FUDMA Journal of Sciences (FJS)
ISSN online: 2616-1370
ISSN print: 2645 - 2944
Vol. 10 No. 18, September, 2026, pp 171 – 180
DOI: https://doi.org/10.33003/fjs-2026-1018-5863

Storage Fungal Load, Community Diversity, and Mycotoxigenic Risk in Stored Groundnut Seeds Across Niger State, Nigeria

***[1]Musa Muhammad Liman, [1]Adebola Matthew Omoniyi, [2]Muhammad Hadiza Lami, [1]Bello Ismail Muhammad, [3]Aremu Mariam Bukola, [1]Kabaraini Maryam Alfa and [1]Ishaq Aisha Muhammad**

[1]Department of Plant Biology, Federal University of Technology Minna, Niger State, Nigeria.
[2]African Centre of Excellence for Mycotoxin and Food Safety, Federal University of Technology Minna, Niger State, Nigeria.
[3]Nigerian Stored Products Research Institute, Ibadan, Oyo State, Nigeria.

*Corresponding authors' email: musaliman25@gmail.com

Received: 07 Sep. 2026
Accepted: 15 Sep. 2026
Published: 24 Sep. 2026

ABSTRACT
Postharvest losses in stored groundnut remain high across Niger State, Nigeria, driven substantially by fungal colonization under the region's humid, high-temperature storage conditions. This study assessed fungal load, mycoflora community structure, and qualitative toxigenic potential across twelve Local Government Areas (LGAs) spanning three agro-ecological zones, using 98 seed samples analyzed by standard microbiological isolation and toxigenic screening on Coconut Agar Medium under UV fluorescence (365 nm). Fungal load ranged from 11 × 10^3 CFU/g (Chanchaga) to 28 × 10^3 CFU/g (Mokwa), with the highest-burden LGAs concentrated in the wetter south-western storage belt. A total of 346 isolates spanning six genera were recovered, dominated by *Aspergillus* spp. (67.4%; principally *A. niger*, *A. flavus*, *A. fumigatus*), and 58.0% (n = 201) of isolates showed potential for mycotoxin production. Multivariate community analysis (PCA, hierarchical clustering) and diversity indices (mean H' = 2.02, J' = 0.92) resolved three geographically coherent storage-risk zones, extending prior isolate-frequency surveys of Nigerian stored groundnut mycoflora by linking community structure directly to spatial storage risk. These findings support targeted, zone-specific postharvest management to reduce losses and consumer exposure to mycotoxins.

Keywords: Groundnut, diversity, *mycoflora*, *aflatoxin*, *toxigenic fungi*, food safety, Niger State

INTRODUCTION

The groundnut (*Arachis hypogaea* L.) is one of West Africa's highest-priority food legumes, valued for its edible oil, protein, and role in farmer income, livestock feed, and agro-industry (Pedro et al., 2022; Abdullahi et al., 2023; Çiftçi and Suna, 2022). Nigeria is among Africa's leading producers, with cultivation concentrated in the northern Guinea and Sudan savannah zones (Bakoye et al., 2019). Despite strong production and market demand, postharvest losses remain high, driven substantially by poor storage practices, inadequate drying, and fungal deterioration (Amaechi et al., 2021; Adetunji et al., 2021). The high lipid and nutrient content of stored groundnut seeds makes them particularly susceptible to fungal colonization once in storage (Adetunji et al., 2021); losses of this kind are generally expected to reduce farmer income and seed viability and to constrain access to export markets where contamination limits are strictly enforced, though this study did not directly measure economic loss, seed germination, or trade outcomes, and these connections should be read as motivation for the work rather than as findings.

