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Research Article

An assessment of the antioxidant potential and nutritional makeup of native landraces of foxtail millet (*Setaria italica*) from Shamator District, Nagaland

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Abstract

Foxtail millet (*Setaria italica*) is an important crop species with vast genetic resources highly valued for its nutritional profile and adaptability to harsh environments. This study investigated the nutritional composition and antioxidant properties of indigenous foxtail millet genotypes grown in the Shamator district of Nagaland. Proximate analysis, including carbohydrates, proteins, ashes, moisture, crude fibre and bioactive compounds such as total phenolic content (TPC) and total flavonoids content (TFC) were screened on eight different genotypes. Antioxidant potential was also determined through DPPH and FRAP assays. In the eight-millets recorded good stability and low variability among the genotypes in ash content (1.12%-1.60%; CV 11.19%) and carbohydrates (36.7%-39.7%; CV 2.51%). However, high variability was observed among the genotypes in relation to their protein content (53%-80%; CV 13.0%). Significant variation was observed between the genotypes for crude fibre (0.28%-0.72%) and moisture content (7.8%-15.8%, CV 19.82%). TPC exhibited significant variability (CV ~28.8%), indicating variations in phenolic accumulation. Whereas TFC (CV ~35.43%), showed genotypic heterogeneity in secondary metabolites. Among the landraces, LS consistently exhibit the utmost levels of phenolics and flavonoids. Antioxidant profiles revealed that LS has the highest radical scavenging activity with the lowest IC_{50} value and highest FRAP, followed by TS and WS, while AST exhibit the lowest antioxidant capacity. Overall, this study conveyed considerable variability in nutritional and antioxidant profiles in indigenous cultivars of foxtail millets in Shamator district of Nagaland. Genotype of LS, TS and WS demonstrates the promising functional food production and parental lines enhancing millet quality and health promoting traits.

Keywords: Foxtail millet, Antioxidant capacity, Genotypes, Nutritional, Landraces

Introduction

The Poaceae family comprises of diverse group of small-seeded cereals such as millets. Among the different millets, foxtail millets are the oldest millet cultivated 8,000 years ago in China (Austin, 2006). These plants are currently cultivated in semiarid and tropical regions in Africa, Asia, Australia, South America, China, India, Nigeria, and Niger (Saleh *et al.,* 2013; Yang *et al.,* 2018). Foxtail millet plants have gained significance for several reasons, such as rapid growth cycle, salt tolerance, disease and pest resistance, photosynthesis efficiency, and nutrition (Liu *et al.,* 2011; Vetriventhan *et al.,* 2012). These millets are historically classified as poor man crop. Being gluten-free, nutritious, easy to digest, and low in glycaemic index, this cereal can be used nutritionally by diabetics and coeliac patients (Ramashia *et al.,* 2019). Flavonoids, phenolic acid, essential amino acids, B complex vitamins, and several minerals like potassium, iron, phosphorous, zinc and calcium are among the numerous phytochemical compositions found in millets (Singh *et al.,* 2012; Saleh *et al.,* 2013; Bandyopadhyay *et al.,* 2017). The crude fibre in foxtail millet helps to maintain healthy digestion and proper bowel movements (Sharma & Niranjan, 2018). Millets have systematic health benefits including reduction in blood cholesterol, weight management, cancer, and heart problems (Gupta *et al.,* 2012; Zhang *et al.,* 2015). The vital nutrients and bioactive compounds present in millets depend on their farming locations (Kitta *et al.,* 2005; Wen *et al.,* 2014). Challenges in millet farming due to Climate change, droughts, and soil degradation are causing an ever-growing quantity of farmland to become marginal and less suitable for cultivating staple foods. Unexploited millets, referred to as future grains, can flourish on marginal soils due to their ability to withstand harsh environments (Rodríguez *et al.,* 2020). Different types of millets have diverse levels of phenolics and flavonoids, which offer various health benefits, especially in addressing type II diabetes (Shukla & Srivastava, 2014; Ren *et al.,* 2016). Millets provide sustainable agriculture and food security since they can grow in harsh, hot, and arid conditions where most cereal crops cannot thrive. Poverty and malnutrition have escalated owing to the decline in millet cultivation despite advances in agriculture. Millets' nutritional, environmental, and agricultural benefits have garnered fresh attention due to socioeconomic challenges such as market dynamics and dietary changes (Patil *et al.,* 2023). Natural compounds derived from food have long been significant sources of medicine and drug development platforms (Harvey, 2007; Anand *et al.,* 2008). Nutraceuticals and phytochemicals found in abundance in millet seeds aid in preventing numerous diseases. Whole grains, particularly millets, have garnered interest recently due to their dietary fibre and bioactive components that enhance human health, such as phytochemicals and antioxidants (Yao *et al.,* 2004; Holtekjølen *et al.,* 2006). The present study was conducted to explore the nutritional and antioxidant profiles of indigenous germplasm of foxtail millet in Shamator district, Nagaland, India.

Materials and methods

Sample materials

The foxtail millet samples were collected from seven village of Shamator district, Nagaland and Cultivars were assigned sample codes as per the local classification as presented in Table 1. One sample per genotypes were collected.

