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KERNEL PROTEIN PROFILING, VARIABILITY ASSESSMENT AND TRAIT ASSOCIATION STUDIES IN CONFECTIONERY SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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ABSTRACT

Sunflower stands as a major oilseed crop globally, yet the predominant focus on oilseed types has considerably diminished breeding efforts for confectionery sunflower. This research enhances the understanding of confectionery sunflower through a comprehensive characterization of 72 advanced breeding lines for various qualitative and quantitative traits. Morphological DUS characterization revealed distinctive pigmentation and seed coat patterns serving as valuable identification markers. Quantitative traits including yield, seed characteristics and hull content, exhibited high heritability with substantial genetic advance, indicating excellent selection and trait improvement potential. Principal component analysis consolidated 75.26% of total variation into three components, with seed and kernel characteristics contributing much towards the variability. Cluster analysis identified Cluster IV as a valuable genetic reservoir with superior seed and kernel dimensions and desirable low oil content. Trait association studies revealed a significant positive association between yield and both hull proportion and oil content, alongside strong intercorrelations among seed and kernel dimensions. Protein profiling of selected elite genotypes identified RCSF-18 as a superior entry with 31.34% kernel protein, showing 4.87% more protein than the confectionery check KBSH-44 (26.47%). These findings provide crucial baseline information for strategic parent selection and development of superior confectionery sunflower hybrids with enhanced nutritional quality and market acceptability.

Keywords : Confectionery sunflower, Diversity, Kernel protein, Principal component analysis, Trait association, Variability.

Introduction

Sunflower (*Helianthus annuus* L.) ranks third among global oilseed crops, after soybean and rapeseed-mustard. Archaeological evidence suggests that the domestication of sunflower occurred ~4000 years ago in eastern North America, with the oldest evidence found in Tennessee. Spanish explorers introduced it to Europe (Seiler *et al.*, 2017), where it was initially an ornamental crop before gaining prominence as a major oilseed crop following its agricultural development in Russia, from where improved high-oil cultivars were later reintroduced to North America.

According to the USDA data for 2024-25, global sunflower production stands at 52.31 million metric tons, cultivated across 28.20 million hectares. Russia, being the largest producer, contributes 32% of the total global output (16.90 million tons) from 10.5 million hectares. In India, sunflower cultivated over 0.18 million hectares, generating a production of 0.11 million metric tons (Annon., 2025). Karnataka emerges as the predominant sunflower-producing state, accounting for 1.03 lakh hectares of cultivation area with 1.05 lakh tons of production (Annon., 2024).

Cultivated sunflower has two main types: oilseed and confectionery (non-oilseed), both developed in

Eastern Europe and Russia during the late 19th century. Consumer demand for confectionery type has grown consistently due to its exceptional nutritional qualities and snack adaptability. These seeds are characterized by black, white or grey seed coats with stripes, significantly larger (>2 cm) than oil-type seeds, with high hull percentage (~40%) and thicker hulls loosely connected to kernels for easy dehulling (Fernandez-Martinez *et al.*, 2009; Hladni *et al.*, 2012). They contain less fat but higher protein with superior protein solubility, foam formation, foaming stability and emulsification properties, rendering them particularly suitable for bakery and confectionery applications.

The major confectionery sunflower producing countries are Ukraine, Russia and Turkey's Middle and East Anatolia region. In India, confectionery acreage remains undocumented, though consumption for human use and bird feed has increased (Basavarajappa, 2017). Oilseed types dominate global sunflower cultivation (83%), resulting in limited breeding emphasis on confectionery types (17%). However, confectionery sunflower commands a premium price, offering enhanced profitability for farmers. With this context, 72 confectionery sunflower genotypes were evaluated for confectionery traits to identify superior lines for future breeding programs.

Material and Methods

Location and climatic conditions

A field trial was conducted during *Rabi*-2024-25 at the Main Agricultural Research Station, University of Agricultural Sciences, Raichur at an elevation of 398.9 m above mean sea level and located at approximately 16°06 N latitude and 77°06 E longitude. The research station recorded an average annual rainfall of approximately 66.1 mm during *Rabi* season. The soil is primarily black cotton and the climate is semi-arid.

