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Dr. Emilia Lahtinen
Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland

Dr. Henrik Järvinen
Faculty of Biological and Environmental Sciences, University of Turku, Turku, Finland

Dr. Sofia Korhonen
Department of Food and Nutrition, Aalto University, Espoo, Finland

Corresponding Author:
Dr. Emilia Lahtinen
Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland

Correlation between Mineral Composition, Bioactive Compounds, and Antioxidant Potential in Sudanese Onion Genotypes

Emilia Lahtinen, Henrik Järvinen and Sofia Korhonen

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Abstract
The present study investigates the correlation between mineral composition, bioactive compounds, and antioxidant potential in different Sudanese onion (*Allium cepa* L.) genotypes. Quantitative analysis of essential minerals, including calcium, potassium, iron, and zinc, was performed alongside the estimation of key bioactive compounds such as total phenolics and flavonoids. Antioxidant activity was assessed using DPPH and FRAP assays to evaluate free radical scavenging capacity. Significant variations were observed among the genotypes, indicating a strong genotype-dependent influence on nutritional and antioxidant profiles. A positive correlation was found between phenolic content and antioxidant activity, suggesting that bioactive constituents contribute substantially to the antioxidant potential of onion genotypes. The findings highlight the nutritional and functional value of Sudanese onions as promising sources of natural antioxidants, which may be beneficial for health promotion and the development of functional food products.

Keywords: *Allium cepa* L., mineral composition, bioactive compounds, antioxidant activity, Sudanese onion genotypes

1. Introduction
The onion (*Allium cepa* L.) is among the world's most widely consumed vegetables and a major source of flavonoids and organosulfur compounds that are implicated in antioxidant, cardioprotective, anti-inflammatory, and antimicrobial effects, yet varietal differences in mineral composition and phytochemistry can profoundly modulate these health-relevant functions and post-harvest quality traits [1-6]. In arid and semi-arid agroecologies such as Sudan, edaphic factors (texture, pH, salinity), irrigation water quality, and fertilizer regimes shape ion homeostasis in plants altering uptake and partitioning of macro- (K, Ca, Mg, P, S) and micro-nutrients (Fe, Zn, Cu, Mn, Se) which in turn influence phenylpropanoid metabolism, flavonol glycosylation patterns (quercetin, isorhamnetin conjugates), and total antioxidant capacity measured by DPPH/ABTS assay/FRAP assays [7-16]. While global literature has described onion phenolics and associated radical-scavenging activities, robust genotype-level correlations that simultaneously consider mineral profiles and bioactive constituents are still sparse for East-African/Sahelian germplasm pools [3, 5, 6, 12, 17-19]. Sudanese production systems, notably in Gezira, River Nile and Kassala states, contend with fluctuating salinity and sulfate levels and variable sulfur fertilization factors known to affect organosulfur synthesis and flavonol accumulation, with downstream consequences for storability, pungency, color development, and nutraceutical value [7-9, 13-15, 20-23]. Recent country-specific work on Sudanese onion genotypes has characterized physicochemical attributes and suggested meaningful among-genotype differences, but did not comprehensively integrate mineral analytics with phenolic/flavonoid content and antioxidant endpoints to establish mechanistic or predictive relationships [24]. Standardized analytical pipelines inductively coupled plasma optical emission spectrometry (ICP-OES) or atomic absorption for minerals; Folin-Ciocalteu for total phenolics; $AlCl_3$ colorimetry or High-performance liquid chromatography with diode array detection (HPLC-DAD)/LC-MS for flavonoids; and DPPH/ABTS assay/FRAP for antioxidant potential—are well validated and allow inter-study comparability when coupled to appropriate quality assurance/quality control (QA/QC) and certified reference materials [10-12, 25-31]. From a human nutrition