Sample preparation

The grains were allowed to air dry. The air-dried grains were then dehusked and milled into a fine powder using a grinder or mortar and pestle.

Moisture content

In a pre-weighed petri dish about 2 grams of the sample were precisely weighed and dried for four to six hours at 105 °C in a hot air oven. Then final weight of sample also taken for calculation (Pojić *et al.,* 2015).

Calculation

$$Moisture\,(\%) = \frac{Loss\,in\,Weight}{Initial\,sample\,weight} \times 100$$

Ash content

The pre-weighed crucible was added with 2 g of the sample and burnt for 4-6 hours in a muffle furnace at 550 °C to obtain ash of light grey or white colour. The crucible was cooled in a desiccator, and its weight was measured (Harris & Marshall, 2017).

Calculation

$$Ash\ (\%) = \frac{Weight\,of\,ash}{Sample\,weight} \times 100$$

Crude fibre content

2 g of the millet sample were boiled with 200 mL of 1.25% sulphuric acid for 30 minutes, then filtered. The residue was boiled again for 30 minutes in 1.25% sodium hydroxide, filtered, and washed well with distilled water. After drying at 105 °C, the residue was weighed, then ashed at 550 °C. The change in weight before and after ashing was recorded (Yadav *et al.,* 2022).

Table 1: List of the foxtail millet varieties with local names and sample codes

S. No.	Local name	Location name	Sample code
1	Jüpai jih	Ayiponger	JP
2	Tamsung sha	Chessore	TS
3	Leekong sha	Hukir	LS
4	Muliu	Kuthur	MUL
5	Jüpo jih	Leangkonger	JJ
6	Amürak shipu tanji	Rurur	AST
7	Wakmei Jih	Shiponger	WJ
8	Khotsaru	Chessore	KS

Calculation

$$Crude\,Fibre\ (\%) = \frac{(W_1 W_2)}{W} \times 100$$

Total carbohydrate content

The Carbohydrate test was done using the anthrone method. A calibration curve is created by reacting freshly made anthrone reagent with a standard glucose solution under carefully regulated heating conditions, producing a range of known colour intensities. The sample extract is treated similarly with anthrone reagent and its absorbance at measured at 620 nm. The dry basis of the result will be expressed in mg of carbohydrate per mL of extract or per g of sample (Arora *et al.,* 2023).

Total protein content

The protein test was done using Lowry's method. In this method BSA (Bovine serum albumin) is used as standard. Diluted Folin-Ciocalteu reagent is added to the samples and incubated for about 20 to 30 minutes at room temperature. The absorbance is measured at 660 nm. The protein content of the unknown sample is calculated and expressed in mg of Protein per mL of extract or per g of sample (Waterborg, 2009; Jenipher *et al.,* 2024)

Total phenol content

The Folin-Ciocalteu reagent method was modified to evaluate the crude extract's total phenolic content. A standard of gallic acid was made at various concentrations (Sudharsan *et al.,* 2022). 2.5 mL of 0.2 mol/L Folin-Ciocalteu reagent was added to 0.5 mL of each extract, gently shaken, and left for five minutes. After adding 2 mL of Na_2CO_3 (7.5%, w/v), the solutions were incubated for 20 minutes at 30 °C. Each experimental procedure had three replicates. The absorbance of the sample was taken using a UV-visible spectrophotometer at a wavelength of 765 nm (Zahin *et al.,* 2017). The concentration of gallic acid equivalent per microgram of extract was calculated using the gallic acid standard curve.

Total flavonoid content (TFC)

TFC was estimated using the $AlCl_3$ method (Qiu *et al.,* 2010). Different concentration of quercetin was used as standard to obtain the standard curve. 1 mL of the extract and 1 mL of 2% $AlCl_3$ were mixed and incubate for 15 minutes. The absorbance was measured at 510 in a spectrophotometer. The total flavonoid content was expressed as QE per microgram of extract.

Extraction of samples for antioxidant properties

Weigh out 500 mg of finely ground foxtail millet flour in a conical flask then add 10 mL of 1% (v/v) hydrochloric acid in methanol. Use a mortar and pestle to homogenize it. Then centrifuge the filtrate for 15 minutes at 10,000 rpm.

Collect the supernatant for further analysis. Until additional analysis, keep the extract at 4 °C and shield it from light (Pradeep & Guha, 2011; Balasubramaniam *et al.,* 2019).

Activity of antioxidants

DPPH radical scavenging activity

Make a 0.1 mM DPPH solution in methanol, dissolve the extracts in methanol to create a range of concentrations. Add equal volumes of the prepared sample and DPPH working solution to each test tube. Thoroughly mix the reaction, then incubate at room temperature for 30 minutes in the dark. Using a spectrophotometer, measure each reaction mixture's absorbance at 517 nm. Methanol was used as a blank and the DPPH reagent as a control (Sharma *et al.,* 2023).

