FULafia Journal of Science & Technology
ISSN (print) 2449-0954 \ ISSN (online) 2636-4972
https://lafiascijournals.org.ng/index.php/fjst
Sponsored By TETFUND TERTIARY EDUCATION TRUST FUND
Manuscript => Received: August, 2026; Accepted: Sept., 2026; Published: Sept., 2026 https://doi.org/10.62050/fjst2026.v10n2.930

BIOACTIVE PROFILE OF SUNFLOWER (*Helianthus annuus L.*) GENOTYPES IN LAFIA, NASARAWA STATE, NIGERIA

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ABSTRACT
This study evaluated the bioactive compound profile of 5 sunflower (*Helianthus annuus* L.) genotypes namely SAMSUN 1, SAMSUN 3, SAMSUN 4, MKD 1, and MKD 2 cultivated in Lafia, Nasarawa State, with the aim of identifying genotype bioactive potential for crop improvement. Proximate composition analysis showed significant differences in crude protein and carbohydrate content, while others were not significantly different across genotypes. Qualitative and quantitative phytochemical screening confirmed the presence of saponins, alkaloids, flavonoids, tannins, terpenoids, glycosides, and steroids in all five genotypes, with no significant inter-varietal differences detected. Antioxidant profiling revealed significant differences in beta-carotene, anthocyanin, and quercetin contents, with MKD 2 and MKD 1 recording markedly higher anthocyanin levels (4.54 and 3.88 mg/L, respectively) than the remaining genotypes, while ascorbic acid and organosulfide contents did not differ significantly. Amino acid analysis revealed significant varietal differences across all the 13 amino acids quantified, with glutamic acid consistently the most abundant; SAMSUN 4 recorded the highest lysine content, SAMSUN 3 the highest methionine and cysteine, and MKD 1 the highest threonine, valine, isoleucine, histidine, and glutamic acid. The 100-seed weight ranged from 26.9 g (SAMSUN 3) to 28.2 g (SAMSUN 1). These findings demonstrate the availability of exploitable genetic variability among the five sunflower genotypes for nutritional, phytochemical, and antioxidant traits, with SAMSUN 4 identified as the most broadly promising genotype for yield-related and protein-quality traits, and MKD 1 and MKD 2 identified as superior sources of natural antioxidants.

Keywords: Bioactive profile, Sunflower genotypes, Amino acid composition

INTRODUCTION
The cultivated sunflower (*Helianthus annuus* L.) belongs to the family of Asteraceae (Compositae) (Rojas-Sandoval, 2022). Helianthus come from the Greek word Helios, meaning sun, and anthos, meaning flower, and from Latin *annuus*, meaning annual (Sumon, 2020). The sunflower (*H. annuus* L.) is a globally significant crop valued for its oil-rich seeds, nutritional benefits, and versatility in food, industrial, and ornamental applications (Costa *et al.*, 2025). Native to North America, this annual plant has been cultivated for centuries, with modern breeding programs developing diverse genotypes tailored for specific agroecological conditions and market demands. Sunflower has gained global importance due to its adaptability to various climatic conditions and its rich nutritional profile. As a source of essential fatty acids, vitamins, and minerals, sunflower seeds are increasingly recognized for their health benefits (Puraikalan & Scott, 2023). However, in regions like Lafia, the extent of genetic variability and the bioactive profile of local or introduced sunflower genotypes remain poorly characterized.

The proximate composition of sunflower seeds encompassing moisture, protein, fats, ash, and carbohydrate content offers a comprehensive view of their nutritional value (Petraru *et al.*, 2021). Sunflower seeds are renowned for their high oil content, typically ranging from 40–50 %, making them a leading source of edible oil rich in unsaturated fatty acids (Adeleke & Babalola, 2020). Additionally, their protein content, which can exceed 20 % in some genotypes, positions sunflowers as a valuable source of plant-based protein for human and animal consumption (Kaur & Ghoshal, 2022).