Experimental material

The 72 confectionery sunflower breeding lines along with three checks (KBSH-44, RSFH-700 and PM-81), were evaluated for qualitative and quantitative traits and an experiment was laid out in an Augmented Block design comprising of four blocks. Each

genotype was sown in two rows of 4.5 meters in length, with inter and intra row spacing of 30×60 cm.

Statistical analysis

In the current study, genetic variability parameters *viz.*, phenotypic and genotypic coefficients of variation, broad sense heritability and genetic advance as a per cent of mean for seven quantitative traits were computed using R software. Principal component analysis was performed in GRAPES to elucidate the pattern of genetic divergence among genotypes and to quantify the relative contribution of individual traits towards total variance. Ward's hierarchical clustering method, based on Mahalanobis D^2 statistics was employed for grouping genotypes based on cluster analysis. Correlation and path analysis were performed using INDOSTAT to determine the inter-relationships among traits. Based on these evaluations, ten superior genotypes were identified and subjected to protein content estimation. Kernel protein profiling was performed using the Kjeldahl method according to AOAC International's Official Methods of Analysis (2023).

Results and Discussion

Morphological characterization

A total of 72 confectionery sunflower breeding lines and three checks (KBSH-44, RSFH-700 and PM-81) underwent morphological characterization following established DUS (Distinctness, Uniformity and Stability) guidelines of PPV&FRA. Based on their morphological traits, the genotypes were classified into distinct categories (Figure-1). Anthocyanin pigmentation in the hypocotyl was rare, with only five genotypes (6.7%) exhibiting strong pigmentation, serving as an early-stage identification marker, while stem pigmentation was uniformly absent. Stigma pigmentation exhibited tripartite variation, where 30 lines lacked pigmentation, 29 lines showed strong and 13 lines displayed medium intensity of pigmentation, suggesting multiple alleles or epistatic interactions controlling anthocyanin biosynthesis, which aids pollinator attraction and provides stress tolerance through antioxidant properties (Hladni *et al.*, 2017).

