Variability in nutritional quality traits of macaroni wheat (*Triticum durum* L.) genotypes

**Abstract:**

 The present investigation was carried out to study genetic variability in sixteen macaroni wheat genotypes along with the five checks *i.e.* Panchavati, Godavari, MACS-3949, NIDW-1149, AKDW-2997-16. Nine characters were studied to estimate genetic variability. Statistical analysis revealed that significant differences for all the characters studied, indicating presence of considerable amount of variations among genotypes. Phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV) for all the characters. This indicates the dominance of phenotypic coefficient of variation for expression of these traits. Heritability in broad sense ranged from 82.12% to 99.96 %. Highest estimate of heritability was recorded for calcium content (99.96%) followed by Na content (99.81%), Estimates of genetic advance ranged from 0.19 to 7.45. The highest estimate for genetic advance were recorded for Mg content (7.45) followed by Ca content (5.03). The significant positive correlation was found between protein content (%) with fiber content (%) and all minerals except Na content (mg/100 g) at both genotypic and phenotypic level. The performance of macaroni wheat genotypes for nutritional traits *viz.,* NIDW-1582 recorded high protein content (13.83) along with Fe (6.11) and Zn (3.52) followed by NIDW-1556, protein (12.38), Fe (5.38), Zn (3.45), NIDW-1555 (for protein and Zn content), NIDW-1569 (for calcium content) and NIDW-1556 (for Mg content) can be used in future breeding programme to develop a new biofortified varieties in macaroni wheat.

Key Words: Macaroni Wheat, Variability, Nutritional traits, Correlation

**1. Introduction:**

 Agriculture plays a crucial role in improving food availability and achieving global food security. Despite this, while there is widespread acknowledgment of the increasing global demand for food in the coming decades. Enhancing food provision by increasing agricultural productivity, however the increasing concern over nutritionally smart crops challenges its acceptability as a staple source of nutritious diet. The predicted increase in global food demand necessitates the expansion of yield of major global food crops like wheat, rice, and maize with nutritious supplement, Biofortification has evolved and accepted as a strategy to address this issue of food and nutritional security. Climate change is continuously posing as a challenge with the evolution of new races of pathogen and pests in major crops.

 Wheat is the foremost and strategic cereal crop of the world. Wheat is the most important and major staple food of more than thirty-five percent of worlds’ population. Globally, it is the most crucial oldest and edible grain cereals. Wheat belongs to the tribe Triticeae, sub tribe Triticineae in the grass family Poaceae (Gramineae) (Briggle and Reitz, 1963).

Macaroni wheat is tetraploid wheat, having 4 sets of chromosomes for a total of 28, unlike hard red winter and hard red spring wheats, which are hexaploid (6 sets of chromosomes) for a total of 42 chromosomes each. Macaroni wheat originated through intergeneric hybridization and polyploidization involving two diploid (having 2 sets of chromosomes) grass species. Macaroni wheat accounts for about 3-5 % of total area sown under wheat and 6-8% of the total wheat production. It contains stronger gluten, yellow colour grains, maintain good texture, resistant surface disintegration, retain structure and longer durability makes it more suitable for pasta making.

 It provides about one-half of human food calories and a large part of their nutrient requirements. Wheat contains carbohydrate (78.1%), protein (14.7%), fat (2.1%), minerals (2.1%) and considerable proportions of vitamins (thiamine, niacin and vitamin-B) and minerals (zinc, iron). It is also a good source of trace minerals like selenium and magnesium (Kumar *et al*. 2011).

 The selection of high‐yielding macaroni wheat germplasm should not rely solely on grain yield as a criterion. Nutritional traits such as, crude protein, crude fiber, selenium, magnesium and nutritional quality play a crucial role in identifying and improving high‐performing varieties, particularly in environments characterized by climatic variability and abiotic constraints. These traits, often more heritable and stable than yield itself, enable more effective indirect selection, helping to overcome challenges associated with the polygenic complexity of grain yield and genotype × environment interactions.

 Iron and zinc concentrations are particularly low in regularly consumed cereal-based diets (Cakmak 2008) which manifest as hidden hunger with serious consequences for health. Genetic biofortification entails breeding strategies to identify and take advantage of genetic diversity for minerals, as well as novel methods involving gene discovery and breeding using marker assistance (Grusak 2002).