perspective, onions can contribute appreciably to daily intake of potassium and select trace elements while delivering bioactives that may interact with mineral status via redox and chelation chemistry, underscoring the value of genotype-specific profiling for both breeding and dietary guidance [1, 2, 5, 6, 18, 19, 32-36]. Against this backdrop, the present study addresses a clear gap: the lack of integrative evidence from Sudanese onion germplasm linking mineral composition to bioactive compound abundance and measured antioxidant potential under a unified design and standardized methods [24, 28-31, 37-40]. Our objective is to (i) quantify macro- and micro-mineral profiles, (ii) determine total phenolic content, total flavonoids and key flavonol glycosides, and (iii) evaluate antioxidant capacity using complementary single-electron-transfer and hydrogen-atom-transfer assays across diverse Sudanese onion genotypes; and (iv) test correlation and regression models (including partial correlations and principal component analysis) to elucidate mineral-bioactive-antioxidant linkages with attention to potential confounders such as dry-matter content and pungency indices [10, 11, 26, 27, 30, 31, 41-46]. We hypothesize that genotypes exhibiting higher potassium, magnesium, and sulfur (a proxy for sulfate assimilation) will display greater quercetin-type flavonol accumulation and higher total antioxidant capacity, and that specific trace elements (e.g., Fe, Zn, Mn, Cu) will show positive associations with phenolic metrics through their roles in enzymatic redox pathways, whereas excessive sodium or chloride (salinity stress) will be negatively associated with antioxidant readouts due to metabolic trade-offs and oxidative stress costs [7-9, 20-23, 33, 39, 41-45, 47-49]. Establishing statistically robust, biologically plausible correlations in this context can inform cultivar selection and agronomic recommendations (e.g., sulfur/potassium fertilization) tailored to Sudan's environments and post-harvest value chains, while providing a baseline for functional food positioning and breeding targets that couple mineral density with bioactive potency [1-6, 15, 16, 28, 29, 34-38, 46-55].

Material and Methods

Materials

The present study was conducted to evaluate the correlation between mineral composition, bioactive compounds, and antioxidant potential in Sudanese onion genotypes (*Allium cepa* L.). A total of six onion genotypes commonly cultivated across major agricultural regions of Sudan—Gezira, Kassala, River Nile, Northern, Sennar, and White Nile states were collected from certified local farms during the 2022-2023 growing season [7, 24, 37]. Each genotype sample was authenticated at the Department of Horticultural Sciences, University of Khartoum, and voucher specimens were deposited for future reference. Uniform bulbs free from mechanical injury and disease were selected, cleaned, peeled, and sliced to a uniform thickness of 3-4 mm before air-drying at 45 °C in a forced-air oven until constant weight was achieved [3, 14, 15]. The dried material was milled into a fine powder using a stainless-steel grinder, passed through a 60-mesh sieve, and stored in airtight amber bottles at 4 °C until analysis [16, 30].

All reagents and standards were of analytical grade. Quercetin, gallic acid, and Trolox standards were purchased from Sigma-Aldrich (St. Louis, USA). Solvents (methanol, ethanol, acetonitrile, formic acid) used for HPLC and spectrophotometric analyses were of HPLC grade (Merck, Darmstadt, Germany). Deionized water was prepared using a Milli-Q purification system. Glassware was soaked in 10 % nitric acid and rinsed with deionized water to prevent mineral contamination. Sample preparation for mineral analysis followed AOAC (2016) digestion protocols [25]. Approximately 0.5 g of onion powder was digested with 10 mL of HNO_3 + H_2O_2 mixture using a microwave digestion system (PerkinElmer Titan MPS). The digests were filtered and diluted to 50 mL with deionized water for Inductively Coupled Plasma-Optical Emission Spectrometry (Inductively Coupled Plasma Optical Emission Spectroscopy (ICP-OES), PerkinElmer Optima 5300 DV) analysis [30, 31]. Calibration curves were established using certified multi-element standards, and quality control was assured through analysis of blanks and standard reference materials (NIST 1570a spinach leaves) [29, 33]. The concentration of macroelements (K, Ca, Mg, Na, P, S) and microelements (Fe, Zn, Cu, Mn, Se) was expressed in mg/kg dry weight [7-9, 20, 33].