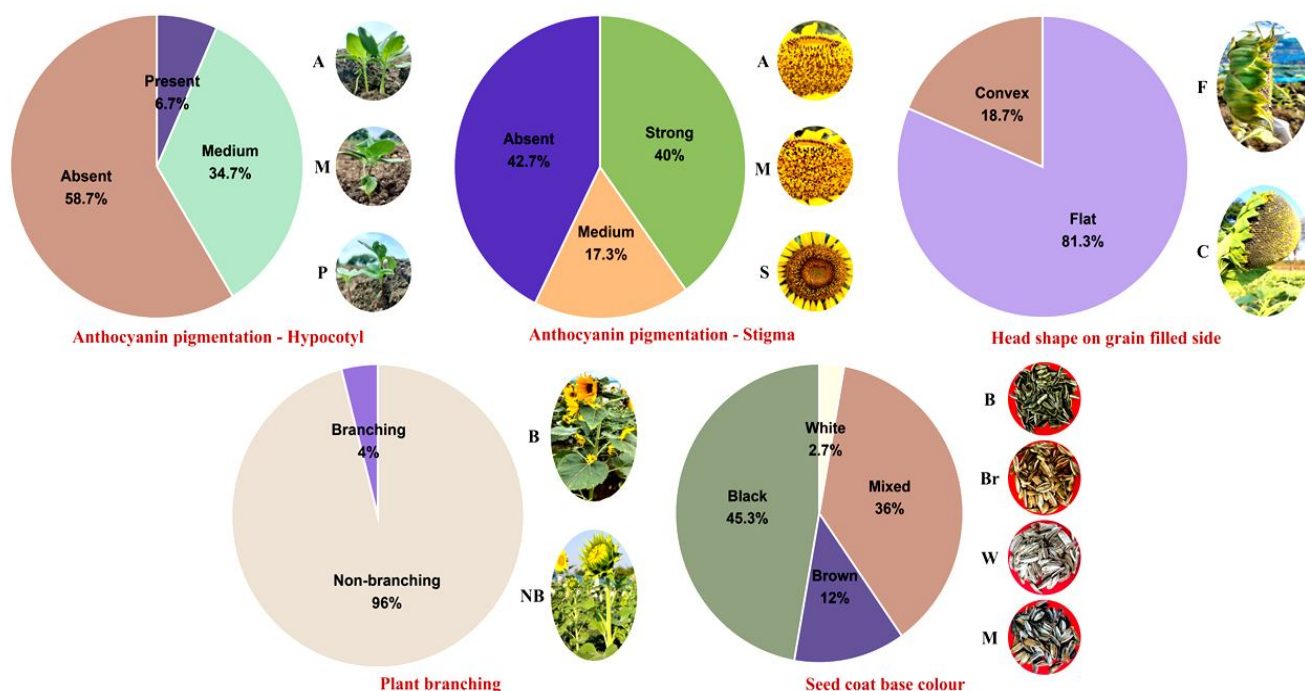


Fig. 1 : Morphological characterization of confectionery sunflower genotypes on DUS guidelines

Head morphology revealed flat heads predominated (59 lines resembling KBSH-44 and PM-81) over convex heads (13 lines similar to RSFH-700), with convex configuration facilitating uniform seed development. Plant architecture showed 70 non-branching types, maximizing photosynthate partitioning to primary heads, while only two lines (RCSF-5 and RCSF-39) exhibited branching similar to PM-81. Seed coat colour variation includes black (34 lines, including all checks), brown (9 lines) and white (2 lines) with 27 lines displaying heterogeneous colouration. Striped seed patterns were nearly universal (72 lines and two checks), reflecting strong selection for this commercially distinguishing trait, though 21 lines showed heterogeneous striping patterns. This variation in seed coat base colour and striping characteristics within genotypes may be attributed to genetic segregation or multiple alleles, consistent with findings by Gorohivets and Vedmedeva (2016) and Kaur (2021). The morphological diversity documented will provide information for germplasm management, parent selection and IPR issues, while unique morphological variants offer opportunities for developing distinct market classes, facilitating varietal registration and expanding the genetic base for future breeding initiatives.

Genetic variability of confectionery seed traits

Genetic variability is essential for developing superior cultivars in plant breeding programs. Mean, genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean are fundamental parameters facilitating strategic trait improvement (Table-1). Yield per plant showed substantial variation, ranging from 4.8-43.1 g with a mean of 16.0 g, where RCSF-67 demonstrated superior performance (31.5 g), followed by RCSF-4 (30.8 g) and RCSF-7 (29.5 g). The PCA was marginally higher than the GCA, with high heritability and substantial genetic advance as per cent of mean, indicating predominance of additive gene action and excellent scope for yield improvement, similar to findings of Kaur (2021). Seed length and width, critical determinants for confectionery value, exhibited reduced variation with high heritability and moderate genetic advance. RCSF-49 produced the largest seeds (18.37 mm), while RCSF-45 displayed the maximum width (7.36 mm) with 63 genotypes surpassing KBSH-44 for both traits (12.24 mm and 5.10 mm, respectively).

Table 1 : Genetic parameters for yield and yield component traits in confectionery sunflower

Trait	Mean	Range		GCV (%)	PCV (%)	h ² BS (%)	GAM (%)
		Min	Max				
Yield per plant (g)	16.0	4.8	43.1	34.67	35.44	95.71	69.98
Seed length (mm)	14.56	9.22	18.37	8.73	9.06	92.86	17.35
Seed width (mm)	5.87	3.37	7.36	9.07	10.18	79.48	16.68
Kernel length (mm)	10.37	6.39	12.04	3.20	7.61	17.62	2.77
Kernel width (mm)	4.15	2.64	5.17	7.63	10.49	52.80	11.43
Hull content (%)	35.75	23.33	54.33	11.63	14.37	65.50	19.42
Oil content (%)	29.82	26.32	37.79	3.95	5.64	48.99	5.70

Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Broad sense heritability (h² BS), Genetic advance as per cent of mean (GAM)

Kernel dimensions showed promising variations, with length averaging 10.37 mm, where RCSF-2 and RCSF-5 achieved maximum values of 12.04 mm, while kernel width averaged 4.15 mm, with RCSF-19 attaining a superior width of 5.17 mm. Despite over 50 genotypes exceeding KBSH-44 for kernel traits (9.50 mm and 3.97 mm, respectively), the low to moderate heritability and genetic advance were observed, reflecting non-additive genetic architecture requiring alternative breeding strategies (Kaur, 2021). Hull content averaged 35.75%, with RCSF-71 showing the highest proportion (54.33%) and exhibiting high heritability and moderate genetic advance, indicating effective scope for genetic improvement. Oil content averaged 29.82%, desirably lower for non-oilseed types, with RCSF-58 recorded the highest value (34.3%). Moderate heritability and low genetic

advance suggest limited potential for improvement. These findings align with Girishraj and Uma (2016).

Principal component analysis of confectionery traits in sunflower

Principal component analysis represents a dimensionality reduction method, where in the current study, it consolidated multiple variables into seven principal components while retaining substantial original variation. PCA was performed on 72 confectionery sunflower breeding lines for seven quantitative traits, reducing 75.26% of the variability in the first three components with eigen values more than unity. The first principal component (PC1) captures the highest variation at 37.61%, while PC2 and PC3 contribute 19.94% and 17.71%, respectively (Table-2).

Table 2 : Eigen values and contributions of each PCs to the total variance

Principal components	Eigen values	Percentage of variance	Cumulative percentage of variance
PC1	2.63	37.61	37.61
PC2	1.40	19.94	57.55
PC3	1.24	17.71	75.26
PC4	0.71	10.16	85.41
PC5	0.46	6.53	91.94
PC6	0.31	4.40	96.34
PC7	0.26	3.66	100.00

Component loadings above 0.4 were designated as important contributors (S1). PC1 primarily represented seed and kernel characteristics with the highest negative loadings, suggesting these confectionery traits are negatively correlated with yield, with their mutual correlation evident from clustering together on the right portion of the biplot (Figure-2) with acute angles between their vectors. PC2 was predominantly influenced by hull proportion and oil content, where their contrasting signs reflecting antagonistic association between them, which is also apparent in the biplot, where both traits lie near the y-axis but extend in opposite directions from the origin. PC3 was

characterised solely by yield per plant (0.815), which exhibited the only substantial loading for this component.

The proportional contributions of variables to the principal components revealed that yield per plant exerted the greatest influence on diversity, as elucidated by PC3, followed by hull proportion and oil content by PC2, with seed and kernel morphometric characteristics predominant in PC1 (Table-2). According to the spatial distribution of genotypes within the biplot, genotypes RCSF-22, 32, 37, 38, 49, 54, 58 and 72 exhibited substantial divergence across multiple phenotypic attributes, indicating their

distinctiveness within the germplasm array. These findings are quite similar with the results of Latif et al. (2024), who reported that seed characteristics and oil

content contribute much towards the variability in sunflower hybrids.