FRAP (Ferric reducing antioxidant power)

The FRAP assay for evaluating the millets were done by Sharma *et al.* (2023). The Frap reagent was prepared by combining 25 mL of acetate buffer (300 mmol/L, pH 3.6), 2.5 mL of 10 mmol TPTZ solution and 2.5 mL of $FeCl_3$ solution (20 mmol/L) in the ratio 10:1:1 (v/v). The above-prepared mixture was incubated for 10 minutes at 37 °C in a water bath. In a 10 mL test tube, 0.5 mL of foxtail millet extract and 3 mL of FRAP reagent were mixed. The resulting mixture was kept in the dark for 15 minutes and the absorbance measured at wavelength 593 nm. Calibration graphs were drawn with the help of ascorbic acid (aa) standards, and the results were expressed in micromoles of AA per gram of dry weight (Sharma *et al.,* 2023).

Statistical analysis

All experiments were performed in triplicates and reported as mean standard deviations. Data were analyzed using analysis of variance (ANOVA) test comparing each cell mean with the other cell mean in that row (Sidak's multiple comparisons test) and the significance of mean differences was compared using Graph pad prism 11.

Result

Moisture content

The moisture content varied between lower 7.8% (LS) and highest 15.8% (AST) among the eight samples. The genotypes showed a moderate moisture content. AST was the genotype with the good moisture content, followed by WS (13.4%) and TS (12.6%), showing significant water retention in these lines, as Table 2 illustrates. LS observed the lowest moisture level (7.8%), while JP, KS, and JJ showed intermediate levels. The 2.35 standard deviation (SD) indicates a wide range of values surrounding the mean. Furthermore, as Figure 1 illustrates, a comparatively high level of variability among the samples is indicated by the coefficient of variation (CV) of 19.82%.

Ash content

The eight indigenous foxtail millet samples were analyzed for the ash contents and found 1.12% (JJ) to 1.60% (LS). The average ash concentration was 1.34%, suggesting that the genotypes' mineral composition was largely consistent. According to Table 3, LS had the greatest ash content among the genotypes, followed by KS (1.46%), JP (1.39%), and WS (1.36%), suggesting that these lines had relatively greater mineral levels. In contrast, JJ (1.12%) and MUL (1.16%) recorded the lowest values, while AST and TS showed moderate ash content. The standard deviation (SD) of 0.15 suggests that the values are closely distributed around the mean. Additionally, the coefficient of variation (CV) of 11.19% reflects a moderate level of variability among the samples as shown in Figure 2. Overall, the variation observed suggests slight genotypic differences, which can be effectively utilized in breeding programs focused on improving mineral composition in foxtail millet.

Table 2: List of millet samples with the moisture content

Sample code	Moisture content
Ls	7.8
JP	10.29
Ks	11.13
JJ	11.46
MUL	12
Ts	12.54
Ws	13.42
Ast	15.89

Table 3: List of the millet samples showing the ash content

Sample code	Ash content
JJ	1.13
Mul	1.17
TS	1.33
Ast	1.34
Ws	1.36
JP	1.39
Ks	1.46
Ls	1.61

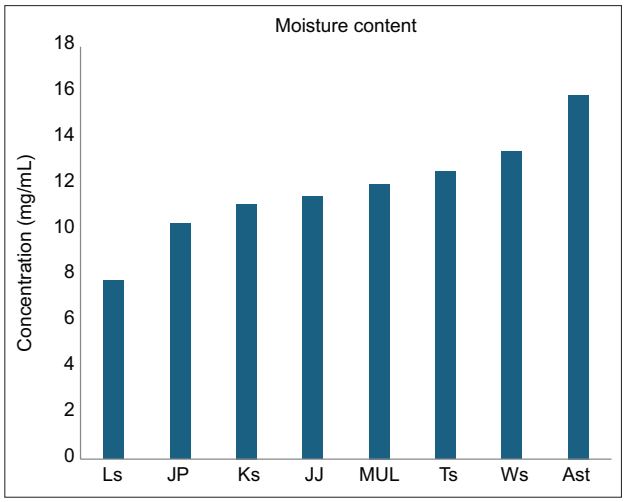

Figure 1: A comparatively high level of variability among the samples is shown by the coefficient of variation (CV) of moisture content 19.82%

Crude fibre

The crude fibre concentration varied significantly among the eight samples, ranging from 0.28 mg (JP) to 0.72 mg (WS). Figure 3 showed the genotypes generally

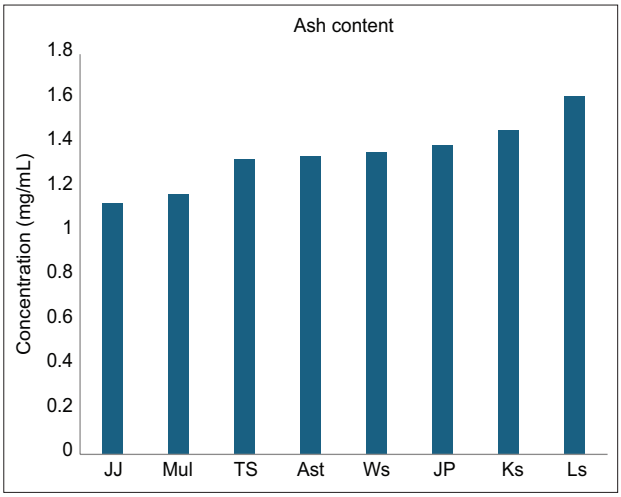

Figure 2: The coefficient of variation (CV) of ash content 11.19% reflects a moderate level of variability among the samples