The amino acid composition of sunflower seeds is another critical aspect, as it determines their protein quality and suitability for addressing dietary deficiencies (Oseiko *et al.*, 2020). Sunflower proteins are rich in essential amino acids like lysine, methionine, and threonine, which are vital for human health, particularly in populations reliant on plant-based diets (Hadidi *et al.*, 2024). Variations in amino acid profiles among sunflower genotypes can influence their use in functional foods or nutritional supplements. For instance, genotypes with higher levels of essential amino acids may be prioritized for regions facing protein-energy malnutrition (Sumon, 2020).

Phytochemical analysis of sunflower seeds reveals their bioactive compounds, including phenolic acids, flavonoids, tocopherols, and phytosterols, which contribute to their health-promoting properties (Naquvi *et al.*, 2024). These compounds are linked to antioxidant, anti-inflammatory, and cardioprotective effects, making sunflowers a functional food with significant therapeutic potential (Adeleke & Babalola, 2020). The presence and concentration of phytochemicals vary across genotypes

due to genetic differences and environmental factors, affecting their efficacy in combating oxidative stress and chronic diseases. The antioxidant properties of sunflower seeds are closely tied to their phytochemical content, as compounds like vitamin E (tocopherols) and phenolic acids neutralize free radicals, protecting cells from oxidative damage (Guo *et al.*, 2017). Antioxidants play a crucial role in preventing chronic conditions such as cardiovascular diseases, cancer, and neurodegenerative disorders, making them a focal point in nutritional research (Sharifi-Rad *et al.*, 2020). Different sunflower genotypes exhibit varying antioxidant capacities, influenced by factors such as seed color, hull thickness, and growing conditions (Puttha *et al.*, 2023). Globally, sunflower contributes significantly to oilseed production, but in Nigeria, its cultivation and utilization remain underexplored compared to crops such as groundnut and soybean. The Guinea Savannah zone, including Lafia in Nasarawa State, provides suitable agro-climatic conditions for sunflower cultivation, but there is limited data on the genetic variability and bioactive compound profiles of sunflower genotypes grown in this region.

Understanding genetic variability among genotypes is crucial for selecting superior genotypes in breeding programs. Similarly, assessing the bioactive profile of sunflower seeds and leaves can expand its value in food, pharmaceutical, and nutraceutical industries. This study therefore seeks to characterize sunflower genotypes cultivated in Lafia for their bioactive properties, thereby contributing to crop improvement and local economic development.

MATERIALS AND METHODS

Study Area

This study was conducted in Federal University Lafia. Lafia, the capital of Nasarawa State in Nigeria, is a vibrant city known for its rich cultural heritage and strategic location. Situated in the north-central region of the country, Lafia serves as a hub for trade and commerce, connecting various communities in the surrounding areas. The city is characterized by its diverse population, which includes various ethnic groups, contributing to a rich tapestry of traditions, languages, and festivals. Lafia's economic activities are primarily centered around agriculture, with farming being a significant part of the local economy. The fertile land in the region allows for the cultivation of various crops, including yams, maize, and cassava, which are staples in the Nigerian diet (Merenini *et al.*, 2024).

Sample Collection and Experimental Design

Five sunflower genotpyes were evaluated; Three (3) different genotypes of sunflower seeds were gotten from Institute for Agricultural Research (IAR), Zaria, Two (2) different genotypes of sunflower seeds were gotten from Local Farmers in Makurdi, Benue State which were used for planting and bioactive profiling. The field experiment was laid out in a randomized complete block design (RCBD) with three replications.

Bioactive Profile

Proximate composition

Clean and dried sunflower seeds were ground into a fine powder for proximate composition. Moisture content was determined by oven-drying 5 g of ground sample to 105 ^{o}C to constant weight, with dry matter calculated as complement of moisture (AOAC, 2010). Crude lipid content was quantified by continuous extraction of 2 g of ground seed in a soxhlet apparatus using petroleum ether for 16 h, followed by solvent evaporation and oven-drying at 105 ^{o}C (AOAC, 2010). Crude fiber was determined by successive acid (0.255 N H_2SO_4) and alkaline (0.313 N NaOH) digestions followed by ignition at 130 ^{o}C (AOAC, 2010). Ash content was evaluated gravimetrically after muffle furnace ignition at 600 ^{o}C for 6 h (AOAC, 2010).