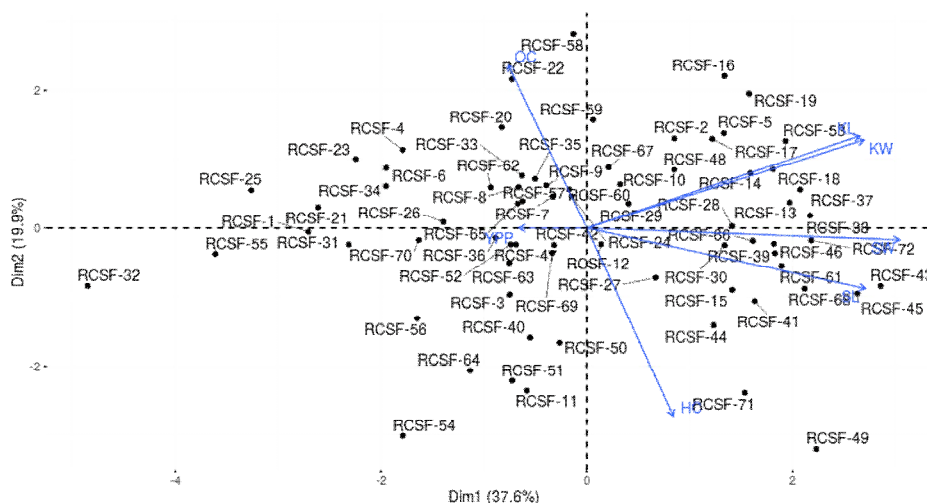


Fig. 2 : Biplot analysis and grouping of confectionery sunflower genotypes based on PC1 and PC2

Cluster analysis

Employing a multivariate analytical technique, the 72 confectionery sunflower genotypes were grouped into four discrete clusters based on genetic divergence (Figure-3). Cluster II emerged as the most populous assemblage (27 genotypes) followed by Clusters I and IV with 19 genotypes in each cluster and Cluster II (seven genotypes). The intra-cluster D^2 values ranged from 1.55 to 2.30, with cluster III exhibiting the maximum intra-cluster distance (2.30). Conversely,

inter-cluster distances revealed that the maximum divergence existed between Cluster I and IV (3.54), while the minimum separation was detected between clusters II and IV (2.53). The narrow range between the minimum (2.53) and the maximum (3.54) inter-cluster distances suggests a structured genetic diversity rather than a random distribution, indicating all the advanced breeding lines share common ancestry but have diverged over time through selection or breeding (Table-3).

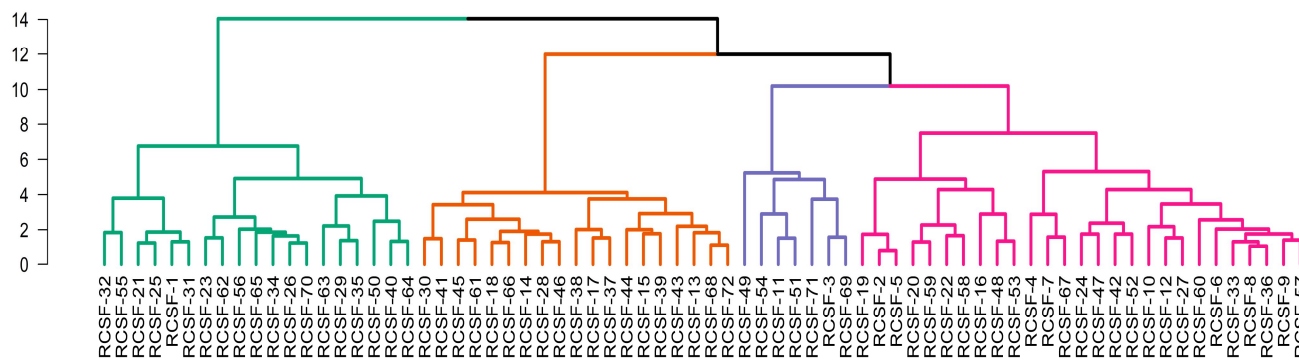


Fig. 3 : Dendrogram of confectionery sunflower genotypes based on phenotypic divergence data

Table 3 : Intra and inter cluster distance D^2 values for confectionery sunflower genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	1.88	2.56	3.42	3.54
Cluster II		1.97	3.06	2.53
Cluster III			2.30	3.38
Cluster IV				1.55

Table 4 : Cluster means concerning yield and confectionery attributes in confectionery sunflower genotypes

Cluster	YPP	SL	SW	KL	KW	HC	OC
I	12.5	13.88	5.31	9.63	3.81	33.54	29.19
II	19.0	14.21	5.96	10.72	4.30	34.79	30.73
III	20.3	15.47	5.92	10.04	3.87	47.22	29.20
IV	12.0	16.01	6.50	11.05	4.48	36.43	28.51

Yield per plant (YPP), Seed length (SL), Seed width (SW), Kernel length (KL), Kernel width (KW), Hull content (HC), Oil content (OC)