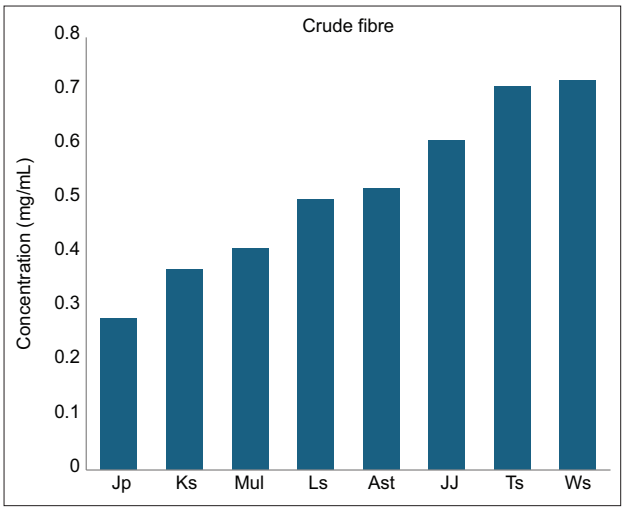

Figure 3: The mean crude fibre content of roughly 0.52, shows that genotypes have generally moderate fibre levels

have moderate fibre levels, as indicated by the mean crude fibre content of roughly 0.52 mg. WS had the greatest crude fibre content of all the genotypes, with TS (0.71) and JJ (0.61) following closely behind, indicating their aptitude as fibre-rich lines as shown in Table 4. On the other hand, KS (0.37), MUL (0.41), LS (0.50), and AST (0.52) revealed low to moderate levels of crude fibre content whereas JP (0.28) express the lowest level.

Total carbohydrate content

The carbohydrate content across the eight samples showed minimal variation, spanning from 36.7% (JJ) to 39.7% (JP and LS), as shown in Table 5. The average carbohydrate level was 38.83%, indicating that all samples possess relatively high carbohydrate content with slight differences among them. Among the genotypes, LS and JP exhibited the highest carbohydrate content (39.7%), followed by KS (39.3%), WS (39.1%), and AST (39.0%), which can be considered high carbohydrate content. JJ, on the other hand, recorded a significantly lower (36.7%), indicating possible genetic variations influencing the accumulation of carbohydrates. MUL and TS, the other

Table 4: List of the millet samples showing the crude fibre content

Sample code	Crude fibre content
Jp	0.28
Ks	0.37
Mul	0.41
Ls	0.5
Ast	0.52
JJ	0.61
Ts	0.71
Ws	0.72

Table 5: List of millet samples with the carbohydrate content

Sample code	Carbohydrate content
JJ	36.7
TS	38.3
MUL	38.8
AST	39
WS	39.1
KS	39.3
JP	39.7
LS	39.7

samples, have moderate or intermediate quantities of carbohydrates. The results are tightly clustered around the mean, as indicated by the computed standard deviation (SD) of 0.98. Furthermore, as shown in Figure 4 coefficient of variation (CV) of 2.51%, which suggests low variability and strong uniformity among the samples. This low CV% implies that the carbohydrate content is very constant throughout the samples.

Total protein content

The protein concentration of the eight samples varied significantly, ranging from 53% (JP) to 80% (LS) as shown in Table 6. With a mean protein content of 65.025%, the genotypes had moderate to high protein levels. Among the genotypes, LS showed the most protein content, indicating that AST (72%), WS (69%), and MUL (68%) recorded as protein-rich lines. On the other hand, JP (53%) had the lowest protein level, while TS, KS, and JJ had moderate levels. The 9.07% standard deviation (SD) indicates a wide range of values surrounding the mean. Additionally, as illustrated in Figure 5, the coefficient of variation (CV) of 13.0% denotes a considerable level of variability among the samples.

Total phenolic content

The assessment of Total Phenolic Content (TPC) among specific foxtail millet genotypes showed notable variance due to genetic influences on the accumulation of bioactive compounds. Table 7 demonstrates TPC values increased steadily, with LS having the highest content, followed by JJ and MUL, while AST had the lowest. Moderate levels were noted in WS and TS. The small standard deviations indicate good experimental precision, and the variations in TPC are linked to genotype specific metabolic pathways affecting phenolic biosynthesis. A substantial dispersion of data around the mean is shown by the standard deviation (SD) of roughly 0.15. Moreover, Figure 6 represents the coefficient of variation (CV) of roughly 28.8%, indicating a comparatively