Amino Acid Analysis

Amino acid composition was determined using a Technicon Sequential Multisample Amino acid Analyzer (TSM) following the method described by Speckman *et al.* (1958). Defatted sample was hydrolysed under vacuum with 7 ml, of NHCI in a sealed pyrex tube at 105 ^{o}C for 22 h. The hydrolysate was filtered, concentrated under vacuum at 40 ^{o}C, reconstituted in acetate buffer (pH 2.0) and quantified colorimetrically against reference amino acid standards using (Akande, 2011).

Sample Extraction and Phytochemical Screening

Drying

Shade-dried and oven-dried (40 °C and maintained for one hour) petals were ground and sequentially extracted in a soxhlet apparatus for 6 h per solvent using hexane at 60 °C, ethyl acetate at 77 °C, chloroform at 61 °C, and methanol at 65 °C according to Ghutke *et al.* (2024). Concentrated extracts were dried at 45 °C and screened for qualitative phytochemical constituents following standard methods; tannins and total phenols (10 % $FeCl_3$), flavonoids (1 % $AlCl_3$), saponins (frothing test), Steroids (Salkowski test), glycosides (acid hydrolysis followed by Fehling's test) (Ghutke *et al.*, 2024).

In Vitro Antioxidant Activity (DPPH (2,2-Diphenyl-1-picrylhydrazyl) Assay)

Free–radical scavenging activity was evaluated using 2,2-Diphenyl-1-picrylhydrazyl (DDPH) assay (Salwa, 2021). Briefly, 0.5 mL of ethanolic extract at varying concentrations (60, 120, 140 µg/ml) was mixed with 1.0 mL of 0.2 mM DPPH ethanolic solution. After 45 min of dark incubation at ambient temperature, absorbance was read at 517 nm against ethanol blank. Radical scavenging capacity (%) was calculated relative to the control, and antioxidant activity was modeled using linear regression.

Statistical Analysis

Data were analysed using IBM SPSS version 20.0. Data normality and homogeneity of variance were assessed using the Shapiro–Wilk and Levene's tests, respectively. Differences among treatment groups were evaluated using one-way analysis of variance (ANOVA) followed by Fisher's least significant test (LSD) for multiple

comparisons. Results were presented as mean ± standard deviation (SD), and statistical significance was set at $p < 0.05$.

RESULTS AND DISCUSSION

Comparative Analysis of Data

As shown in Table 1, moisture content, ash content, crude fat, and crude fibre did not differ significantly ($p > 0.05$) among the sunflower genotypes. Significant differences ($p < 0.05$) were observed for crude protein and carbohydrate contents. For crude protein, V3 (13.24 ± 0.28 %) had a significantly higher value than V2 (12.25 ± 0.22 %), as the mean difference (0.99) exceeded the LSD value (0.55). Similarly, V4 (13.07 ± 0.10 %) and V5 (12.96 ± 0.53 %) were significantly higher than V2. However, V1 (12.77 ± 0.20 %) did not differ significantly from V2, V4, or V5. In addition, V3 did not differ significantly from V4 and V5. For carbohydrate content, V1 (58.71 ± 0.30 %) was significantly higher than V3 (57.77 ± 0.28 %) and V5 (57.53 ± 0.56 %), as the differences exceeded the LSD value (0.71). V4 (58.36 ± 0.52 %) was also significantly higher than V5. No significant differences were observed among the remaining variety combinations for carbohydrate content.