Storage-associated fungal contamination is a globally recognized threat to grain and oilseed quality, safety, and marketability (Pedro et al., 2022; Gide et al., 2025). High relative humidity, poor ventilation, and temperature fluctuations within storage facilities promote colonization by xerophilic and storage-associated fungi (Kumar et al., 2022), and the resulting losses are compounded where storage infrastructure and drying technology remain rudimentary. Fungal toxin production frequently begins well before visible spoilage, which limits the reliability of visual inspection as a storage-monitoring tool in many Nigerian systems (Olukosi and Yusuf, 2021; Abdullahi & Dandago, 2022) and underscores the need for laboratory-based screening embedded within routine postharvest handling.

Beyond the storage-loss dimension, several of the fungal genera implicated in postharvest spoilage majorly *Aspergillus*, *Penicillium*, and *Fusarium* also produce secondary metabolites responsible for carcinogenic and nephrotoxic mycotoxins (Martínez-Culebras et al., 2021; Najjar, 2023). Aflatoxins, produced mainly by *Aspergillus flavus* and *A. parasiticus*, are linked to hepatocellular carcinoma, immunosuppression, and acute aflatoxicosis (IARC, 2023; Mwanza et al., 2021), while fumonisins, ochratoxins, and alternariol derivatives are associated with nephrotoxicity and chronic metabolic dysfunction (Najjar, 2023; Saleh et al., 2024). Nigerian studies have repeatedly reported high aflatoxin levels in stored feeds, legumes, cereals, and nuts, with consequences for both public health and trade access (Suleiman and Atehnkeng, 2022; Adebiyi et al., 2024).

Given this toxin burden, a screening method that is cheap, fast, and deployable at or near the point of storage is of direct practical value: Coconut Agar Medium (CAM) fluorescence screening under UV light remains widely used in Nigerian laboratories for exactly this purpose, offering a low-cost, operationally simple preliminary method for flagging likely aflatoxigenic isolates within storage-monitoring programs (Mahato et al., 2019; Naveen and Vidyasagar, 2021).

Existing surveys of Nigerian stored-groundnut mycoflora have largely reported isolate frequencies and toxigenic screening in isolation, without linking fungal community structure to spatial risk patterns across contiguous storage zones (Bakoye et al., 2019; Gide et al., 2025). This study

interprets community structure through the lens of niche differentiation and, where richness tracks total abundance, the intermediate disturbance hypothesis: storage conditions act as an environmental filter shaping which taxa co-occur at a given site, so diversity indices and multivariate ordination are used here as proxies for storage-environment heterogeneity rather than as purely descriptive statistics humidity, ventilation, and residue load were not measured directly at each facility, so the fungal community's structure stands in for the storage conditions that produced it. From a storage-management standpoint, this leaves a practical gap: postharvest interventions are typically designed at the level of individual facilities or LGAs, yet the ecological drivers of contamination risk operate at the scale of agro-ecological zones. The present study addresses this gap by combining fungal-load assessment with multivariate community analysis (principal component and hierarchical cluster analysis), diversity indices, and GIS-based spatial mapping, alongside qualitative toxigenic screening, to characterize storage-risk zones across Niger State rather than isolated storage sites.

Accordingly, this study investigated fungal load, community diversity and spatial distribution, and qualitative toxigenic potential of fungi isolated from stored groundnut seeds across twelve selected Local Government Areas of Niger State, Nigeria, with the aim of informing zone-specific postharvest storage and monitoring recommendations. The predominance of Aspergillus and the high prevalence of *A. flavus* and *A. parasiticus* corroborate earlier Nigerian surveys; the contribution specific to this study is the spatial zonation derived from community structure, which has not previously been used to prioritize storage interventions within the state.

MATERIALS AND METHODS

Study Area

The study was carried out using stored groundnut seed samples collected from twelve selected Local Government Areas (LGAs) across the three agricultural zones of Niger State, Nigeria: Zone I (Bida, Mokwa, Lavun, Agaie), Zone II (Chanchaga, Bosso, Shiroro, Suleja), and Zone III (Wushishi, Kontagora, Borgu, Mashegu). These LGAs represent major agricultural and storage regions for groundnut production and commercialization.