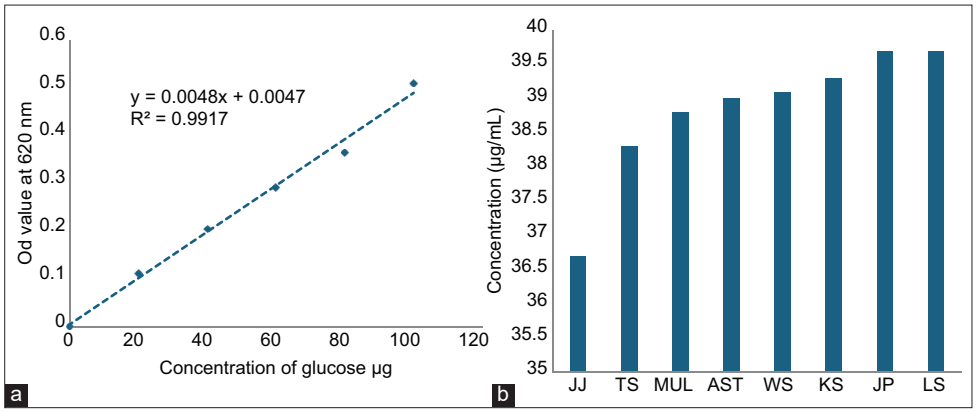

Figure 4: a) Carbohydrate content standard graph and b) The samples' great homogeneity and low variability are indicated by the coefficient of variation (CV) of 2.51%

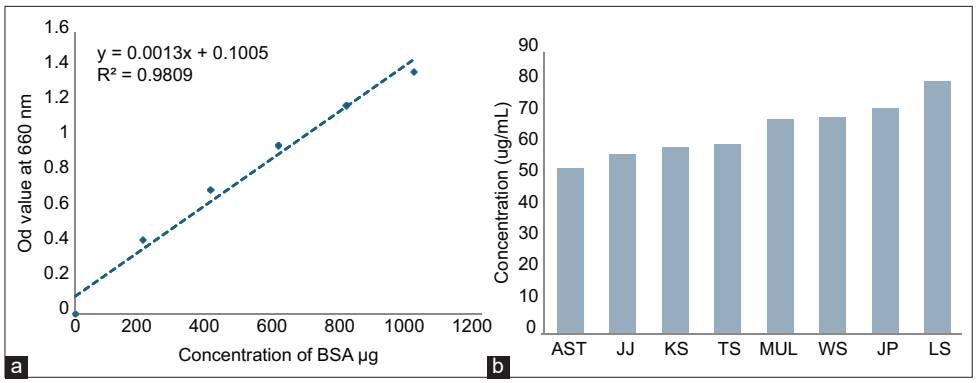

Figure 5: a) Standard protein content graph and b) A moderate level of variability among the samples is indicated by the coefficient of variation (CV) of 13.0%

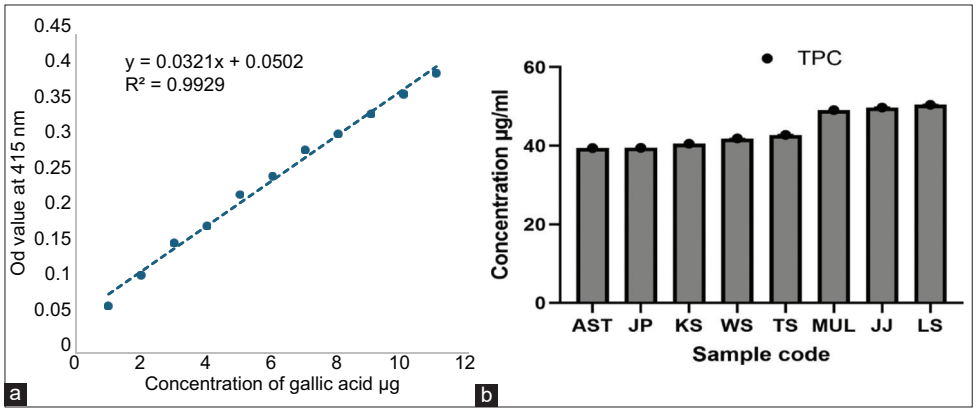

Figure 6: a) Standard graph for Phenolic content and b) Total phenolic content (TPC) of foxtail millet genotypes expressed as µg GAE/mL

Table 6: List of millet samples with the protein content

Sample code	Protein content
AST	52.9
JJ	57.3
KS	59.4
TS	60.5
MUL	68.4
WS	69.1
JP	72.1
LS	80.5

Table 7: List of the millet samples showing the phenolic content

Sample code	Mean	SD
AST	39.43333	0.005774
JP	39.49333	0.005774
KS	40.52	0.017321
WS	41.85	0.017321
TS	42.77	0.086603
MUL	49.08333	0.005774
JJ	49.73667	0.11547
LS	50.40667	0.11547

higher level of variability among the samples. Overall, the diversity found reveals important genotypic variations that can be successfully utilised in breeding initiatives meant to increase foxtail millet's dietary fibre content.

Total flavonoid content

The assessed foxtail millet genotypes' total flavonoid content (TFC) varied significantly, suggesting a strong genotypic influence on the accumulation of flavonoid

molecules. LS had the greatest TFC (~0.155 mg QE/g) of all the samples, followed by TS (~0.138 mg QE/g) and WS (~0.132 mg QE/g), as shown in Table 8, indicating that these genotypes had higher secondary metabolite production levels. On the other hand, JJ, MUL, KS, and JP showed moderate values between ~0.115 and 0.125 mg QE/g, whereas AST recorded the lowest flavonoid concentration (~0.112 mg QE/g). Good analytical precision and reproducibility were shown by the comparatively low standard error values seen in all samples, as shown in Figure 7.