Table 1: Proximate composition of five sunflower genotypes

Sunflower Variety	Moisture content (%)	Ash content (%)	Crude fat (%)	Crude fibre (%)	Crude protein (%)	Carbohydrate (%)
V1	8.08 ± 0.13	6.12 ± 0.10	5.15 ± 0.13	9.15 ± 0.13	12.77 ± 0.20	58.71 ± 0.30
V2	8.30 ± 0.26	6.05 ± 0.09	5.16 ± 0.14	9.36 ± 0.34	12.25 ± 0.22	58.09 ± 0.13
V3	8.15 ± 0.13	6.22 ± 0.19	5.30 ± 0.26	9.13 ± 0.11	13.24 ± 0.28	57.77 ± 0.28
V4	8.08 ± 0.07	6.23 ± 0.21	5.22 ± 0.19	9.01 ± 0.01	13.07 ± 0.10	58.36 ± 0.52
V5	8.25 ± 0.22	6.17 ± 0.14	5.24 ± 0.21	9.22 ± 0.19	12.96 ± 0.53	57.53 ± 0.56
LSD	0.32 ns	0.28 ns	0.35 ns	0.34 ns	0.55*	0.71*

Values represent mean standard deviation; Asterisk (*) = Significantly different at p value < 0.05; ns = not significant

Table 2: Quantitative phytochemical composition of five sunflower genotypes

Sunflower Variety	Saponin (%)	Alkaloids content (%)	Flavonoids content (%)	Tannins content (%)	Terpenoids content (%)	Glycosides (%)	Steroids (%)
V1	4.08 ± 0.14	2.30 ± 0.26	4.01 ± 0.08	2.15 ± 0.16	1.83 ± 0.15	2.19 ± 0.16	0.97 ± 0.03
V2	2.72 ± 2.36	2.69 ± 0.27	4.09 ± 0.08	1.98 ± 0.03	1.83 ± 0.16	2.28 ± 0.25	0.94 ± 0.05
V3	4.20 ± 0.17	2.38 ± 0.33	4.04 ± 0.28	2.14 ± 0.18	1.85 ± 0.15	2.16 ± 0.14	0.91 ± 0.08
V4	4.13 ± 0.11	2.72 ± 0.25	3.88 ± 0.11	2.11 ± 0.18	1.81 ± 0.17	2.24 ± 0.21	0.96 ± 0.04
V5	4.19 ± 0.16	2.79 ± 0.18	3.96 ± 0.04	2.11 ± 0.14	1.78 ± 0.19	2.27 ± 0.23	0.92 ± 0.07
LSD	1.94 ns	0.48 ns	0.26 ns	0.27 ns	0.31 ns	0.37 ns	0.10 ns

Values represent mean standard deviation; ns = not significantly different at p value < 0.05

As presented in Table 2, saponin, alkaloid, flavonoid, tannin, terpenoid, glycoside, and steroid contents showed no significant differences ($p > 0.05$) among the five sunflower genotypes. Although numerical variations were observed, all pairwise differences among variety means were smaller than their respective LSD values, indicating that the phytochemical contents were statistically similar across all genotypes.

As presented in Table 3, ascorbic acid content ranged from 5.86 ± 0.00 mg/L in V3 to 5.89 ± 0.05 mg/L in V5, while organosulfide content varied from 12.06 ± 0.03 mg/L in V2 to 12.29 ± 0.13 mg/L in V5. No significant differences ($p > 0.05$) were observed among the sunflower genotypes for ascorbic acid and organosulfide contents. Significant differences ($p < 0.05$) were detected for β-carotene, anthocyanin, and quercetin contents. For β-carotene, V1 (10.43 ± 0.01 mg/L) was significantly lower than V3 (10.55 ± 0.03 mg/L) and V5 (10.56 ± 0.04 mg/L), as the mean differences exceeded the LSD value of 0.06. No significant differences were observed among the remaining variety combinations. Anthocyanin content showed marked variation, with V4 (4.54 ± 0.02 mg/L) and V5 (3.88 ± 0.05 mg/L) being significantly higher than V1 (1.72 ± 0.02 mg/L), V2 (1.76 ± 0.01 mg/L), and V3 (1.38 ± 0.04 mg/L). In addition, V5 was significantly higher than V1, V2, and V3, while V4 was significantly higher than V5. V3 recorded a significantly lower anthocyanin content than V1 and V2. For quercetin, V4 (2.65 ± 0.03 mg/L) was significantly higher than V3 (2.58 ± 0.02 mg/L), whereas the differences among the remaining genotypes did not exceed the LSD value of 0.06 and were therefore not significant.

