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Research Article

Amino Acid Composition of Selected Sesame Accessions and the Effect of Accelerated Ageing on Catalase Activity

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Abstract

This study investigated the influence of accelerated ageing on the amino acid composition and catalase (CAT) activity of various sesame (*Sesamum indicum* L.) seed accessions. Sesame seed accessions (NCRIBEN131, NCRIBEN106, NCRIBEN201, NCRIBEN121, and NCRIBEN203) were sourced from the experimental farm of the National Cereals Research Institute (NCRI) in Badeggi, Niger State, Nigeria. To simulate rapid deterioration, seeds were subjected to accelerated ageing at 42°C and 100% relative humidity for up to 6 days. Amino acid profiles were quantified using an automated amino acid analyzer, while catalase activity was determined spectrophotometrically at regular intervals (Day 0 to Day 6). The amino acid profiling revealed that the Total Non-Essential Amino Acids (TNEAA) class exhibited the highest concentration across all accessions, ranging from 147.24±5.28 mg/100g in NCRIBEN131 to 183.47±3.52 mg/100g in NCRIBEN106. The Total Essential Amino Acids (TEAA) and Total Aromatic Amino Acids (TARAA) concentrations were highest in accession NCRIBEN201 (72.54±0.95 mg/100g and 27.54±0.71 mg/100g, respectively), while accession NCRIBEN131 had the lowest TEAA (61.87±0.84 mg/100g) and accession NCRIBEN121 had the lowest TARAA (21.71±0.28 mg/100g). Among the individual amino acids, glutamic acid and arginine were highly prominent, peaking in concentration at 55.83±0.12 mg/100g (NCRIBEN203) and 37.89±0.01 mg/100g (NCRIBEN201), respectively Accelerated ageing significantly influenced catalase activity across the accessions. Accession NCRIBEN106 consistently exhibited the highest catalase activity throughout the ageing period, decreasing slightly from 31.96±0.21 mg/ml/min on Day 0 to 29.10±0.03 mg/mL/min on Day 6 (an 8.95% reduction). Conversely, accession NCRIBEN121 exhibited the highest vulnerability to ageing, demonstrating the largest percentage reduction in catalase activity (46.03%), dropping from 26.33±0.22 mg/mL/min on Day 0 to 14.21±0.81 mg/mL/min on Day 6 These results demonstrate that these sesame accessions are excellent sources of both essential and non-essential amino acids. Additionally, accelerated ageing leads to a significant, accession-dependent decline in catalase activity, reflecting a loss of cellular antioxidant defense capacity during seed deterioration.

Keywords: Accelerated ageing, Amino acid, Catalase activity, seed deterioration, Accessions Sesame seeds.

Introduction

Sesame (*Sesamum indicum*), belonging to the Pedaliaceae plant family, is among the world's most significant and ancient oilseed crops (Abou-Gharbia *et al.,* 2017). Its cultivation dates back to around 1500 BC in regions such as the Middle East, Asia, and Africa (Ali *et al*., 2017). These small, oil-rich seeds are widely used in cooking, salad, confectionary, and sesame oil production (Babagana *et al.,* 2021). The nutritional profile of sesame seeds, comprising proteins, fats, carbohydrates, fiber, minerals, vitamins, and bioactive compounds, makes them a valuable food source with numerous health benefits, including

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antioxidant properties, cholesterol reduction, blood lipid regulation, liver and kidney protection, cardiovascular system protection, as well as anti-inflammatory and anti-tumor effects (Wei *et al*., 2022).

Amino acids, the fundamental components of proteins, are vital for human nutrition and health. The amino acid profile of sesame seeds is crucial as it determines the seed's protein quality and its ability to meet human dietary needs (Sibt-e-Abbas *et al*., 2022). Catalase, an enzyme, is instrumental in protecting seeds from oxidative damage during storage and germination. The activity of catalase in sesame seeds indicates their capacity to withstand oxidative stress, maintain seed viability, and preserve overall quality.

Accelerated ageing is a technique that simulates the natural ageing and deterioration of seeds at an accelerated rate. It is used to predict seed storage potential and assess seed quality by exposing them to environmental stress factors such as high temperature and humidity. This method mimics real-world storage conditions, allowing for the examination of changes in various seed parameters, including amino acid composition and enzyme activity (Zhang *et al*., 2021). Understanding how accelerated ageing impacts the amino acid profile and catalase activity of sesame seeds is crucial for maintaining their nutritional quality and resilience to oxidative stress.