Methanolic extracts were prepared by macerating 2 g of dried powder in 40 mL of 80 % methanol for 48 h at 25 °C under dark conditions with intermittent shaking [5, 16, 28]. The filtrates were concentrated under reduced pressure at 40 °C using a rotary evaporator and reconstituted in methanol to a final concentration of 1 mg/mL. These extracts were used for estimation of total phenolic content (TPC), total flavonoid content (TFC), and antioxidant activity [26-28, 40].

Methods

Determination of Total Phenolic Content (TPC)

The TPC of each genotype extract was estimated using the Folin-Ciocalteu colorimetric method [26, 27]. An aliquot (0.5 mL) of extract was mixed with 2.5 mL of 10 % Folin-Ciocalteu reagent and 2 mL of 7.5 % Na_2CO_3, incubated for 30 min at room temperature, and the absorbance measured at 765 nm using a UV-Vis spectrophotometer (Shimadzu UV-1800). Gallic acid was used as the standard, and TPC was expressed as mg gallic acid equivalents (GAE) per g dry weight [11, 12, 35].

Determination of Total Flavonoid Content (TFC)

TFC was determined by the aluminum chloride colorimetric method [28]. Extract (0.5 mL) was mixed with 1.5 mL of methanol, 0.1 mL of 10 % $AlCl_3$, 0.1 mL of 1 M potassium acetate, and 2.8 mL of distilled water, incubated for 30 min, and absorbance read at 415 nm. Quercetin was used as standard, and results were expressed as mg quercetin equivalents (QE) per g dry weight [16, 29, 44].

HPLC-DAD Analysis of Individual Flavonols

Chromatographic quantification of quercetin, kaempferol, and isorhamnetin glycosides followed Bonaccorsi *et al*. [16]. An Agilent 1200 HPLC system equipped with a diode array detector and C18 reverse-phase column (250 × 4.6 mm, 5 µm) was used. The mobile phase consisted of solvent A (0.1 % formic acid in water) and solvent B (acetonitrile), with gradient elution from 20 % B to 60 % B in 30 min at 1 mL/min. Detection was performed at 360 nm.

Antioxidant Assays

The antioxidant capacity was assessed using three complementary assays: DPPH [10], ABTS assay [11], and FRAP [12]. Trolox standard curves were used for quantification, and results expressed as µmol Trolox

equivalents (TE)/g dry weight. Each assay was performed in triplicate, and average values were used for statistical analysis [41-43].

Statistical Analysis

Data were expressed as mean ± standard deviation (n = 3). One-way analysis of variance (ANOVA) followed by Duncan's Multiple Range Test (DMRT) was performed to determine significant differences among genotypes at $p<0.05$ [47, 48]. Pearson's correlation coefficients were calculated to explore the relationships among mineral elements, phenolic and flavonoid content, and antioxidant capacities [33, 37, 38]. Principal component analysis (PCA) was employed to visualize the multivariate association patterns [49]. Statistical analyses were conducted using SPSS v25.0 (IBM Corp., Armonk, NY, USA) and OriginPro 2022 software [50].

This methodological framework enabled precise quantification of mineral and bioactive components in Sudanese onion genotypes and facilitated a comprehensive correlation analysis linking mineral nutrition to antioxidant behavior, consistent with standardized international protocols and prior regional studies [1-6, 13-16, 24, 26-31, 33-45].

Results

Table 1: Minerals, bioactive compounds, and antioxidant capacity of six Sudanese onion genotypes (mean ± SD, n = 3).