Examination of cluster means (Table-4) unveiled distinct phenotypic patterns across groups. Genotypes assigned to Cluster III demonstrated superior performance for yield per plant. Notably, Cluster IV, showed elevated mean values for confectionery attributes, thereby establishing this cluster as a valuable genetic reservoir for confectionery traits improvement. Concomitantly, this cluster registered the lowest mean oil content (28.51), a desirable characteristic for non-oilseed cultivar development. Furthermore, genotypes belonging to Cluster III displayed the highest mean values for hull proportion (47.22). These results correlate with the findings of Kholghi *et al.* (2011) and Kaur *et al.* (2021).

Correlation studies and path analysis for confectionery traits in sunflower

The phenotypic correlation analysis across seven quantitative traits aimed to identify direct associations between these characteristics and to develop effective selection strategies for yield attributes. The correlation matrix (Table-5) revealed that hull content (0.247) and oil content (0.244) exhibited a highly significant positive association with yield per plant, while seed length (-0.246) demonstrated a significant negative correlation. These findings partially align with Sri *et*

al. (2025), who reported positive yield-hull correlations but negative yield-oil content correlations, contrasting the present study. Among morphometric parameters, seed length displayed significant positive correlations with seed width (0.546), kernel length (0.456), kernel width (0.360) and hull content (0.357), while seed width demonstrated the strongest positive correlation with kernel width (0.628), followed by seed length (0.546) and kernel length (0.532), consistent with Kaur and Kaila (2023). Kernel length exhibited significant positive associations with kernel width (0.574), seed width (0.532) and seed length (0.456), while kernel width maintained strong positive relationships with seed width (0.628), kernel length (0.574), and seed length (0.360), demonstrating genetic linkages among morphometric parameters that corroborate PCA results. Hull proportion showed significant positive correlations with seed length (0.357) and yield per plant (0.247), but displayed a significant inverse relationship with oil content (-0.247), while oil content exhibited significant positive associations with yield per plant (0.244). This hull-oil antagonism benefits confectionery breeding, requiring thicker hulls and lower oil for improved kernel quality, consistent with Kaya *et al.* (2025).

Table 5 : Phenotypic correlation coefficient between yield and confectionery traits in confectionery sunflower genotypes

	SL	SW	KL	KW	HC	OC	YPP
SL	1.000	0.546**	0.456**	0.360**	0.357**	-0.151	-0.246*
SW		1.000	0.532**	0.628**	0.220	-0.214	-0.056
KL			1.000	0.574**	-0.064	0.048	-0.038
KW				1.000	-0.043	0.021	-0.062
HC					1.000	-0.247*	0.247*
OC						1.000	0.244*
YPP							1.000

Seed length (SL), Seed width (SW), Kernel length (KL), Kernel width (KW), Hull content (HC), Oil content (OC), Yield per plant (YPP)

Note: *Significance at 5% **Significance at 1%

Path coefficient analysis, developed by Wright (1921), partitions correlation coefficients into direct and indirect components, elucidating the causal pathways through which independent variables influence a dependent variable (S2 and Figure-4). At the phenotypic level, hull content (0.4843) exhibited the strongest positive direct effect on yield per plant

followed by oil content (0.3030) which is contrary to Hladni *et al.* (2017). Kernel length (0.1649) and seed width (0.1021) showed positive direct effects contributing to yield enhancement, while seed length (-0.4931) and kernel width (-0.0281) demonstrated negative effects reflecting resource allocation trade-offs, comparable with Gjorgjieva *et al.* (2015). Despite