DPPH radical scavenging activity

The DPPH free radical scavenging experiment was used to assess the antioxidant activity of different foxtail millet genotypes. Figure 8 illustrates the significant variance in both % inhibition and IC_{50} values. With the largest radical scavenging potential and the lowest IC_{50} value, genotype LS demonstrated the strongest antioxidant activity, showing its better efficacy in neutralising free radicals. Strong antioxidant qualities were also demonstrated by genotypes TS and WS, which were favourably positioned among the investigated genotypes due to their high scavenging percentages and low IC_{50} values. AST, on the other hand, exhibited the lowest antioxidant activity, as shown by its highest IC_{50} value and decreased scavenging capacity. With intermediate IC_{50} values, the other genotypes (JJ, MUL, KS, and JP) showed moderate antioxidant potential.

FRAP

The ferric reducing antioxidant power (FRAP) assay revealed considerable differences in the antioxidant capacity of the evaluated foxtail millet genotypes, reflecting differences in their overall reducing potential and electron-donating ability. Among the samples, LS showed the greatest FRAP value, indicating superior ferric ion (Fe^{3+}) reduction activity. WS and TS, both of which demonstrated quite strong antioxidant potential, and AST had the lowest FRAP value, indicating a significantly lower lowering capacity, while JJ, MUL, KS, and JP displayed moderate antioxidant activity as shown in Table 9 and Figure 9.

Table 8: List of the millet samples showing the Flavonoid content

Sample code	Mean	SD
AST	4.266667	0.047258
JJ	5.073333	0.015275
MUL	5.08	0.017321
KS	5.433333	0.152753
JP	6.533333	0.152753
WS	7.466667	0.11547
TS	8.436667	0.120139
LS	11.53333	0.152753

Discussion

The current study demonstrated that the proximate composition and antioxidant characteristics of the eight foxtail millet genotypes varied significantly, underscoring the important role that both genetic and environmental factors play in grain quality. The discovered variations in nutritional composition show that every genotype has a distinct biochemical profile, which makes them useful genetic resources for programs aimed at improving crops and nutrition. The genotypes' differences in carbohydrate content were comparatively small, ranging from 36.7% to 39.7%. Compared to other nutritional characteristics, the limited range indicates that carbohydrate accumulation is a reasonably stable trait that is less affected by changes in the environment. However, the LS and JP genotypes' relatively larger carbohydrate content suggests that they could be better suppliers of energy. Strong genetic control over starch production and accumulation pathways in foxtail millet grains may be the cause of this stability in carbohydrate concentration. On the other hand, between around 5.3% and 8.0%, the protein concentration varied significantly among the genotypes under study. The significant variations between LS, JP, WS, and MUL imply that genotype-specific traits and environmental factors have a significant impact on protein accumulation. Cereal grain protein production and deposition are known to be influenced by soil fertility, nitrogen availability, climate, and genetic background. The relatively low protein level seen in AST could be related to variations in the efficiency of nitrogen intake, assimilation, and translocation during grain development. Arora *et al.* (2023), Kalita *et al.* (2025) and Makwana *et al.* (2025) have published similar findings, showing that differences in nitrogen utilization efficiency have a substantial impact on grain protein content in millet species. These results imply that foxtail millet cultivars' protein content could

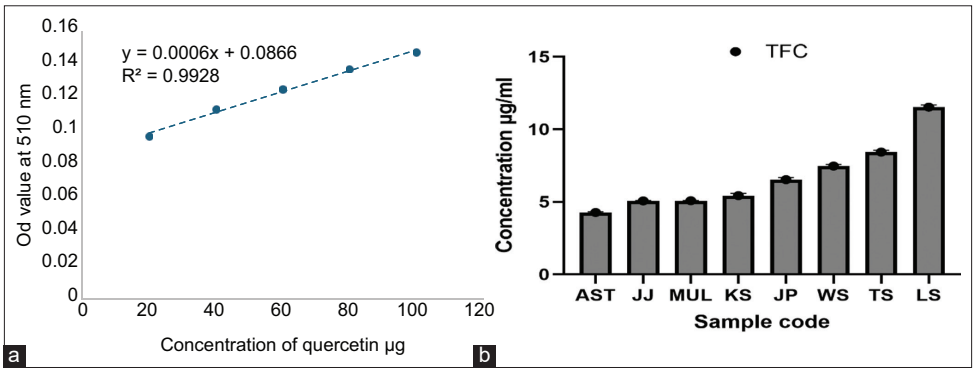

Figure 7: a) Standard graph for Flavonoid content and b) Quantification of total flavonoid content (TFC) in foxtail millet genotypes, expressed as µg QE/mL