In the context of sustainable agriculture, enhanced knowledge of sesame seed quality and storage can lead to more efficient seed management practices, reducing seed wastage and promoting agricultural sustainability. Therefore, this study aims to evaluate the influence of accelerated ageing on amino acid composition and catalase activity of selected sesame seed accessions.

Materials and Methods

Samples collection

Sesame seeds were collected from the experimental farm of the National Cereal Research Institute (NCRI) in Badeggi, Niger State, Nigeria. Approximately 100 grams of mature sesame seeds were gathered, properly labeled, and air-dried. These seeds were then transported to the laboratory for further analysis. Twenty sesame accessions were initially characterized for oil yield, and five accessions (NCRIBEN201, NCRIBEN203, NCRIBEN131, NCRIBEN121, and NCRIBEN106) were selected for accelerated ageing. Prior to the initiation of the experiments, seed lots were screened to ensure high initial germination viability (>90%) and standardized to an initial moisture content of approximately 6.0%. The laboratory experiments were arranged in a Completely Randomized Design (CRD) with three independent replications.

Accelerated ageing treatment

To simulate rapid post-harvest seed deterioration, the sesame accessions were subjected to an accelerated ageing protocol. Replicate seed samples from each accession were distributed in a single layer over a nylon mesh suspended inside sealed plastic ageing boxes. The bottom of each box was filled with 100 mL of double-distilled water to maintain a relative humidity of 100% within the sealed headspace. The boxes were placed in a digital incubator at a constant temperature of 45^{o} c for five different durations: 0, 24, 48, 72, and 96 hours. Upon removal at each time point, the seeds were immediately transferred to a drying chamber at 25^{o}C and 45% relative humidity for 24 hours to restore their original moisture content before physiological and biochemical testing. Physiological Viability and Membrane Integrity Measurements Standard seed germination was assessed by placing three replicates of 100 seeds from each treatment on double-layered Whatman No. 1 filter papers moistened with sterile distilled water in 9cm Petri dishes. The dishes were were incubated at 25 pm 1^{o}C under a 12-hour light/dark cycle.

Amino acid analysis

Aminoacid profiling was performed using a validated pre-column pheynylisothiocyanate (PITC) derivatization method (Bindlingmeyer *et al*., 1984) for standard amino acids, sample aliquots (5g) were weighed into sterile furnace hydrolysis tubes, spiked with 5nmol of norleucine as an internal standard, and dried under vacuum. Vapor phase acid hydrolysis was conducted using10.5N HCL containing phenol at 180^{o} c for 20-23 hours under vacuum. To ensure reliable quantification of sensitive amino acids, separate preparation steps

were employed; Trptophan was determined following separate alkaline hydrolysis using 4.2 M NaOH at 110^{c} for 20 hours. (Bindlingmeyer *et al*., 1984).

Sulfur containing amino acids (cysteine/cysteine and methionine) were determined after pre-oxidation with performic acid at 0 C overnight to convert them to stable derivatives (cysteic acid and methionine sulfone, respectively) prior to acid hydrolysis step (Bindlingmeyer *et al*., 1984). Following hydrolysis, stage lasted for 20-23 hours at 180°C. Following hydrolysis, the samples were dissolved in ultrapure water (HPLC grade) containing ethylenediaminetetraacetic acid (EDTA) to chelate the metals and stored in analyzer vials.

The hydrolyzed samples were automatically derivatized on the Waters 616/626 HPLC by reacting the amino acids under basic conditions with thiocyanate (PITC) to obtain phenylthiocarbamyl (PTC) amino acid derivatives. This step lasted 45 minutes per sample, as calibrated on the instrument. A set of standard solutions of amino acids was prepared from Pierce Reference Standards H (1000 µmol) into autosampler vials, and they were also derivatized. These standards (0.0, 0.5, 1.0, 1.5, 2.0 µmol) were used to generate a calibration file to determine the amino acid contents of the samples. After derivatization, a methanol solution (1.5N) containing the PTC-amino acids was transferred to a narrow-bore Waters 616/626 HPLC system for separation. The separation and quantitation of the PTC-amino acids were performed on a reverse-phase (C18 silica) column, and the PTC chromophore was automatically and digitally detected at a wavelength of 254 nm.

The buffer system used for separation consisted of 140 mM sodium acetate at pH 5.50 as buffer A and 80% acetonitrile as buffer B. The program was run using a gradient of buffer A and buffer B concentrations, ending with a 55% buffer B concentration at the end of the gradient. The elution of all amino acids in the samples took 30 minutes.