its negative direct effect (-0.4931), seed length contributed positively to yield *via* hull content (0.1727), kernel length (0.0751) and seed width (0.0557), demonstrating compensatory mechanisms where seed elongation enhances yield by facilitating hull deposition and kernel expansion, though negative contributions occurred through oil content (-0.0459) and kernel width (-0.0101). Seed width (0.1021) showed considerable indirect effects through hull content (0.1065) and kernel length (0.0876), while kernel length (0.1649) contributed through seed width (0.0542) and oil content (0.0147). Kernel width (-0.0281), despite negative direct effects, compensated through kernel length (0.0946), seed width (0.0641) and oil content (0.0062). Hull content (0.4843) exhibited positive indirect contributions through seed width (0.0224) and kernel width (0.0012), though negative indirect effects through seed length (-0.1759), oil content (-0.0749) and kernel length (-0.0106), indicating competitive resource allocation constraints. Oil content (0.3030) contributed indirectly through seed length (0.0747) and kernel length (0.0080). These results correspond with Sanju *et al.* (2018), emphasizing balanced selection strategies integrating morphological and biochemical traits for yield maximization. The residual value of 0.8342 indicated that 83.42% of yield variation remained unexplained by the studied traits, suggesting other unmeasured factors significantly influence yield per plant.

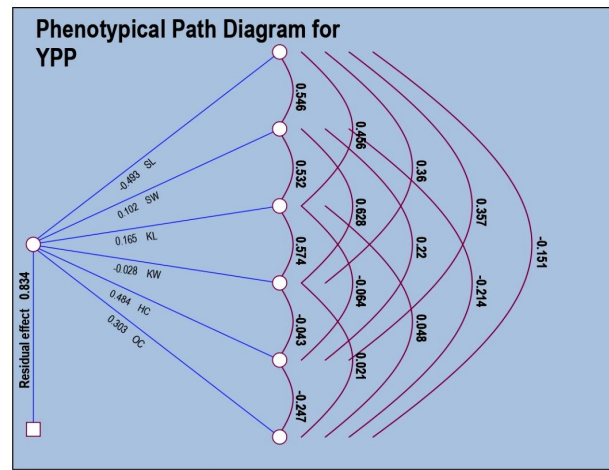


Fig. 4 : Path diagram depicting direct and indirect effects of quantitative traits on yield per plant at phenotypic level

Assessment of kernel protein in prominent confectionery sunflower genotypes

Confectionery sunflower genotypes are characterised by the production of large, distinctly striped achenes exhibiting diminished lipid concentrations and elevated protein levels ranging from 24-27% (Salehipour *et al.*, 2025). For comprehensive protein profiling, 10 genotypes were strategically selected from 72 confectionery sunflower breeding lines along with three checks (KBSH-44, RSFH-700 and PM-81) based on superior performance for key morphological determinants, specifically: seed length, seed width, kernel length, kernel width and hull content (Plate-1). Manually dehulled kernels served as the analytical substrate for protein quantification using the Kjeldahl method. This methodology yields the per cent nitrogen content within the analysed sample. Conversion to crude protein percentage was accomplished through multiplication by the established conversion factor (5.30) (Jones, 1941).

Table 6 : Assessment of kernel protein in prominent confectionery sunflower genotypes

Genotypes	SL (mm)	SW (mm)	KL (mm)	KW (mm)	HC (%)	OC (%)	PC (%)	Rank
RCSF-18	15.54	5.93	11.88	4.85	28.33	27.77	31.34	1
RCSF-5	13.94	5.97	12.04	4.94	30.33	28.94	29.31	2
RCSF-13	16.22	5.82	11.54	5.09	36	29.46	29.27	3
RCSF-40	15.21	6.08	8.79	4.02	40.33	29.14	29.16	4
RCSF-15	16.36	6.2	10.27	4.67	34.33	27.65	28.39	5
RCSF-43	16.98	6.74	10.58	4.9	42.67	29.17	27.56	6
RCSF-16	16.08	5.96	10.81	5.16	32	34.01	27.01	7
KBSH-44 (Check)	12.24	5.1	9.5	3.97	33	31.46	26.47	8
RCSF-53	16.57	6.65	11.24	4.49	35.67	32.59	25.59	9
RCSF-54	13.43	5.76	8.77	3.65	52.33	29.38	24.66	10
RCSF-49	18.37	6.27	11.22	3.74	48.67	26.74	24.41	11
RSFH-700 (Check)	10.93	4.97	9.4	4.15	25.67	37.79	23.8	12
PM-81 (Check)	9.22	3.37	6.39	2.64	23.33	36.92	22.59	13