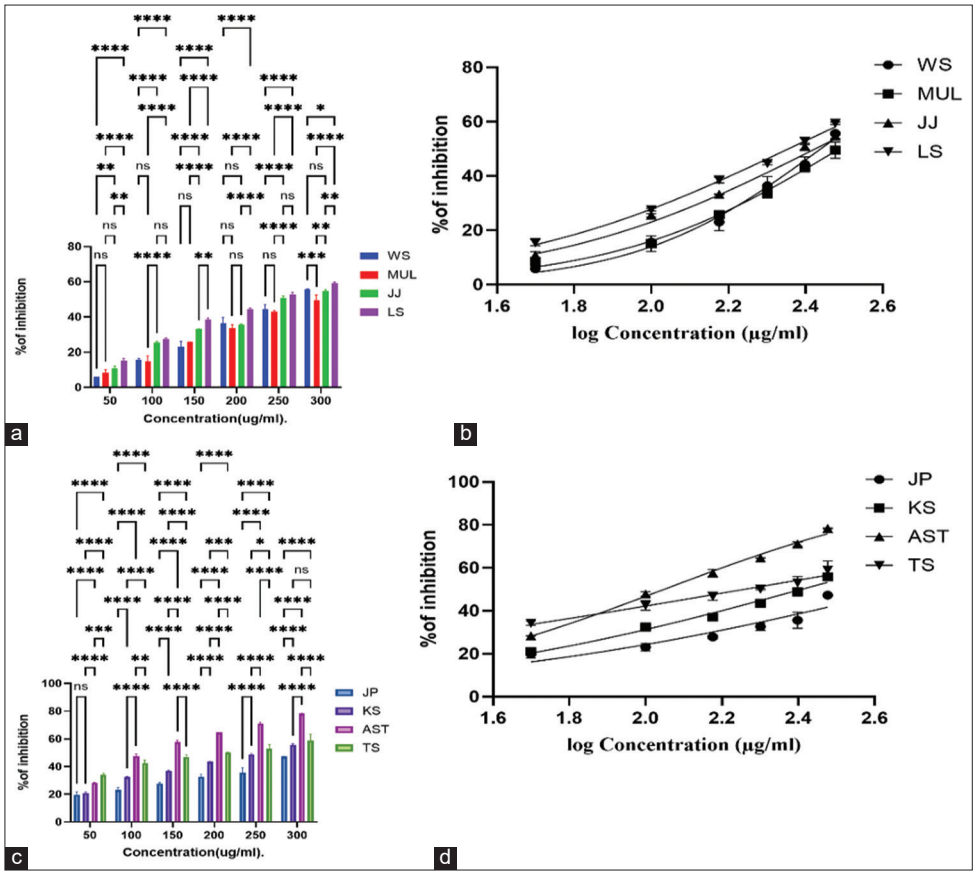

Figure 8: (a-d) Assessment of foxtail millet genotypes' DPPH radical scavenging capacity

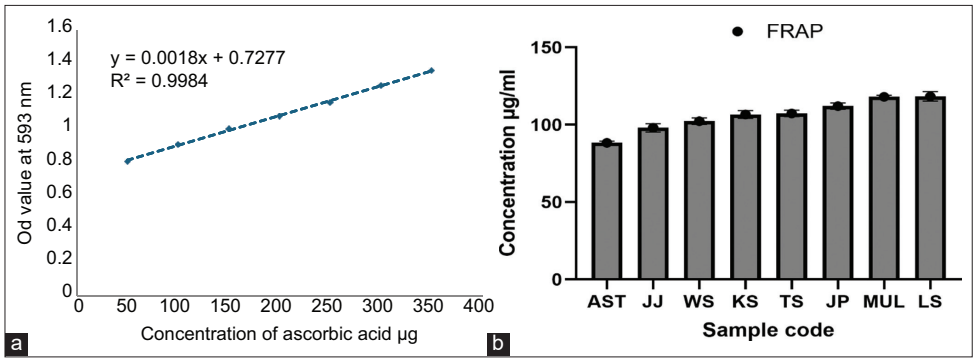

Figure 9: a) Frap content standard graph and b) Evaluation of foxtail millet genotypes' ferric reducing antioxidant power (FRAP), measured in µg AAE/mL

Table 9: List of the millet samples showing the FRAP content

Sample code	Mean	SD
AST	88.3333	1.1547
JJ	98	2.64575
WS	102.333	2.08167
KS	106.667	2.51661
TS	107.333	2.08167
JP	112	2
MUL	118	1
LS	118.333	3.05505

be increased by selective breeding techniques aimed at increased nitrogen-use efficiency.