Data interpretation and calculations

The intensity of the chromatographic peak areas was automatically and digitally identified and quantified using a Dionex Chromeleon data analysis system integrated with the Waters 616/626 HPLC System. A calibration curve, prepared from the average values of the retention times (in minutes) and areas (in Au) from 5 standard runs of amino acids, was used. Since a known amount of each amino acid in the standard was loaded into the HPLC, a response factor (Au/pmol) was calculated by the software integrated with the HPLC. This response factor was used to calculate the amount of each amino acid (in pmols) in the sample, which was displayed on the system digitally. The amount of each amino acid in the sample was ultimately calculated by the software by dividing the intensity of the peak area of each amino acid (corrected for the differing molar absorptivity of the various amino acids) by the internal standard (i.e., Pierce) in the chromatogram and multiplying this by the total amount of the internal standard added to the original sample. After determining the picomole intensity of the height of each amino acid by the software, the data and the digital chromatographic software extrapolated back to 5 nmoles of the internal standard (norleucine) and displayed the total amount that was pipetted into the hydrolysis tube at the beginning of the analysis.

$$\text{mg/ml (in Extract)} = \text{Dilution factor x Peak height intensity}$$

$$\text{mg/ml (in sample)} = \frac{\frac{ug}{ml}\ in\ extract\ X\ sample\ volume}{weight\ of\ sample}$$

Determination of catalase activity (CAT)

Two grams (2 g) of the seed were homogenized in an extraction buffer (pH 7.6) containing 10 mM EDTA and 10% (w/v) PVPP. The homogenates were then centrifuged at 12,000g for 15 minutes. Catalase activity was determined spectrophotometrically by monitoring the decomposition of H_2O_2 at 240 nm. The reaction mixture contained 50 mM potassium phosphate buffer (pH 7.0), the sample, and 10 mM H_2O_2. The assay was performed at 25°C in a 3 ml cuvette. Protein concentration was measured according to the Bradford method (1976) using bovine serum albumin as a standard.

$$\text{Catalase activity} = \frac{\Delta A240/\min(\text{sample}) - \Delta A240/\min(blank)}{0.0436}\ \text{X}\ 1.6$$

Where:
Δ240/min = change in absorbance at 240 nm/min of sample or blank
0.0436 = millimolar extinction coefficient of H_2O_2 at 240 nm
1.6 = total reaction mixture volume

Data analysis
Physiological and biochemical data were subjected to two-way ANOVA using the general linear model procedure of SAS. Significant differences among treatment means were determined using Duncan's Multiple Range Test at significant value of $p \leq 0.05$.

Results and Discussion
The essential amino acid content of sesame seed accessions is presented in Table 1. The essential amino acids are isoleucine, phenylalanine, methionine, tryptophan, valine, histidine, and threonine. The results showed that phenylalanine had the highest concentration in all the sesame accessions, ranging from 14.74±0.11 mg/100g in NCRIBEN201 to 12.22±0.04 mg/100g in NCRIBEN121, followed by valine, which ranged from 14.59±0.21 mg/100g in NCRIBEN201 to 12.06±0.10 mg/100g in NCRIBEN121. Tryptophan was observed to have the lowest concentration in all the accessions analyzed, ranging from 3.17±0.26 mg/100g in NCRIBEN131 to 3.88±0.01 mg/100g in NCRIBEN201. There was a significant ($P < 0.05$) difference in the concentrations of methionine, valine, histidine, and threonine amino acids in the accessions of sesame seed samples. The non-essential amino acid content of sesame seed accessions is presented in

Table 2. Non-essential amino acids, including alanine, cystine, glutamine, tyrosine, serine, asparagine, arginine, glycine, and proline, were listed. The results showed that glutamic acid had the highest concentration in all the sesame accessions, ranging from 55.83±0.12 mg/100g in NCRIBEN203 to 41.17±0.01 mg/100g in NCRIBEN131, followed by arginine, which ranged from 37.89±0.01 mg/100g in NCRIBEN201 to 33.90±0.10 mg/100g in NCRIBEN121. Cystine was observed to have the lowest concentration in all the accessions analyzed, ranging from 22.19±1.00 mg/100g in NCRIBEN106 to 4.30±0.08 mg/100g in NCRIBEN121.