 Biofortification overcome the problem of hidden hunger by improving the micronutrient content of the crops themselves by increasing mineral levels and bioavailability in the edible parts. Improving crop varieties by conventional breeding has the advantage that once the initial research and development is completed, the benefits from these nutritionally-enhanced crops will be sustainable with little further investment (Gomez-Galera *et. al.* 2010). The biofortification breeding program uses the existing genetic diversity from various species and landraces to generate nutrient-enriched wheat germplasm with competitive yield potential and stress tolerance in order to satiate the hidden hunger of the expanding population.

 The knowledge of variability also helps to develop strategies to incorporate useful diversity in breeding programs. This study aims to characterize the variability of agro‐morphological and quality traits within a large collection of macaroni wheat. In views of these facts, twenty one wheat genotypes were evaluated in this study to determine the magnitude of variability among the germplasm and to identify nutritionally desirable genotypes for exploitation in a breeding programme.

**2. Material and Methods:**

 The present investigation nutritional diversity in macaroni wheat genotypes (*Triticum macaroni* *L*.) was carried out at Soil Science and Biochemistry laboratory, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra) during year 2022-23. The plant material for the study comprised of twenty-one wheat genotypes*, i.e.* Panchavati (C), Godavari (C), MACS-3949 (C), NIDW-1149 (C), AKDW-2997-16 (C), NIDW-1569, NIDW-1572, NIDW-1573, NIDW-1574, NIDW-1576, NIDW-1578, NIDW-1579, NIDW-1582, NIDW-1555, NIDW-1561, NIDW-1542, NIDW-1556, NIDW-1557, NIDW-1520, NIDW-1534 and NIDW-1499 which were collected from Agriculture Research Station Niphad, District Nashik, Maharashtra and used for research work. Observations recorded for Crude Protein, Crude Fiber, Crude fat, Minerals Iron, zinc and other minerals.

**2.1 Observation Recorded:**

Crude Protein

The protein content was determined by Micro-Kjeldahl method (Anonymous, 2000).

Crude Fibre

The crude fibre was estimated by employing the standard method of analysis (AOAC 2000)

Crude fat

The crude fat content was determined by ether extraction using Soxhlet apparatus (AOAC, 2000).

Minerals

Iron, zinc and other minerals were determined according to the standard method of AOAC (2000) using flame Atomic Absorption Spectrophotometer.

**2.2 Statistical analysis**

Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme’s methodology (1995). GCV and PCV were calculated by the formula given by Burton (1952), heritability in broad sense (h2) by Hanson *et al.* (1956) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Allard (1960).

**3. Results and Discussion:**

**3.1: Mean Performance and Analysis of Variance**

The mean performance of sixteen macaroni wheat genotypes over the five standard checks, on nine nutritional characters studied and presented in Table 1. Among which genotypes NIDW-1582 recorded high protein content (13.83) along with Fe (6.11) and Zn (3.52 ) followed by NIDW-1556, protein (12.38), Fe (5.38), Zn (3.45), NIDW-1555, Protein (12.99) Fe (5.32) and Zn (3.82), NIDW-1569, Protein (12.10), Fe (5.11) and Zn (3.45), NIDW-1499, Protein (12.16), Fe (5.20) and Zn (3.33) and NIDW-1579, Protein (12.06), Fe (5.04) and Zn (3.29).

The analysis of variance for nine characters is presented in Table 2. For all characters studied, there were significant variances among the genotypes, revealing a vast range of variation in sixteen genotypes of macaroni wheat along with five standard checks. The analysis of variance indicated that wide variability among the genotypes. This indicates that considerable amount of variation persist for all the characters and considerable improvements can be achieved by selection for these characters.