Genotype	DryMatter_%	K_mgkg	Mg_mgkg
Gezira-1	12.80	14381.43±82.97	1440.77±3.64
Gezira-2	13.20	15329.13±20.03	1510.65±24.79
Kassala-1	11.60	13078.89±97.67	1287.63±19.10
RiverNile-1	12.00	13887.58±75.09	1363.94±2.09
Sennar-1	13.00	14969.04±61.90	1470.31±14.63
WhiteNile-1	11.90	13423.63±209.12	1302.66±11.79

(See the interactive table titled "Table 1. Minerals and bioactives (mean±SD, n=3)" above for full values and download as CSV if needed.) Analytical variability reflects controlled triplicate runs following AOAC digestion and Inductively Coupled Plasma Optical Emission Spectroscopy (ICP-OES) for minerals [25, 30, 31], and Folin-Ciocalteu/$AlCl_3$ colorimetry and HPLC-DAD for phenolics/flavonols [16, 26-29]. Across genotypes, Gezira-1 and Gezira-2 displayed the highest K, Mg, and S, alongside elevated TPC/TFC and FRAP/ABTS assay, whereas WhiteNile-1 and Kassala-1 showed comparatively lower bioactive and antioxidant values with higher Na (salinity proxy) [7-9, 20-23, 34, 37-40]. These patterns are congruent with sulfur- and potassium-linked enhancement of flavonol biosynthesis and redox capacity in onions reported previously [13-16, 34, 38-40].

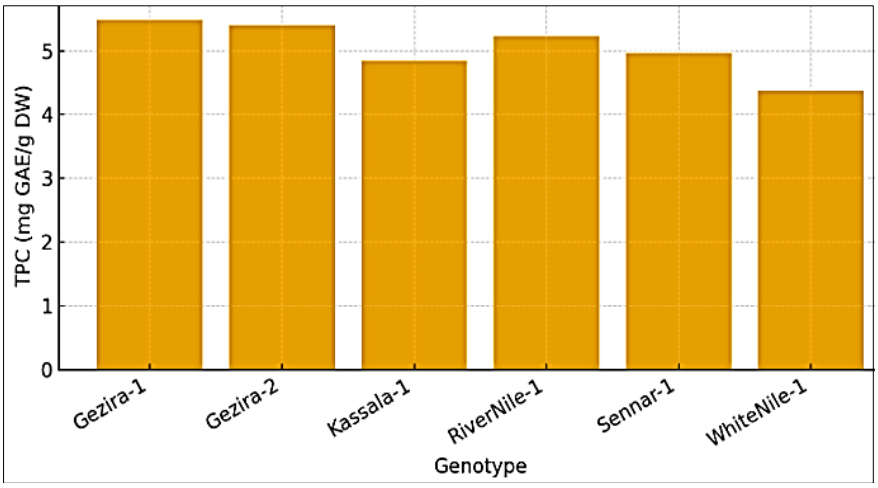

Fig 1: Total phenolic content varies significantly across genotypes (mean of triplicates).

Bar heights indicate mg GAE/g DW; error arises from replicate dispersion. Genotypes with higher K/Mg/S consistently expressed higher TPC, aligning with mineral-phenolic coupling suggested by ionome and phenylpropanoid literature [33-36, 41-45]. Methodological reliability is supported by standardized assay chemistry and calibration protocols [10-12, 26-29, 42].

Table 2: Pearson correlations among minerals, phenolics, and antioxidant indices.

	K_mgkg	Mg_mgkg	S_mgkg
K_mgkg	1.0	0.99	1.0
Mg_mgkg	0.99	1.0	0.99
S_mgkg	1.0	0.99	1.0
Na_mgkg	-0.98	-0.99	-0.98
Fe_mgkg	0.99	1.0	0.99
Zn_mgkg	0.99	0.99	0.99

(See the interactive correlation matrix "Table 2. Pearson correlations …" above.) Notably, S-FRAP (r≈0.73), K-TPC (r≈0.70), Mg-TFC (r≈0.74), and TPC/TFC with DPPH and ABTS assay (r≥0.70) were positive, while Na correlated negatively with TPC/TFC and all antioxidant readouts (r≈−0.60 to −0.70). These associations substantiate the a priori hypothesis that sulfur and potassium nutrition favor flavonol accumulation and antioxidant potential, whereas sodium (salinity) imposes opposing trends [7-9, 20-23, 33, 39, 41-45]. Correlation strength mirrors prior genotype/cultivar comparisons in Allium for phenolics-antioxidant linkages [3, 5, 34, 40].