Table 3 shows the aromatic amino acid content of sesame seed accessions. The aromatic amino acids, including phenylalanine, tyrosine, and tryptophan, were analyzed. The results revealed that phenylalanine had the highest concentration in all sesame accessions, ranging from 14.74±0.08 mg/100g in NCRIBEN201 to 12.22±0.03 mg/100g in NCRIBEN121. Tryptophan was observed to have the lowest concentration in all the analyzed accessions, ranging from 3.17±0.10 mg/100g in NCRIBEN131 to 3.88±0.11 mg/100g in NCRIBEN201. There was no significant ($p > 0.05$) difference in the concentrations of tyrosine, tryptophan, and phenylalanine amino acids among the accessions NCRIBEN201, NCRIBEN203, and NCRIBEN106.

Table 4 shows the summing of raw values of the individual amino acids reveals a high nutritional concentration in all tested accessions. Total non-essential amino acids (TEAA) formed the largest fraction across all sesame accessions, ranging from 147.24mg/100g in NCRIBEN131 to 182.25mg/100g in NCRIBEN201. Total essential amino acids (TEAA) were highest in NCRIBEN 201(72.54mg/100g) and lowest in NCRIBEN121 (65.51mg/100g). Similarly, total aromatic amino acids (TARAA) were most abundant in accession NCRIBEN 201 (27.54mg/100g) and the lowest in NCRIBEN121 (21.71mg/100g).

The amino acid compositions determined in this study demonstrate that sesame (*Sesamum indium* L.) seeds represent an excellent source of both essential and non-essential amino acids. Sesame proteins are rich in glycine, leucine, methionine, phenylalanine, arginine, aspartic acid, and glutamic acid. Compared to other oilseeds, such as melon seeds, sesame profiles feature significantly higher levels of vital essential amino acids, including lysine, methionine, serine, leucine, glycine, and valine (Crews *et al*., 2016).

Consistent with the findings of Darmstadt *et al*. (2017), who demonstrated that aspartic acid among the five NCRIBEN varieties point toward genetic diversity, matching observations by Tashiro *et al*. (2017) regarding the control exerted by crop genotypes on amino acid biosynthesis.

Comparative analysis reveals that raw and locally processed seeds of *Ricinus communis* contain higher overall concentrations of TEAA, TNEAA, and TARAA than those recorded in our sesame accessions (Igwe *et al*., 2017). However, the relative proportions of these amino acid groups within the overall protein content of *S. indicum* L. are comparable. Furthermore, our findings for accession NCRIBEN106 are in alignment with those of Grieshop and Fahey (2016) and Karr-Lilienthal *et al*. (2015), who reported lower relative concentrations of TEAA and TNEAA in soybean meals from northern zones of the United States. In contrast, (Goel *et al*., 2012) observed higher TEAA concentrations in soybean compared to our highest-performing accession, NCRIBEN201. Additionally, kidney beans and cowpea (*Vigna unguiculata* L. Walp) seeds exhibit higher concentrations of TNEAA and TARAA than those recorded here (Goel *et al*., 2012; Crews *et al*., 2016). Despite these comparisons, the overall TEAA concentration of sesame seeds (66.37±0.16 mg/100g) exceeds that documented for chicken eggs (50.12±0.16 mg/100g) by the Food and Agriculture Organization (FAO, 2019), underlining the high biological value of sesame seed protein.

The effect of accelerated ageing on catalase (CAT) activity is summarized in Table 5. On Day 0, catalase activity was highest in NCRIBEN106 (31.96±0.21 mg/mL/min) and lowest in NCRIBEN203 (20.21±0.76 mg/mL/min). Intriguingly, rather than demonstrating a direct, continuous decline, accession NCRIBEN106 showed a minor initial increase in catalase activity from Day 0 (31.96±0.21 mg/mL/min) to Day 3 (33.05±0.02 mg/mL/min) before dropping significantly on Day 6 (29.10±0.03 mg/mL/min). This initial transient spike on Day 3 likely represents an adaptive cellular defence mechanism triggered by early oxidative stress. By Day 6, all sesame seed accessions experienced a significant decline in catalase activity. The rate of catalase activity depletion varied sharply across genotypes. NCRIBEN121 exhibited the highest vulnerability to accelerated ageing, experiencing a 46.03% reduction in activity by Day 6. Conversely, NCRIBEN131 proved to be the most resilient accession, exhibiting a minimal catalase reduction of only 9.19%.