The genotypes' differences in the ash content, an indirect measure of the overall mineral composition, were quite minor. On the other hand, LS and KS regularly showed higher ash content than JJ and MUL, indicating better nutritional quality and mineral buildup. Because minerals like iron, zinc, calcium, magnesium, and phosphorus are important for human health, genotypes with increased ash content could be useful sources of micronutrients in food. Genetic variations in nutrition absorption, transport, and storage processes may be responsible for the reported discrepancies. The genotypes also varied in terms of moisture content, with LS having the lowest. In general, reduced grain moisture is linked to longer shelf life, better storage stability, and less vulnerability to insect invasion and microbiological deterioration. AST, WS, and TS, on the other hand, maintained comparatively higher moisture levels, which could have a detrimental effect on storage quality and raise the possibility of post-harvest degradation. These results highlight the need of choosing parental lines for breeding operations while taking storage stability and nutritional quality into account. Abedin *et al.* (2022), Lv *et*

al. (2023) and Zhang *et al.* (2025) have revealed similar findings, highlighting the crucial significance of grain moisture content in determining storage performance and product quality. Ferric Reducing Antioxidant Power (FRAP) and DPPH radical scavenging activity assays were used to assess the antioxidant capacity of the foxtail millet genotypes. The DPPH test is frequently used to evaluate bioactive substances' capacity to transfer electrons or hydrogen atoms in order to neutralize free radicals. Since a lower extract concentration is needed to block 50% of the free radicals present, lower IC_{50} values imply higher antioxidant action. Girish *et al.* (2023) and Gulcin and Alwasel (2023) claim that DPPH radical scavenging activity is a trustworthy measure of antioxidant efficacy in materials produced from plants. Similarly, the FRAP assay quantifies antioxidants' capability to convert ferric ions (Fe^{3+}) to ferrous ions (Fe^{2+}). Greater reducing power and improved antioxidant potential are indicated by higher FRAP levels. Reducing capacity and antioxidant efficacy are strongly positively correlated, according to research by Gülçin (2014) and Gulcin and Alwasel (2025). LS continuously showed better antioxidant activity across the assessed genotypes, indicating the availability of higher amounts of bioactive phytochemicals. The increased concentration of phenolic chemicals and flavonoids, which are known to be important contributors to antioxidant activity in cereals, may be responsible for the improved antioxidant performance seen in LS. By acting as efficient hydrogen donors and free-radical scavengers, phenolic substances shield biological systems from oxidative damage. Increased phenolic content is directly linked to improved radical-scavenging activity and reducing power in cereal grains, according to Hernández-Rodríguez *et al.* (2019) and Sarker *et al.* (2020). Additionally, Shi *et al.* (2022) showed that phenolic compounds have potent antioxidant qualities and play a major role in neutralizing reactive oxygen species. Another significant class of secondary metabolites that support antioxidant defence mechanisms are flavonoids. By scavenging free radicals, chelating metal ions, inhibiting oxidative enzymes, and preventing lipid peroxidation, these substances increase antioxidant activity. Patil *et al.* (2024) emphasized the several ways whereby flavonoids enhance the antioxidant activity of diets produced from plants. The differences in flavonoid concentration between the genotypes of foxtail millet found in this study are in line with earlier findings by Wei *et al.* (2021) and Ye *et al.* (2025), who found that environmental factors and genotype were the main factors influencing flavonoid accumulation in cereal crops. The results of this study collectively show that genotypic variation and its interaction with environmental factors play a major role in determining the nutritional and antioxidant qualities of foxtail millet. This study's strong correlation between polyphenol content and antioxidant activity confirms earlier findings that flavonoids and phenolic compounds play a major role in millets' ability to promote health. Because of its advantageous combination of higher carbohydrate content, superior mineral composition, reduced moisture content, and enhanced antioxidant activity, LS stood out as the most promising genotype among those assessed. Because of these qualities, LS is a useful genetic resource for upcoming breeding initiatives meant to enhance functional food applications, storage stability, and nutritional quality. Additionally, as previously suggested by Sharma *et al.* (2015), the better antioxidant profile of LS supports its potential use in the creation of nutraceutical goods and health-promoting food compositions.

Conclusion

This study has provided several possibilities for future research and practical used for the improvement of foxtail millet. High-producing varieties, which are nutritional and rich in antioxidant were improved, through crossbreeding and selection procedures, using genetically improved varieties like LS, TS, and WS. Further, conducting field trial and property test research the outcome will determine the genes responsible for high protein, phenolic content, and antioxidative qualities through molecular markers and genomic analysis. Environmental effects could influence nutritional qualities, so multi-location and multi-season studies are important to conduct as well. The potential of flavonoids and phenolics as functional foods and health benefits quality will be validated by in vitro and in vivo studies on their bioavailability and metabolic effects. The discovered nutrient-rich genotypes may be used to produce functional foods, such as high nutraceuticals, and fortified foods, to boost customer acceptance and market value. More studies on shelf life, storage stability, and processing effects on nutritional and antioxidant characteristics would help commercialize and broaden use. This involves promoting the crop in development creation of better landraces and safeguarding indigenous genetic resources through community-based initiatives, sustainable usage and biodiversity preservation. The combination of nutritional, biochemical, and molecular approaches will hasten the development and use of foxtail millet as a climate-resilient and health-promoting crop.

Author contributions

Nokenketla Jamir: Writing original manuscript, methodology, formal analysis. Giridharan Bupesh: Supervision, interpretation of results, Validation. Longnyu M. Konyak and Sudharsan Parthasarathy: Formal analysis, interpretation of results, writing review and editing. Sidhartha Saikia: Writing review and editing. Chandresh Kumar Singh: contributed for Manuscript drafting, corrections and justification. All authors approved the final manuscript.

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