Sample Collection

Ninety-eight stored groundnut seed samples were randomly collected from local storage facilities, farmer warehouses, and retail outlets across the selected LGAs, aseptically packaged in sterile polyethylene bags, labeled, and transported to the Mycology Laboratory, Department of Plant Biology, Federal University of Technology, Minna, Nigeria.

Media Preparation

Potato Dextrose Agar (PDA): 39 g of PDA powder was suspended in 1000 mL distilled water, dissolved by heating, and sterilized by autoclaving at 121 °C for 15 minutes (Adebola et al., 2020).

Coconut Agar Medium (CAM): 50 g of shredded coconut was mixed with 200 mL hot distilled water, boiled for five minutes, and filtered through four layers of cheesecloth; the filtrate was adjusted to pH 7, combined with 10 g agar, boiled for 10 minutes, made up to 500 mL, and sterilized at 121 °C for 15 minutes (Sowmya and Ramalingappa, 2024).

Determination of Fungal Load

Fungal load was determined by serial dilution as described by Adebola et al. (Adebola et al., 2020). One gram of homogenized groundnut seed sample was suspended in 9 mL sterile distilled water and serially diluted to the third fold (10^{-3}); 1 mL of the third-fold dilution was inoculated onto PDA supplemented with 0.5 mL chloramphenicol, plated in triplicate, and incubated at 28 ± 2 °C for 5 days. Fungal load was expressed as mean ± SD CFU/g across replicates.

Isolation and Purification

Fungal colonies were sub-cultured repeatedly on fresh PDA to obtain pure cultures, which were stored on PDA slants at 4 °C for subsequent identification and toxigenic screening (Adebola et al., 2020; Yakubu et al., 2022).

Identification of Fungal Isolates

Isolates were identified from macroscopic colonial characteristics (texture, pigmentation, growth rate, sporulation pattern, reverse plate coloration) and microscopic examination using lactophenol cotton blue staining, with reference to standard mycological identification keys (Sarah et al., 2016).

Community Structure Analysis (PCA and Hierarchical Clustering)

To resolve storage-risk groupings among LGAs, the standardized 12 × 10 species-by-site abundance matrix (z-score normalized) was analyzed by principal component analysis via singular value decomposition (scikit-learn v1.3 (Pedregosa et al., 2011)), retaining components by scree-plot inflection and projecting site scores and species-loading vectors jointly onto the PC1–PC2 plane as a biplot, and by Ward's minimum-variance hierarchical clustering on squared Euclidean distance (Ward, 1963), with cluster number set by Mojena's stopping rule (Mojena, 1977) and validated against PCA site scores. The 12 × 10 matrix is comparatively small for SVD-based ordination, so higher-order component loadings (PC5–PC10) were not interpreted; the 98-sample, triplicate-plate design was set to balance laboratory feasibility against adequate power for the ANOVA and correlation analyses reported in Section 3.

Mycological Diversity Indices

Four alpha-diversity metrics were computed per LGA (Robertson et al., 2023): the Shannon–Wiener index (H'), Simpson's index (1-D), Margalef's richness index (D_Mg), and Pielou's evenness index (J' = H'/ln S). One-way ANOVA tested whether total isolate abundance, each diversity index, and abundance across the ten recovered taxa differed significantly among the three hierarchical clusters and among taxa, respectively; Pearson's product-moment correlations assessed relationships between H', species richness, and total isolate abundance.

GIS Spatial Distribution Mapping

Bubble maps of total isolate abundance and Shannon diversity were constructed from georeferenced LGA centroids using matplotlib v3.8 (WGS 84), with symbol size proportional to metric magnitude and colour encoding cluster membership; spatial patterns were interpreted relative to agro-ecological zone boundaries (Robertson et al., 2023).