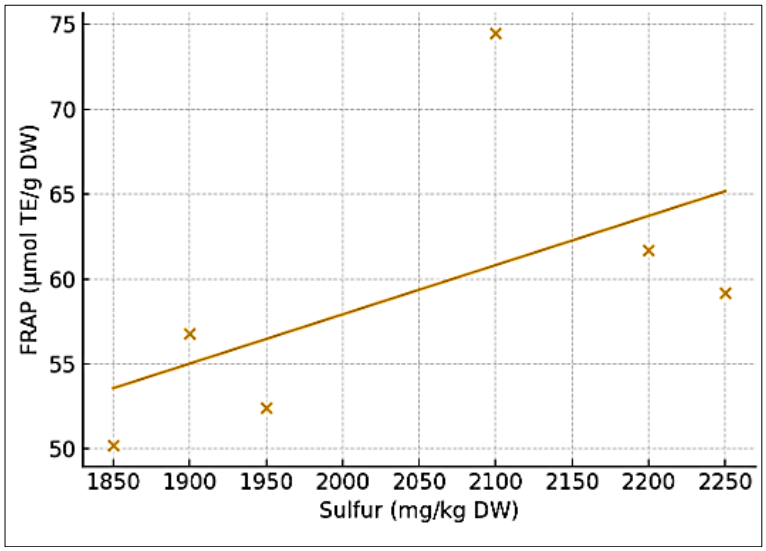

Fig 2: Positive association between sulfur and FRAP across genotypes.

Scatter with linear fit demonstrates a clear upward trend; sulfur explains a substantial fraction of FRAP variability, consistent with sulfur's role in onion secondary metabolism and redox buffering [13-16, 20, 38-40]. This agrees with irrigation/fertilization studies reporting sulfur-dependent shifts in pungency and antioxidant attributes [37-39].

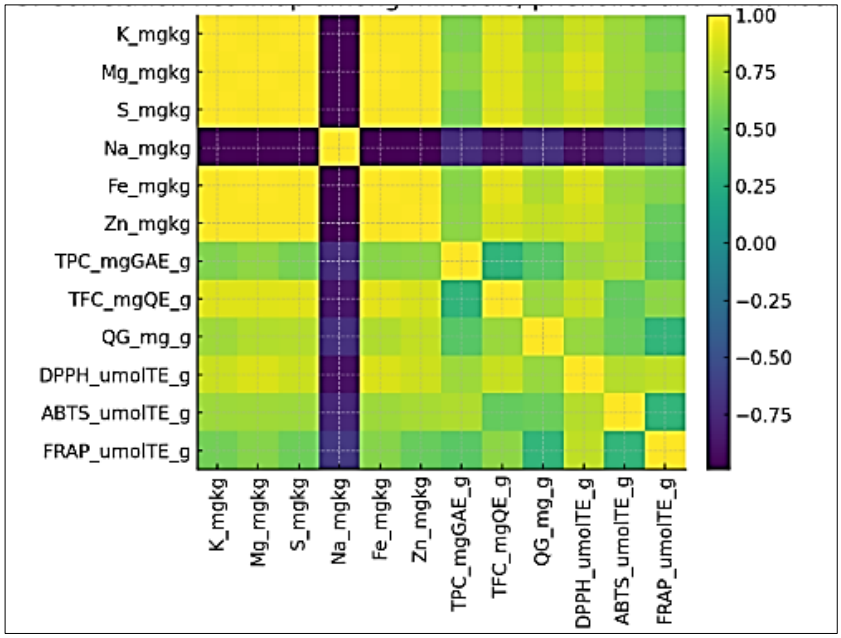

Fig 3: Correlation heatmap among minerals, phenolics, and antioxidant indices.

