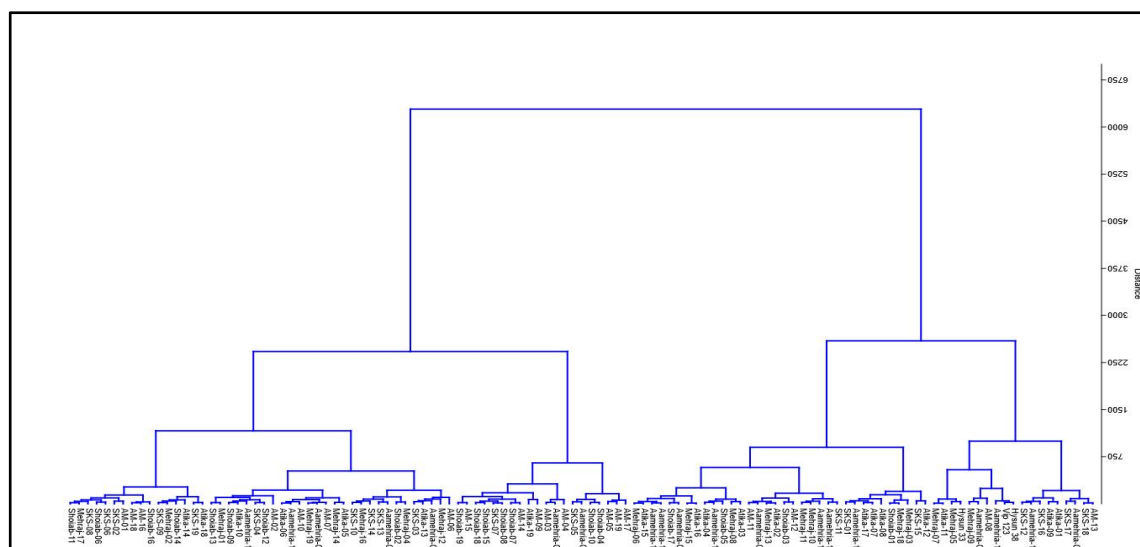


Figure 2. Dendrogram showing the distribution of 117 sunflower (*Helianthus annuus L.*) genotypes.

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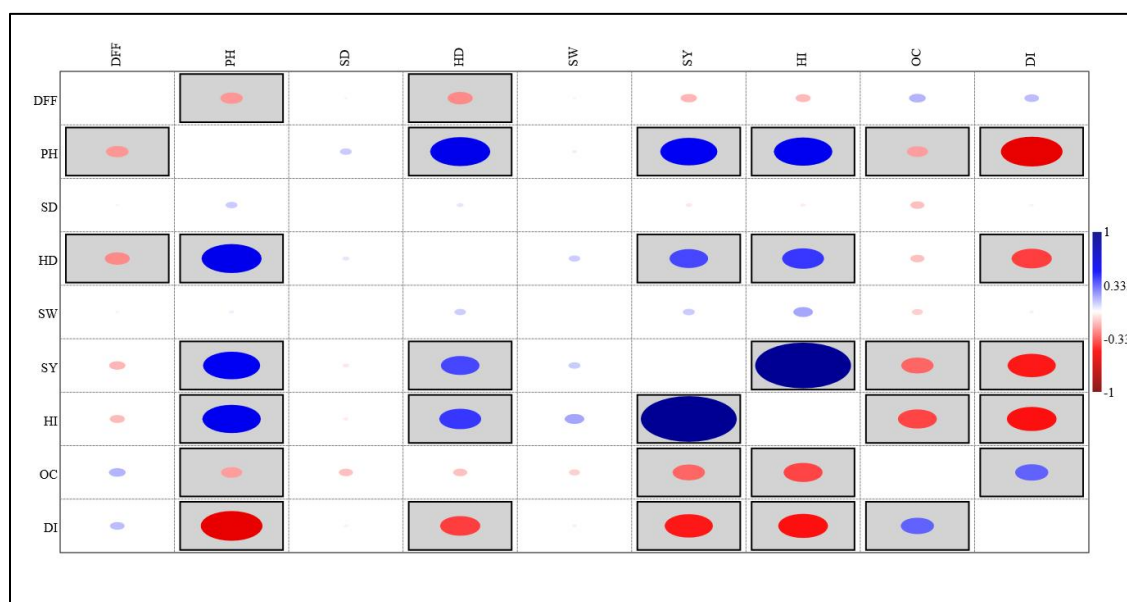


Figure 3. Correlation among morpho-yield traits (red = negative, blue = positive and boxed significant at 5%). DFF (Days to 50% flowering), PH (Plant height), SD (Stem diameter), HD (Head diameter), SW (1000-Seed weight), SY (Seed yield), HI (Harvest index), OC (Oil content), DI (Disease incidence).