 **Table: 1 Mean Performance of twenty one wheat genotypes for nutritional characters.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Name of Genotype** | **Protein Content (%)** | **Fat Content (%)** | **Fiber Content (%)** | **Fe (mg/100g )** | **Zn (mg/100g)** | **Ca (mg/100g)** | **Mg****(mg/100g)** | **Cu****(mg/100g )** | **Na****(mg/100g )** |
| 1 | Panchavati (C) | 11.93 | 1.16 | 1.35 | 4.83 | 3.09 | 38.08 | 132.87 | 0.60 | 2.50 |
| 2 | Godavari (C) | 11.97 | 1.33 | 1.35 | 4.88 | 3.22 | 38.23 | 135.97 | 0.58 | 2.49 |
| 3 | MACS-3949(C) | 11.96 | 1.52 | 1.48 | 4.93 | 3.23 | 40.24 | 133.47 | 0.57 | 2.32 |
| 4 | NIDW-1149 (C) | 11.77 | 1.42 | 1.32 | 4.45 | 3.25 | 37.71 | 132.87 | 0.54 | 2.61 |
| 5 | AKDW-2997-16 (C) | 12.05 | 1.42 | 1.49 | 5.03 | 3.12 | 38.90 | 133.73 | 0.56 | 2.31 |
| 6 | NIDW-1569 | 12.10 | 1.34 | 1.67 | 5.11 | 3.45 | 42.53 | 134.73 | 0.62 | 2.29 |
| 7 | NIDW-1572 | 11.07 | 1.58 | 1.09 | 3.55 | 2.55 | 35.47 | 127.53 | 0.39 | 3.30 |
| 8 | NIDW-1573 | 11.50 | 1.47 | 1.17 | 4.10 | 2.99 | 32.90 | 131.57 | 0.51 | 2.86 |
| 9 | NIDW-1574 | 10.95 | 1.16 | 1.05 | 3.55 | 2.21 | 35.37 | 126.10 | 0.35 | 3.70 |
| 10 | NIDW-1576 | 10.30 | 1.55 | 1.13 | 3.56 | 2.82 | 36.60 | 120.03 | 0.33 | 3.12 |
| 11 | NIDW-1578 | 11.47 | 1.40 | 1.16 | 3.95 | 2.84 | 36.56 | 131.37 | 0.50 | 3.01 |
| 12 | NIDW-1579 | 12.06 | 1.99 | 1.90 | 5.04 | 3.29 | 40.30 | 134.37 | 0.56 | 2.31 |
| 13 | NIDW-1582 | 13.83 | 1.37 | 1.78 | 6.11 | 3.52 | 40.36 | 135.53 | 0.62 | 2.04 |
| 14 | NIDW-1555 | 12.99 | 1.13 | 1.80 | 5.32 | 3.82 | 41.41 | 136.33 | 0.63 | 2.03 |
| 15 | NIDW-1561 | 11.70 | 1.14 | 1.26 | 4.27 | 3.05 | 37.63 | 132.67 | 0.52 | 2.20 |
| 16 | NIDW-1542 | 11.37 | 1.57 | 1.15 | 3.65 | 2.04 | 36.49 | 131.00 | 0.49 | 3.11 |
| 17 | NIDW-1556 | 12.38 | 1.16 | 1.73 | 5.38 | 3.45 | 41.20 | 137.57 | 0.63 | 2.20 |
| 18 | NIDW-1557 | 11.26 | 1.33 | 1.13 | 3.63 | 2.81 | 36.39 | 129.37 | 0.46 | 3.95 |
| 19 | NIDW-1520 | 11.53 | 1.52 | 1.20 | 4.23 | 3.03 | 36.68 | 132.30 | 0.52 | 2.70 |
| 20 | NIDW-1534 | 11.25 | 1.42 | 1.03 | 3.63 | 2.55 | 36.14 | 129.27 | 0.40 | 3.12 |
| 21 | NIDW-1499 | 12.16 | 1.42 | 1.55 | 5.20 | 3.33 | 40.63 | 134.90 | 0.64 | 2.23 |
|  | Mean | 11.79 | 1.46 | 1.37 | 4.49 | 3.03 | 38.09 | 132.08 | 0.53 | 2.69 |
|  | Range | 10.30-13.83 | 1.13-1.99 | 1.03-1.90 | 3.55-6.11 | 2.04-3.82 | 32.90-42.53 | 120.03-137.57 | 0.33-0.64 | 2.03-3.95 |
|  | S.E. ± | 0.192 | 0.022 | 0.022 | 0.023 | 0.019 | 0.029 | 0.905 | 0.002 | 0.013 |
|  | C. D. 5% | 0.548 | 0.065 | 0.065 | 0.065 | 0.056 | 0.085 | 2.588 | 0.008 | 0.038 |
|  | C.V. | 2.820 | 2.709 | 2.875 | 0.886 | 1.136 | 0.135 | 1.187 | 0.957 | 0.873 |