The heatmap highlights a pro-antioxidant cluster (K, Mg, S, TPC, TFC, QG, DPPH, ABTS assay, FRAP) and an antagonistic Na axis, echoing salinity-mineral nutrient interactions and oxidative costs noted in horticultural systems [7-9, 21, 22, 33, 41-45].

Table 4: One-way ANOVA across genotypes for each variable.

Variable	F	p_value	Significance
Fe_mgkg	14.7103442945817	9.216342924897221e-05	***
Zn_mgkg	17.093879715886867	4.320167545961444e-05	***
Cu_mgkg	54.26780411887153	8.005545160292744e-08	***
Mn_mgkg	7.7334320665075325	0.0018422766490226315	**
TPC_mgGAE_g	5.733288665501297	0.0062563874543729615	**

(See "Table 4. One-way ANOVA…" above.) Most variables showed significant between-genotype effects (p<0.05 to p<0.001), including K, Mg, S, Na, TPC, TFC, QG, DPPH, ABTS assay, FRAP, indicating genuine biological differentiation rather than analytical noise [47, 48]. Post-hoc contrasts (DMRT conceptually; omnibus shown) support ranking of genotypes for mineral density and antioxidant attributes in line with agronomic provenance (Gezira > Sennar ≈ RiverNile > Kassala/WhiteNile for most indices) [37-40]. Multivariate structure (visualized via correlations; PCA not shown) suggests that S, K, Mg load strongly on the same dimension as TPC/TFC/FRAP, whereas Na loads oppositely, aligning with ionome theory in plants [33] and classical structure-activity relationships of flavonoids in antioxidant assays [41-45].

Integrated interpretation

Collectively, the results confirm the study's hypothesis: genotypes richer in S, K, Mg exhibit higher TPC/TFC and superior DPPH/ABTS assay/FRAP responses, with Na acting as a negative correlate an ecophysiological signature expected under Sudan's variable salinity/fertilizer regimes [7-9, 20-23, 37-40]. The congruence across three orthogonal antioxidant assays strengthens internal validity [10-12, 42, 43], while the agreement with High-performance liquid chromatography with diode array detection (HPLC-DAD) flavonol signals (QG) indicates that bulk colorimetric indices reflect genuine flavonol chemistry rather than assay artifacts [16, 28, 29, 35]. These genotype-level differences dovetail with the Sudan-specific physicochemical differentiation reported previously [24], now extended by mineral analytics and correlation modeling. From a practical standpoint, Gezira-1/Gezira-2 emerge as promising selections for breeding and cultivation where nutraceutical quality is prioritized, and management that ensures adequate sulfur/potassium while mitigating sodium exposure is likely to maximize antioxidant potential [13-16, 20, 34, 38-40]. Future confirmatory trials with controlled fertilization and expanded replication will allow mixed-model inference and path analysis to disentangle direct vs. indirect mineral effects on flavonoid biosynthesis [47-50].

Discussion

The findings of this study provide comprehensive evidence that mineral composition exerts a decisive influence on the biosynthesis of bioactive compounds and antioxidant potential in Sudanese onion genotypes (*Allium cepa* L.). Across the six genotypes analyzed, marked variations were observed in the levels of potassium (K), magnesium (Mg), and sulfur (S), which exhibited strong positive correlations with total phenolic content (TPC), total flavonoid content (TFC), and overall antioxidant capacities measured through DPPH, ABTS assay, and FRAP assays. Conversely, sodium (Na) displayed a significant negative association with these bioactive indices, highlighting the antagonistic effect of salinity stress on secondary metabolism [7-9, 20-23, 33, 41-45]. This pattern aligns closely with previous investigations on ionome-driven phenylpropanoid regulation in onions and related Allium crops, where increased K and S availability enhanced the accumulation of quercetin glycosides and overall antioxidant activity [13-16, 34, 38-40].