Seed length (SL), Seed width (SW), Kernel length (KL), Kernel width (KW), Hull content (HC), Oil content (OC), Protein content (PC)



Plate 1 : Seed and kernel characteristics of RCSF-18 and RCSF-5 relative to confectionery check KBSH-4

The evaluated genotypes demonstrated considerable phenotypic variation for kernel protein content (Table-6), exhibiting a range from 24.66-31.34%. Genotype RCSF-18 emerged as the superior line, manifesting the maximal protein concentration of 31.34%, succeeded by RCSF-5 (29.31%), RCSF-13 (29.27%), RCSF-40 (29.16%) and RCSF-15 (28.39%). Seven of the assessed genotypes demonstrated superior performance relative to the confectionery check (KBSH-44: 26.47%) for kernel protein accumulation, while genotypes RCSF-54 and RCSF-49 exhibited comparatively reduced protein concentrations relative to the reference cultivar.

Breeding efforts in confectionery sunflower have been reduced because of the emphasis on oilseed types and a lack of genetic materials for improving confectionery specific traits. The present study provides valuable insights into 72 advanced breeding lines through various analyses. Distinctive morphological markers were identified and key quantitative traits showed much variation coupled with substantial heritability and genetic advance. Principal component and cluster analyses highlighted seed and kernel characteristics as major variability sources, with Cluster IV offering superior genetic resources. Yield correlated positively with hull proportion and oil content, while seed and kernel traits were strongly interlinked. Among genotypes, RCSF-67 (31.5 g) achieved exceptional yield performance, followed by

RCSF-4 (30.8 g) and RCSF-7 (29.5 g). For morphometric superiority, RCSF-49 (18.37 mm) produced larger seeds, while RCSF-45 excelled in seed width (7.36 mm). RCSF-2 (12.04 mm) displayed maximum kernel length and RCSF-19 exhibited a superior kernel width (5.17 mm). Protein profiling identified RCSF-18 (31.34%) as the most promising genotype with high kernel protein content followed by RCSF-5 (29.31) and RCSF-13 (29.27). These findings offer a valuable foundation for developing nutritionally superior confectionery sunflower hybrids.

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Supplementary Table 1 : Loading of each variable in various principal components

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Yield per plant (g)	0.116	0	0.815	0.323	-0.214	0.184	-0.371
Seed length (mm)	-0.474	0.213	-0.046	-0.576	-0.119	0.197	-0.585
Seed width (mm)	-0.533	0.042	0.077	0.232	0.268	0.662	0.38
Kernel length (mm)	-0.465	-0.323	0.076	0.002	-0.716	-0.252	0.312
Kernel width (mm)	-0.472	-0.309	0.065	0.29	0.503	-0.505	-0.293
Hull content (%)	-0.147	0.656	0.412	-0.222	0.15	-0.407	0.376
Oil content (%)	0.134	-0.569	0.385	-0.613	0.282	0.07	0.225

Supplementary Table 2 : Phenotypic path coefficient of confectionary traits on yield per plant in confectionary sunflower genotypes

	SL	SW	KL	KW	HC	OC	r _g
SL	-0.4931	0.0557	0.0751	-0.0101	0.1727	-0.0459	-0.2456
SW	-0.2694	0.1021	0.0876	-0.0176	0.1065	-0.0649	-0.0557
KL	-0.2247	0.0542	0.1649	-0.0161	-0.0312	0.0147	-0.0382
KW	-0.1778	0.0641	0.0946	-0.0281	-0.0207	0.0062	-0.0617
HC	-0.1759	0.0224	-0.0106	0.0012	0.4843	-0.0749	0.2465
OC	0.0747	-0.0219	0.0080	-0.0006	-0.1197	0.3030	0.2435

Residual=0.8342

Seed length (SL), Seed width (SW), Kernel length (KL), Kernel width (KW), Hull content (HC), Oil content (OC), Yield per plant (YPP).