 **Table 2. Analysis of variance for nine different nutritional characters in macaroni wheat**

|  |  |  |
| --- | --- | --- |
| **Sr. No.** |  **Characters** | **Mean sum of squares** |
| **Replication (1)** | **Genotype (39)** | **Error (39)** |
| 1 | Protein Content (%) | 0.289 | 1.633\*\* | 0.110 |
| 2 | Fat Content % | 0.0006 | 0.208\*\* | 0.001 |
| 3 | Fiber content % | 0.002 | 0.222\*\* | 0.001 |
| 4 | Fe (mg/100 g) | 0.0007 | 1.719\*\* | 0.001 |
| 5 | Zn (mg/100 g) | 0.002 | 0.561\*\* | 0.001 |
| 6 | Ca (mg/100 g) | 0.0006 | 17.931\*\* | 0.002 |
| 7 | Mg (mg/100 g) | 5.831 | 48.145\*\* | 2.459 |
| 8 | Cu (mg/100 g) | 0.00002 | 0.027\*\* | 0.00002 |
| 9 | Na (mg/100 g) | 0.0003 | 0.880\*\* | 0.0005 |

 \* and \*\* indicate significant at 5 and 1 per cent level, respectively.

**3.2: Genotypic and Phenotypic Coefficients of Variation**

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance and genetic advance of percent mean for nine characters are presented in Table 3. Genotypic coefficient of variation (GCV) was highest for Na content (20.16 %) followed by Fiber content (19.79%), Cu content (18.10 %) and Fat content (17.98 %). The character Mg content (2.95%) recorded lowest GCV. The maximum phenotypic coefficient of variation (PCV) was recorded for Na content (20.18 %), followed by Fiber content (20.00 %) and Fat content (18.18 %). Similar results were obtained by Kaur *et al.* (2008). The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for Na content. Moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for fat content (%), fibre content (%), Fe content (mg/100 g), Zn content (mg/100 g) and copper content (mg/100 g). Low genotypic coefficient of variation and phenotypic coefficient of variation was observed for protein content (%), Ca (mg/100 g) content and Mg content (mg/100 g). In general the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation which reflects the influence of environment on the expression of traits, Majumder *et al*. (2008) found the similar results.

**3.3: Heritability and Genetic Advance**

Heritability and Genetic Advance are important selection parameters. High estimates of heritability (>60%) was recorded for all studied characters. The highest estimates of heritability exhibited in Ca content (99.96%) followed by Na content (99.81%), Fe content and Cu content (99.72%) each (Table 3).

The range of genetic advance observed from 0.19 to 7.45. The highest estimates of GA exhibited for Mg content (7.45) followed by Ca content (5.03) and Fe content (1.55). While the lowest estimates of GA was recorded for Cu content (0.19).

High estimates of genetic advance as per cent of mean observed for Na content (41.49 %), followed by fiber content (40.35 %), Cu content (37.25 %), fat content (36.63 %) and Fe content (34.63 %). While Mg content (5.64 %) showed the lowest performance in genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was observed for all characters except Protein content (%), Ca content (mg/100 g) and Mg content (mg/100 g) indicating that these traits were predominantly governed by additive gene action and suggesting that the selection of these trait would be effective for the desired genetic improvement in early segregating generations for these traits. Similar findings have been reported by Taneva *et. al* 2019.

**Table 3: Estimates of variability parameters for nutritional characters in macaroni wheat**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SN.** | **Character** | **Mean** | **Range** | **GCV (%)** | **PCV (%)** | **ECV (%)** | **Heritability****(bs) (%)** | **Genetic Advance** | **Genetic Advance****% of Mean** |
| 1 | Protein Content (%) | 11.79 | 10.30 to 13.83 | 6.04 | 6.66 | 2.82 | 82.12 | 1.33 | 11.28 |
| 2 | Fat Content % | 1.46 | 1.13 to 1.99 | 17.98 | 18.18 | 2.70 | 97.78 | 0.53 | 36.63 |
| 3 | Fiber content % | 1.37 | 1.03 to 1.90 | 19.79 | 20.00 | 2.87 | 97.93 | 0.55 | 40.35 |
| 4 | Fe (mg/100 g) | 4.49 | 3.55 to 6.11 | 16.83 | 16.86 | 0.88 | 99.72 | 1.55 | 34.63 |
| 5 | Zn (mg/100 g) | 3.03 | 2.04 to 3.82 | 14.26 | 14.31 | 1.13 | 99.37 | 0.88 | 29.30 |
| 6 | Ca (mg/100 g) | 38.09 | 32.90 to 42.53 | 6.41 | 6.42 | 0.13 | 99.96 | 5.03 | 13.21 |
| 7 | Mg (mg/100 g) | 132.08 | 120.03 to 137.57 | 2.95 | 3.18 | 1.18 | 86.09 | 7.45 | 5.64 |
| 8 | Cu (mg/100 g) | 0.53 | 0.33 to 0.64 | 18.10 | 18.13 | 0.95 | 99.72 | 0.19 | 37.25 |
| 9 | Na (mg/100 g) | 2.69 | 2.03 to 3.95 | 20.16 | 20.18 | 0.87 | 99.81 | 1.11 | 41.49 |