Concerning enzyme degradation under storage stress, the marked decrease in catalase (CAT) activity under accelerated ageing observed in this study conforms to trends noted in soybean seeds (Kabinza *et al*., 2016; Nadeem *et al*., 2015). This pattern of cellular decline matches reports by Rao *et al*. (2017) on onion seed storage, as well as observations by Chauhan *et al*. (2017) on enzyme activity decay in naturally and accelerated aged wheat seeds.

Crucially, our study captured an early, transient upregulation of catalase activity on Day 3 (notably in accession NCRIBEN106). This fluctuation suggests a momentary surge in the plant's antioxidant defences to scavenge accumulating reactive oxygen species (ROS) before the onset of advanced physiological decay on Day 6. Catalase acts as an essential antioxidant within plant seeds, protecting vital structures from oxidative stress and supporting viability during germination. Depleted catalase activity serves as a primary marker of seed deterioration, warning of reduced germination rates and structural decay (Ayse *et al*., 2017).

Conclusion

This study provides key insights into the impact of accelerated ageing on the amino acid profile and catalase activity of *Sesamum indicum* L. accessions. Sesame seeds are confirmed as excellent reservoirs of essential and non-essential amino acids, characterized by high concentrations of glutamic acid and arginine. Accelerated ageing, however, precipitates a significant decline in catalase activity. This enzymic degradation, likely worsened by seed coat fracturing and intracellular leakage during stressful storage, has serious implications. The resulting oxidative vulnerability compromises seed viability, agricultural yield, industrial shelf-life, and the downstream nutritional benefits of the seeds.

Recommendations

1. Farmers, seed banks, and agricultural organizations should be cautious about the storage conditions of sesame seeds. Implementing proper storage practices, such as maintaining lower temperatures and reducing mechanical damage during handling, can help preserve the catalase activity and overall seed quality.

2. The food industry should consider the high amino acid content of sesame seeds when formulating products, especially those aimed at improving protein quality. This can lead to the development of enhanced food products with improved nutritional profiles.

3. The nutritional value of sesame seeds, particularly their amino acid content, should be promoted in dietary guidelines and public awareness campaigns. Encouraging the consumption of sesame seeds can contribute to a more balanced and nutritious diet.

Authors' Contributions

All authors contributed equally to this research, such as data curation, formal analysis, funding acquisition, investigation, methodology, software supervision, validation, writing review and editing. All authors read and approved the manuscript.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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Table 1: Concentration of essential amino acids (EAA) in mg/100g

Accession	ISO	PHL	TRP	VAL	MET	HIS	THR
NCRIBEN106	11.18±0.11^{c}	13.18±0.07^{bc}	3.71±0.06^{a}	12.96±0.21^{a}	7.27±0.01^{a}	8.12±0.03^{ab}	9.07±0.04^{ab}
NCRIBEN121	10.70±0.01^{ab}	12.22±0.04^{a}	3.19±1.01^{a}	12.06±0.10^{a}	7.51±0.01^{a}	7.55±0.11^{a}	8.28±0.10^{a}
NCRIBEN131	10.56±0.02^{ab}	12.63±0.42^{a}	3.17±0.26^{a}	12.26±0.11^{a}	7.16±0.02^{a}	7.52±0.04^{a}	8.57±0.01^{a}
NCRIBEN201	11.51±0.02^{a}	14.74±0.11^{c}	3.88±0.01^{a}	14.59±0.21^{b}	8.45±0.25^{b}	8.87±0.01^{b}	10.50±0.14^{b}
NCRIBEN203	11.19±0.01^{a}	14.16±0.12^{c}	3.83±0.20^{a}	14.28±0.24^{b}	8.40±0.10^{b}	8.71±0.02^{b}	9.91±0.11^{ab}

Values are mean ± standard error of mean of three determinations. Values with different superscript along the column are significantly ($p < 0.05$) different. ISO = Isoleucine; PHL = Phenylalanine; TRP = Tryptophan; VAL = Valine; MET = Methionine; HIS = Histidine; THR = Threonine

Table 2: Concentration of non-essential amino acids (NEAA)