Qualitative Screening for Mycotoxin Production

Fungi were screened for toxin production by inoculating 4-mm agar plugs onto sterilized CAM, incubating at 28 ± 2 °C for 7 days, and visually evaluating fluorescence under long-wave UV illumination (λ = 365 nm); blue-green or greenish-yellow fluorescence beneath colonies indicated aflatoxin-production capability (B1, B2, G1, G2) (Sowmya and Ramalingappa, 2024).

Statistical Analysis

Fungal-count data were analyzed by descriptive statistics and one-way ANOVA, with means separated using Duncan's Multiple Range Test at $P < 0.05$. Graphs were produced using Python's SciPy package.

RESULTS AND DISCUSSION

Fungal Load of Stored Groundnut Seeds

Fungal load differed significantly among locations ($P < 0.05$; means separated by Duncan's Multiple Range Test). Mokwa recorded the highest fungal load (28 ± 1.29 × 10^3 CFU/g), followed by Agaie (24 ± 1.25 × 10^3 CFU/g), while Chanchaga recorded the lowest (11 ± 2.86 × 10^3 CFU/g). The overall order was Mokwa > Agaie > Borgu = Lavun = Kontagora > Bida > Mashegu > Suleja > Bosso > Wushishi > Shiroro > Chanchaga. Zone I recorded the highest zonal load (23.8 × 10^3 CFU/g), followed by Zone III (19.6 × 10^3 CFU/g), with Zone II lowest (14 × 10^3 CFU/g).

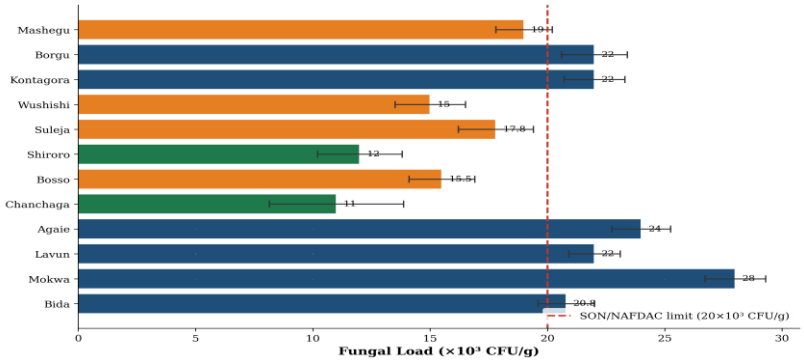

Figure 1: Mean Fungal Load (×10^3 CFU/g) of Stored Groundnut Seeds Across Sampled LGAs (mean ± SEM). Red dashed line = SON/NAFDAC indicative limit. Blue = high load (≥ 20×10^3); orange = moderate (15–20×10^3); green = lower (< 15×10^3).