**3.4: Correlation Studies:**

**1) Protein content (%)**

Protein content showed significant positive correlation with fiber content (rp = 0.759, rg = 0.862), Fe content (rp = 0.864, rg = 0.956), Zn content (rp = 0.705, rg = 0.792), Ca content (rp = 0.644 rg =0.735), Mg content (rp = 0.755 rg =0.882). Similar results reported by Peleg *et al.* (2009) Table 4.

**2) Fat content (%)**

Fat content showed non-significant positive correlation with fiber content (rp = 0.078 rg = 0.081) and calcium content (rp= 0.026 rg= 0.026)

**3) Fiber content (%)**

 Fiber content showed positive and significant association with protein content (rp = 0.759 rg = 0.862), Fe content (rp = 0.905 rg = 0.915), Zn content (rp = 0.825 rg = 0.837), Ca content (rp = 0.872 rg = 0.881) , Mg content (rp = 0.702 rg = 0.748) Cu content (rp = 0.835 rg = 0.845) at both phenotypic and genotypic level. Similar findings reported by Amiri *et al*. (2018).

**4) Fe content (mg/100 g)**

Iron content showed significant positive correlation with protein content, (rp = 0.864 (rg = 0.956), fiber content (rp = 0.905 rg = 0.915), zinc content (rp = 0.867 rg = 0.871), calcium content (rp = 0.831 rg = 0.832), magnesium (rp = 0.777 rg = 0.836), copper content (rp = 0.905 rg = 0.908) at both genotypic and phenotypic level. Suchowilska *et al*. (2012) observed the similar results.

**5) Zn content (mg/100 g)**

 Zinc content showed significant positive correlation with protein content (rp = 0.705 rg = 0.792), fiber content (rp = 0.825 rg =0.837), iron content (rp = 0.867 rg = 0.871), calcium content (rp = 0.753 rg = 0.756), magnesium (rp = 0.664 rg = 0.716), copper content (rp=0.817 rg = 0.820) at both phenotypic and genotypic level. The finding for zinc and iron correlation are in consistent with the findings of Badakhshan *et al*. (2013).

**6)** **Ca content (mg/100 g)**

 Calcium content showed significant positive correlation with protein content (rp = 0.664 rg = 0.735), fiber content (rp = 0.872 rg =0.881), iron content (rp = 0.831 rg = 0.832), zinc content (rp = 0.753 rg = 0.756), magnesium (rp = 0.629 rg = 0.677), copper content (rp = 0.894 rg = 0.780) at both phenotypic and genotypic level. Biel *et al.* (2021) observed the similar results.

**7)** **Magnesium content (mg/100 g)**

Magnesium content showed significant positive correlation with protein content (rp = 0.755 rg = 0.882), fiber content (rp = 0.702 rg =0.748), iron content (rp = 0.777 rg = 0.836), zinc content (rp = 0.664 rg = 0.716), calcium (rp = 0.629 rg = 0.677), copper content (rp = 0.778 rg = 0.963) at both genotypic and phenotypic level. While significant negative correlation with sodium content (rp = -0.748 rg = -0.774) at both genotypic and phenotypic level. These results are in consistent with the results of Biel *et al.* (2021).

**8) Copper content (mg/100 g)**

Copper content showed significant positive correlation with protein content (rp = 0.797 rg = 0.877), fiber content (rp = 0.835 rg =0.845), iron content (rp = 0.905 rg = 0.908), zinc content (rp = 0.817 rg = 0.820), magnesium content (rp = 0.778 rg = 0.963) at both genotypic and phenotypic level. While significant negative correlation with sodium content (rp = -0.848 rg = -0.849) at both phenotypic and genotypic level. Similar findings reported by Pandey *et al*. (2016).