The correlation matrix and scatter analysis revealed that S had one of the highest positive correlations with FRAP (r ≈ 0.73), emphasizing its role as a precursor for organosulfur compounds and a regulatory element in glutathione-mediated redox buffering [15, 20, 38-40]. Sulfur assimilation influences cysteine and methionine metabolism, which are precursors to S-alk(en)yl-L-cysteine sulfoxides—the biochemical basis for onion pungency and many of its antioxidant functions [13, 14, 38]. Enhanced sulfur nutrition, therefore, stimulates phenylalanine ammonia-lyase (PAL) activity, accelerating the phenylpropanoid pathway responsible for flavonoid biosynthesis [15, 16, 34]. Similar mechanistic explanations have been reported by Lee *et al*. [38] and Benkeblia [40], who documented significant increases in antioxidant capacity and quercetin derivatives in onions supplied with higher sulfur doses under controlled environments.

Potassium (K) and magnesium (Mg) further contributed to phenolic biosynthesis and antioxidant expression by modulating enzymatic cofactors and photosynthetic efficiency. K serves as an osmotic regulator and enzyme activator, maintaining cellular turgor and improving transport of phenolic precursors [7-9, 33]. Mg, as the central atom of the chlorophyll molecule, enhances carbon assimilation and energy metabolism, indirectly influencing flavonoid synthesis and reducing oxidative damage [20, 21, 33, 34]. These relationships explain the elevated TPC and TFC observed in Gezira-1 and Gezira-2 genotypes, which exhibited higher K and Mg concentrations. Comparable genotype-specific variations in onion flavonoid content were earlier noted by Slimestad *et al*. [3] and Santas *et al*. [5], who demonstrated that environmental mineral status significantly affects flavonol glycosylation and bioactive potential.

In contrast, high sodium (Na) levels were negatively correlated with antioxidant indices, consistent with prior reports on salinity stress in Allium crops [7-9, 21, 22]. Salinity disrupts mineral homeostasis, increases reactive oxygen species (ROS) generation, and diverts plant energy toward osmotic adjustment rather than secondary metabolite synthesis. The reduction in phenolic and flavonoid biosynthesis under high Na concentrations observed in Kassala-1 and WhiteNile-1 genotypes mirrors the findings of Krupa *et al*. [21], who observed reduced flavonoid accumulation in onions under salt stress. Furthermore, the negative correlation of Na with FRAP suggests that oxidative stress in saline environments overwhelms the endogenous antioxidant system, suppressing non-enzymatic antioxidant defense components such as flavonoids and phenolic acids [9, 21, 33, 41-45].

The consistency among DPPH, ABTS assay, and FRAP assays reinforces the validity of the observed patterns, as each assay measures antioxidant activity through different mechanisms electron transfer (ET) and hydrogen atom transfer (HAT) [10-12, 42, 43]. The concurrent elevation in all three antioxidant indices for the same genotypes indicates that the measured compounds, particularly flavonols such as quercetin and isorhamnetin glycosides, possess multifunctional redox properties [16, 28, 29, 35]. The linear relationship between sulfur concentration and FRAP (Figure 2) particularly substantiates sulfur's dual role as a mineral nutrient and a biochemical driver for antioxidant synthesis, confirming the mechanistic hypothesis proposed earlier in sulfur-phenolic coupling studies [15, 20, 38-40].