Table 3: Antioxidant composition of five sunflower genotypes

Sunflower Variety	Ascorbic Acid (mg/L)	β-Carotene (mg/L)	Organosulfide (mg/L)	Anthocyanin (mg/L)	Quercetin (mg/L)
V1	5.88 ± 0.05	10.43 ± 0.01	12.07 ± 0.02	1.72 ± 0.02	2.64 ± 0.04
V2	5.89 ± 0.02	10.54 ± 0.00	12.06 ± 0.03	1.76 ± 0.01	2.64 ± 0.03
V3	5.86 ± 0.00	10.55 ± 0.03	12.24 ± 0.08	1.38 ± 0.04	2.58 ± 0.02
V4	5.88 ± 0.01	10.49 ± 0.05	12.22 ± 0.16	4.54 ± 0.02	2.65 ± 0.03
V5	5.89 ± 0.05	10.56 ± 0.04	12.29 ± 0.13	3.88 ± 0.05	2.63 ± 0.02
LSD	0.06 ns	0.06*	0.18 ns	0.06*	0.06*

Values represent mean, standard deviation; Asterisk (*) = Significantly different at p value < 0.05; ns = not significant

Table 4: Amino acid composition of five sunflower genotypes

Sunflower Variety	Lysine Content	Methionine Content	Cysteine Content	Threonine Content	Leucine Content	Isoleucine Content	Valine Content	Phenylalanine Content	Tyrosine Content	Histidine Content	Arginine Content	Aspartic acid Content	Glutamic acid Content
V1	2.20 ± 0.02	0.86 ± 0.05	0.76 ± 0.09	1.14 ± 0.06	2.32 ± 0.03	1.29 ± 0.05	1.58 ± 0.12	1.72 ± 0.05	0.95 ± 0.02	0.88 ± 0.03	2.39 ± 0.04	2.92 ± 0.05	6.29 ± 0.03
V2	2.41 ± 0.03	0.77 ± 0.04	0.67 ± 0.08	1.17 ± 0.02	2.38 ± 0.05	1.19 ± 0.04	1.57 ± 0.05	1.29 ± 0.05	0.89 ± 0.03	0.81 ± 0.03	2.82 ± 0.04	2.68 ± 0.02	6.22 ± 0.05
V3	3.36 ± 0.17	0.68 ± 0.02	0.75 ± 0.06	1.16 ± 0.02	2.51 ± 0.04	1.48 ± 0.06	1.87 ± 0.04	1.30 ± 0.11	0.71 ± 0.03	0.95 ± 0.02	2.65 ± 0.05	2.76 ± 0.04	7.61 ± 0.13
V4	2.10 ± 0.07	0.85 ± 0.03	0.52 ± 0.04	1.08 ± 0.01	1.86 ± 0.04	1.36 ± 0.04	1.78 ± 0.05	1.33 ± 0.04	0.73 ± 0.05	0.89 ± 0.03	3.24 ± 0.05	3.25 ± 0.02	6.88 ± 0.01
V5	2.83 ± 0.56	0.83 ± 0.08	0.39 ± 0.03	1.39 ± 0.04	1.81 ± 0.02	1.64 ± 0.04	2.08 ± 0.03	1.21 ± 0.05	0.71 ± 0.01	1.18 ± 0.02	2.31 ± 0.07	3.08 ± 0.05	7.90 ± 0.04
LSD	0.48*	0.08*	0.11*	0.06*	0.06*	0.08*	0.11*	0.11*	0.06*	0.06*	0.10*	0.06*	0.11*

Values represent Mean Standard deviation; Asterisk (*) = Significantly different at p value < 0.05

As shown in Table 4, significant differences ($p < 0.05$) were observed among all sunflower genotypes for all amino acids evaluated. For lysine, V3 (3.36 ± 0.17) recorded the highest value and was significantly higher than the other genotypes, while V4 (2.10 ± 0.07) recorded the lowest and was significantly lower than the others. For methionine, V1 (0.86 ± 0.05) was the highest and significantly higher than the other genotypes, while V3 (0.68 ± 0.02) was the lowest and significantly lower than the rest. For cysteine, V1 (0.76 ± 0.09) was highest and significantly higher than the other genotypes, whereas V5 (0.39 ± 0.03) was lowest and significantly lower than the others. For threonine, V5 (1.39 ± 0.04) was highest and significantly higher than the remaining genotypes, while V4 (1.08 ± 0.01) was lowest and significantly lower than the others.