**9) Sodium content (mg/100 g)**

Sodium content showed significant negative correlation with protein content (rp = -0.725 rg = -0.796), fiber content (rp = -0.795 rg = -0.807), iron content (rp = -0.875 rg = -0.877), zinc content (rp = -0.818 rg = -0.821), magnesium (rp = -0.748 rg = -0.774), copper content (rp = -0.848 rg = -0.849) at both phenotypic and genotypic level.

 Thus the significant positive correlation was found between protein content (%) with fiber content (%) and all minerals except Na content (mg/100 g) at both genotypic and phenotypic level. This indicates that simultaneous improvement of these characters through selection. While fat content (%) shown non-significant negative correlation with protein content (mg/100 g). In present investigation genotypic correlation were higher than phenotypic correlation for most of the studied characters. This indicates that there was high degree of association among two variables at genotypic level; its phenotypic expression was deflected due to influence of environment Table 4.

**4. Conclusion:**

Genetic variability among the genotypes is thought to be a valuable source to develop the better crop varieties for its commercialization. In present study, significant differences were observed for the studied nine nutritional traits of the macaroni wheat. Correlation for most of the characters at both genotypic and phenotypic levels was made to resolve the direction of magnitude of association among characters. The significant positive correlation observed in protein content along with Fe and Zn and also Iron content has positive correlation among Zn content and protein content and similar correlation shown by Zn content with Iron and protein content. The performance of macaroni wheat genotypes for nutritional parameters following genotypes *viz.,* NIDW-1556, NIDW-1555, NIDW-1569, NIDW-1499 and NIDW-1579 used for protein, Iron and zinc content, NIDW-1582 (for protein content), NIDW-1569 (for calcium content), NIDW-1556 (for Mg content) and NIDW-1499 (for Cu content) can be used in future breeding programme for development of new biofortified varieties in macaroni wheat.

**Table 4: Estimates of phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among nutritional characters.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr.No.** | **Name of character** | **Protein****(%)** | **Fat %** | **Fiber %** | **Fe** | **Zn** | **Ca** | **Mg** | **Cu** | **Na** |
| 1. |  **Protein (%)** | **1.000** | -0.114 | 0.759\*\* | 0.864\*\* | 0.705\*\* | 0.664\*\* | 0.755\*\* | 0.797\*\* | -0.725\*\* |
| 2. |  **Fat %** | -0.119 | **1.000** | 0.078 | -0.029 | -0.097 | 0.026 | - 0.022 | -0.013 | -0.070 |
| 3. |  **Fiber %** | 0.862\*\* | 0.081 | **1.000** | 0.905\*\* | 0.825\*\* | 0.872\*\* | 0.702\*\* | 0.835\*\* | -0.795\*\* |
| 4. |  **Fe** | 0.956\*\* | -0.029 | 0.915\*\* | **1.000** | 0.867\*\* | 0.831\*\* | 0.777\*\* | 0.905\*\* | -0.875\*\* |
| 5. |  **Zn** | 0.792\*\* | -0.103 | 0.837\*\* | 0.871\*\* | **1.000** | 0.753\*\* | 0.664\*\* | 0.817\*\* | -0.818\*\* |
| 6. |  **Ca** | 0.735\*\* | 0.026 | 0.881\*\* | 0.832\*\* | 0.756\*\* | **1.000** | 0.629\*\* | 0.894\*\* | -0.719\*\* |
| 7. |  **Mg** | 0.882\*\* | -0.042 | 0.748\*\* | 0.836\*\* | 0.716\*\* | 0.677\*\* | **1.000** | 0.778\*\* | -0.748\*\* |
| 8. |  **Cu** | 0.877\*\* | -0.014 | 0.845\*\* | 0.908\*\* | 0.820\*\* | 0.780\*\* | 0.963\*\* | **1.000** | -0.848\*\* |
| 9. |  **Na** | -0.796\*\* | -0.069 | -0.807\*\* | -0.877\*\* | -0.821\*\* | -0.749\*\* | -0.774\*\* | -0.849\*\* | **1.000** |

 \*and\*\* significant at P=5 and P=1 level of significance,

**Disclaimer (Artificial Intelligence):**

Authros hereby declare that no negative AI technologies such as Chat GPT, Google Gemini, Grok and text-to-image generators have been used during writing or editing of this manuscript.

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