Accession	ALA	CYST	GLY	TY	SE	ARG	ASP	GLU	PRO
NCRIBEN106	12.89±0.01^{b}	22.19±1.00^{c}	13.59±1.14^{bc}	7.28±0.41^{b}	9.63±0.11^{b}	36.35±0.01^{b}	22.89±0.50^{a}	50.33±0.02^{c}	8.36±0.31^{b}
NCRIBEN121	12.17±0.02^{a}	4.30±0.08^{a}	11.98±0.17^{a}	6.30±0.03^{a}	8.54±0.10^{a}	33.90±0.10^{a}	21.64±0.07^{a}	46.18±0.10^{b}	7.67±0.14^{a}
NCRIBEN131	12.61±0.12^{b}	4.41±0.02^{a}	12.72±3.10^{b}	6.81±0.02^{a}	9.21±0.61^{b}	34.16±0.02^{ab}	22.41±1.11^{b}	41.17±0.01^{a}	8.07±0.28^{b}
NCRIBEN201	14.31±0.15^{c}	5.76±0.10^{b}	15.83±0.02^{c}	8.92±0.12^{a}	11.45±0.08^{c}	37.89±0.01^{c}	24.58±0.01^{d}	54.66±0.03^{d}	9.47±0.20^{c}
NCRIBEN203	14.10±0.09^{c}	5.48±0.01^{b}	15.02±1.04^{c}	7.86±0.04^{b}	11.72±0.02^{c}	37.81±0.21^{c}	23.33±0.02^{c}	55.83±0.12^{e}	9.29±0.21^{c}

Values are mean ± standard error of mean of three determinations. Values with different superscript along the column are significantly ($p < 0.05$) different. ALA = Alanine; CYST = Cysteine; GLY = Glycine; TY = Tyrosine; SE = Selenocysteine; ARG = Arginine; ASP = Aspartic Acid; GLU = Glutamic Acid; PRO = Proline

Table 3: Concentration of aromatic amino acids (ARAA)

Accession	PHL	TRP	TY
NCRIBEN106	13.18±0.17^{bc}	3.71±0.06^{a}	7.28±0.01^{c}
NCRIBEN121	12.22±0.03^{c}	3.19±0.12^{b}	6.30±0.13^{a}
NCRIBEN131	12.63±0.13^{c}	3.17±0.10^{b}	6.81±0.42^{b}
NCRIBEN201	14.74±0.08^{a}	3.88±0.11^{a}	8.92±0.52^{d}
NCRIBEN203	14.16±0.11^{ab}	3.83±0.23^{a}	7.86±0.17^{c}

Values are mean ± standard error of mean of three determinations. Values with different superscript along the column are significantly ($p < 0.05$) different. PHL = Phenylalanine; TRP = Tryptophan; TY = Tyrosine

Table 4: Comparison of Total Amino Acid Concentration (TEAA, TNEAA, TARAA)

Accession	**TEAA**	**TNEAA**	**TARAA**
NCRIBEN106	65.49±0.61b	183.47±3.52a	24.17±0.24bc
NCRIBEN121	65.51±1.48c	151.38±0.81b	21.71±0.28d
NCRIBEN131	61.87±0.84c	147.24±5.28b	22.61±0.62cd
NCRIBEN201	72.54±0.95a	182.25±0.70a	27.54±0.71a
NCRIBEN203	70.88±0.80ab	180.51±1.94a	25.85±0.51ab

TEAA (Total Essential Amino Acids) = Sum of ISO, PHL, TRP, VAL, MET, HIS, THR. TNEAA (Total Non-Essential Amino Acids) = Sum of ALA, CYST, GLY, TY, SER, ARG, ASP, GLU, PRO. TARAA (Total Aromatic Amino Acids) = Sum of PHL, TRP, TY.

Note: Cumulative values are compiled and expressed as the sum of means ± propagated standard error of three determinations. Superscript letters denote significant differences ($p<0.05$) among accessions within the same column.

Table 5: Effect of Accelerated Ageing on Catalase Activity (mg/mL/min) and Percentage Reduction

Accession	Day 0	Day 3	Day 6	% Reduction]
NCRIBEN106	31.96±0.21a	33.05±0.02b	29.10±0.03b	8.95%
NCRIBEN121	26.33±0.22a	14.56±0.54b	14.21±0.81b	46.03%
NCRIBEN131	29.36±0.35a	27.02±0.28b	26.66±0.24c	9.19%
NCRIBEN201	22.18±1.03a	21.42±0.47ab	15.16±0.61b	31.65%
NCRIBEN203	20.21±0.76a	19.19±0.55a	18.40±0.47b	8.96%

Note: Values are mean ± standard error of three determinations. Values with different superscript letters along the column for a given accession represent a significant difference ($p<0.05$) across the ageing period.