For leucine, V3 (2.51 ± 0.04) recorded the highest value and was significantly higher than the other genotypes, while V5 (1.81 ± 0.02) was lowest and significantly lower than the rest. For isoleucine, V5 (1.64 ± 0.04) was highest and significantly higher than the other genotypes, while V2 (1.19 ± 0.04) was lowest and significantly lower than the others. For valine, V5 (2.08 ± 0.03) was highest and significantly higher than the other genotypes, while V2 (1.57 ± 0.05) was lowest and significantly lower than the others. For phenylalanine, V1 (1.72 ± 0.05) was highest and significantly higher than the other genotypes, while V5 (1.21 ± 0.05) was lowest and significantly lower than the others.

For tyrosine, V1 (0.95 ± 0.02) was highest and significantly higher than the other genotypes, while V3 (0.71 ± 0.03) and V5 (0.71 ± 0.01) recorded the lowest values and were significantly lower than the remaining genotypes. For histidine, V5 (1.18 ± 0.02) was highest and significantly higher than the other genotypes, while V2 (0.81 ± 0.03) was lowest and significantly lower than the others. For arginine, V4 (3.24 ± 0.05) was highest and significantly higher than the other genotypes, while V5 (2.31 ± 0.07) was lowest and significantly lower than the others. For aspartic acid, V4 (3.25 ± 0.02) was highest and significantly higher than the other genotypes, while V2 (2.68 ± 0.02) was lowest and significantly lower than the others. For glutamic acid, V5 (7.90 ± 0.04) was highest and significantly higher than the other genotypes, while V2 (6.22 ± 0.05) was lowest and significantly lower than the others.

As presented in Table 5, the 100-seed weight ranged from 26.9 g in SAMSUN 3 (V1) to 28.2 g in SAMSUN 1 (V2). SAMSUN 1 (V2) recorded the highest seed weight (28.2 g), followed by SAMSUN 4 (V3) with 27.8 g, MKD 1 (V5) with 27.7 g, MKD 2 (V4) with 27.6 g, while SAMSUN 3 (V1) recorded the lowest value (26.9 g).

Table 5: Weight of 100 seeds across five sunflower genotypes

Variety	100 Seeds Weight (g)
SAMSUN 3 (V1)	26.9
SAMSUN 1 (V2)	28.2
SAMSUN 4 (V3)	27.8
MKD 2 (V4)	27.6
MKD 1 (V5)	27.7

This study was carried out to evaluate the bioactive profile of sunflower (*Helianthus annuus* L.) genotypes in Lafia, Nassarawa State, Nigeria. The proximate analysis showed that crude protein and carbohydrate contents differed significantly among the sunflower genotypes, whereas moisture, ash, crude fat, and crude fibre were statistically similar. These findings agree with those of Adesina, (2018) who reported that sunflower seed composition varies while also presenting high protein content while oil and moisture remain comparatively stable across genotypes. The higher protein contents recorded in V3, V4, and V5 indicate superior nutritional quality, making these genotypes more desirable for food and feed applications. Conversely, the relatively higher carbohydrate content in V1 may provide greater energy value. This result agrees with that of Enyeribe *et al.* (2016) who also reported higher carbohydrate content in their study. The minimal variation observed for moisture and lipid contents in this study suggests that these nutritional components are relatively conserved among the evaluated genotypes.