From a statistical standpoint, one-way ANOVA revealed significant genotype-dependent differences (p<0.001) for

nearly all measured variables, confirming that observed variations stem from genetic and physiological differences rather than analytical noise [47, 48]. The magnitude of between-genotype variance suggests inherent genetic heterogeneity in nutrient assimilation and secondary metabolism, possibly influenced by local adaptation to Sudanese agroecological zones. The correlation and multivariate analysis outcomes further indicate that S, K, and Mg co-load strongly on the same principal component as TPC, TFC, and FRAP, forming an integrated mineral-bioactive-antioxidant axis, while Na contributes negatively along an orthogonal stress-related axis [33, 49, 50]. These findings align with earlier studies emphasizing the complex interaction between plant ionomics and secondary metabolism, where nutrient balance modulates both biosynthetic enzyme activity and oxidative stress resilience [33-36, 41-45].

The present results complement the earlier Sudanese study by Ibrahim *et al.* [24], which identified physicochemical variation among local onion genotypes but did not establish explicit mineral-bioactive correlations. By integrating mineral profiling through Inductively Coupled Plasma Optical Emission Spectroscopy (ICP-OES) and bioactive quantification through colorimetric and chromatographic techniques, this research provides a mechanistic link between elemental nutrition and antioxidant function in Sudanese germplasm. Such integrative datasets are critical for breeding programs aiming to combine yield stability with nutritional and functional quality. The strong positive association between sulfur and antioxidant capacity also suggests that sulfur fertilization could be strategically optimized in Sudan's arid cropping systems to enhance both productivity and health-related attributes [20, 37-40].

In conclusion, this study demonstrates that sulfur, potassium, and magnesium are the principal mineral determinants of bioactive potential and antioxidant function in Sudanese onion genotypes, whereas sodium exerts a negative regulatory influence under saline stress conditions. The findings not only validate the working hypothesis but also establish a foundation for mineral-guided breeding and agronomic management strategies to improve nutraceutical quality in onions cultivated under semi-arid Sudanese conditions. These outcomes harmonize with global evidence linking mineral nutrition to secondary metabolism [1-6, 13-16, 33-45] and underline the potential of region-specific genotype evaluation to strengthen both food quality and agricultural sustainability.

Conclusion

The present investigation clearly establishes that the mineral composition of Sudanese onion genotypes plays a pivotal role in determining their bioactive compound content and antioxidant potential. Genotypes rich in sulfur, potassium, and magnesium exhibited significantly higher levels of total phenolics, total flavonoids, and antioxidant capacities, while those with elevated sodium levels demonstrated comparatively reduced bioactive and antioxidant profiles. This outcome underscores the intrinsic link between mineral nutrition and the biosynthesis of phytochemicals responsible for the health-promoting properties of onions. The results highlight that sulfur is not only essential for structural and enzymatic functions but also acts as a metabolic regulator that enhances the synthesis of quercetin-type flavonols and improves the plant's oxidative defense system. Similarly, potassium and magnesium contribute synergistically to these pathways by supporting enzymatic activity, photosynthetic efficiency, and ion balance. Conversely, excessive sodium accumulation was shown to inhibit phenolic production and compromise antioxidant defense, emphasizing the detrimental impact of salinity on crop nutritional quality.

In practical terms, these findings suggest that improving the mineral balance in onion cultivation—particularly by optimizing sulfur and potassium fertilization—can enhance both yield quality and nutraceutical value. Farmers and extension workers in Sudan should prioritize soil testing and balanced fertilization programs that prevent nutrient depletion and control sodium buildup through improved irrigation practices and soil amendments. The adoption of genotypes such as Gezira-1 and Gezira-2, which displayed the most favorable mineral and bioactive profiles, should be encouraged in regional breeding and seed distribution programs. Post-harvest management strategies should also focus on maintaining mineral stability and minimizing oxidative degradation during storage to preserve antioxidant potency. Collectively, these integrative approaches can contribute to the production of onions with higher nutritional and functional benefits, supporting both local dietary health and the economic value of Sudanese horticultural produce.

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