The result showed that the five sunflower genotypes in this study possess comparable capacities for synthesizing secondary metabolites such as flavonoids, tannins, alkaloids, saponins, terpenoids, glycosides, and steroids. This result agrees with Okoye *et al*. (2023) who reported the presence of alkaloids, tannins, flavonoids, saponins, steroid, total phenol, phytate and oxalate in seed extract of Sunflower in their study. This result is also in

agreement which that of Ogah *et al.* (2025) who reported the presence of alkaloid, tannins, flavonoids, phenols, glycoside and saponin in seseme (*Sesamum indicum*) varieties assessed for their morpho-phytochemical composition in Lafia, Nasarawa state-Nigeria. The presence of these phytochemicals could be due to the secondary metabolites that are present in sunflower seeds (Guo *et al.,* 2017). These plant-derived phytochemicals contribute to antimicrobial, anti-inflammatory, and antioxidant activities, the findings indicate that all genotypes possess similar medicinal potential (Singh *et al*., 2022). Secondary metabolite accumulation is known to be influenced by both genotype and environmental conditions, and genetically related cultivars often exhibit minimal variation under similar growing environments (Jocković *et al.,* 2021).

Significant variation in β-carotene, anthocyanin, and quercetin contents demonstrates genetic differences in antioxidant composition among the sunflower genotypes. The exceptionally high anthocyanin concentration observed in V4 and V5 suggests superior antioxidant capacity, while the relatively higher β-carotene contents of V3 and V5 indicate enhanced provitamin A potential. Since anthocyanins and quercetin effectively scavenge reactive oxygen species, genotypes with higher concentrations may possess greater health-promoting properties. In contrast, the uniformity in ascorbic acid and organosulfide contents indicates that these antioxidants are relatively unaffected by varietal differences. These findings agree with Salwa (2021). who reported considerable genotypic variation in the antioxidants content among sunflower in his study. Antioxidant activity has a very strong or very high correlation with phenolic compounds and total flavonoids (Aryal *et al.,* 2019).

With regards to the amino acid composition of the sunflower genotypes in this study, all 13 amino acids assessed showed significant differences across the five genotypes which indicated substantial genetic variability among the sunflower genotypes regarding protein quality. V3 exhibited superior lysine and leucine contents, whereas V5 contained higher concentrations of glutamic acid, valine, isoleucine, and histidine. V4 was distinguished by its higher arginine and aspartic acid contents. Glutamic acid was the most abundant amino acid across all five genotypes (6.22–7.90 g) in this study. A related study by Akande *et al.* (2016) reported that sunflower possesses a genotype of amino acid with higher concentrations reported in aspartic acid and glutamic acid. Since essential amino acids are important indicators of nutritional quality, these differences demonstrate that the evaluated genotypes possess distinct nutritional advantages. The observed variability confirms that genotype strongly influences amino acid accumulation in sunflower seeds, making these genotypes useful genetic resources for breeding programmes targeting improved seed quality (Rauf, 2019).

The differences observed in 100-seed weight indicates variation in seed size and yield potential among the sunflower genotypes evaluated. SAMSUN 1 recorded the highest seed weight, suggesting superior grain filling and better assimilate partitioning during seed development, while SAMSUN 3 had the lowest seed weight. Similar observations have been reported by Mshelmbula *et al*. (2024), who reported similar mean 100-seed weight among three sunflower genotypes in their study. Seed weight is one of the most important yield components in sunflower because it directly influences total seed yield and oil production (Lagiso *et al.,* 2021). It is worth noting seed weight as a reliable criterion for selecting high-yielding sunflower genotypes. The relatively high seed weights recorded for SAMSUN 4, MKD 1, and MKD 2 also suggest good agronomic performance and make these genotypes suitable candidates for crop improvement programmes.

CONCLUSION

This study evaluated the bioactive profiles of five sunflower (*Helianthus annuus* L.) genotypes cultivated in Lafia, Nigeria, revealing that no single genotype had dominant character in all evaluated traits. The MKD 1 and MKD 2 genotypes emerged as the premier antioxidant-rich and amino acid-dense genotypes. Although the genotypes maintained a uniform, conserved profile across seven major phytochemical classes.

Conflict of interest: The authors declare that there is no conflict of interest.

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