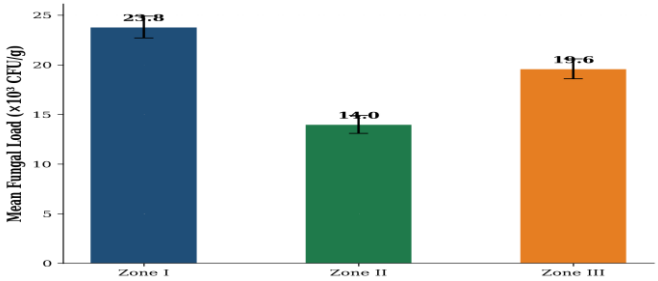

Figure 2: Mean fungal load across agro-ecological zones of Niger State

Occurrence and Distribution of Mycoflora

A total of 346 fungal isolates spanning six genera (*Aspergillus*, *Fusarium*, *Penicillium*, *Alternaria*, *Rhizopus*, *Absidi*a) were recovered. Aspergillus predominated (67.36%), followed by Rhizopus (9.82%), with *Absidia* lowest (2.31%). Within *Aspergillus*, *A. niger* was most frequent (26.30%), followed by *A. flavus* (17.60%) and *A. terreus* (6.69%). Zone I yielded the most isolates (148; 42.77%), while Zone II yielded the fewest (74; 21.39%). *A. flavus* was especially common in Mokwa and Agaie, while *A. parasiticus* was broadly distributed; A. fumigatus and A. terreus occurred at multiple sites with variable abundance, and Fusarium and Penicillium showed notable occurrence relative to Alternaria and Rhizopus, which were confined to selected locations. Abundance differed significantly among the ten recovered taxa (one-way ANOVA, $F(9,110) = 28.12$, $p < 0.0001$, $\eta^2 = 0.70$); *A. niger* recorded the highest mean abundance (M = 7.58, SD = 1.83) and A. flavus the second highest (M = 5.08, SD = 1.78), while *Absidia* sp. recorded the lowest (M = 0.67, SD = 0.65).

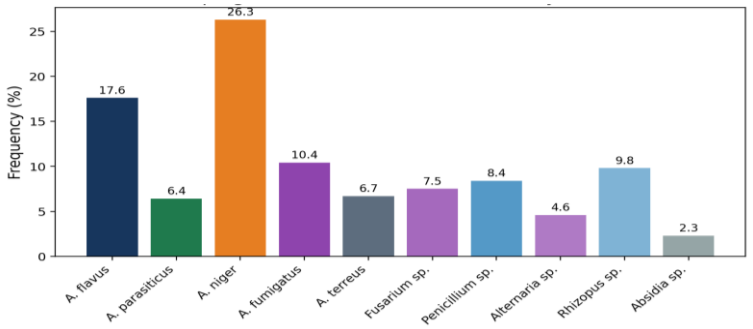

Figure 3: Percentage Frequency Distribution of Fungal Isolates from Stored Groundnut Seeds Across All Sampled LGAs (N = 346 colonies). *Aspergillus* species collectively represent 67.36 % of all isolates.

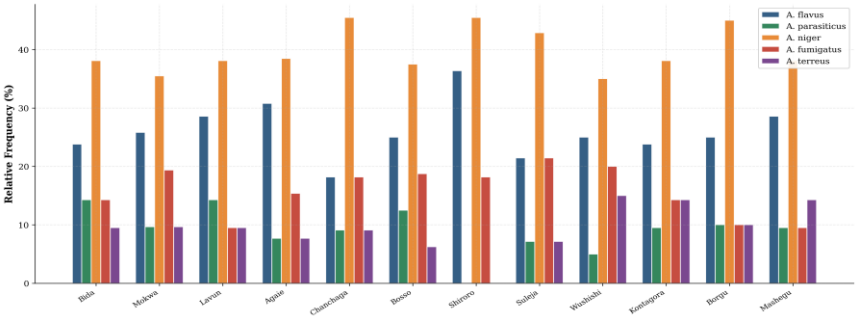

Figure 4: Relative Frequency (%) of Five Major *Aspergillus* Species Across the 12 Sampled LGAs.

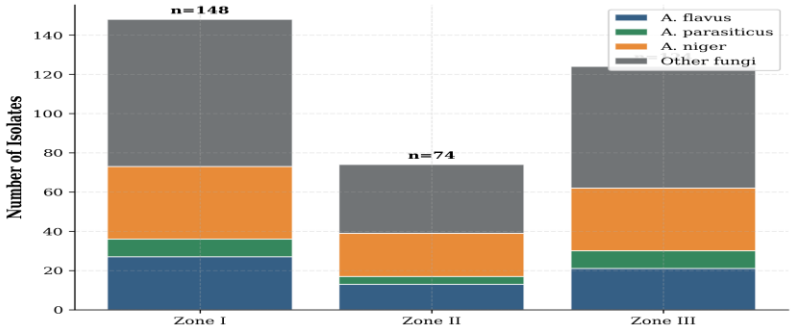

Figure 5: Stacked Distribution of Fungal Isolates across Agro-ecological Zones. Zone I accounted for 42.77 % of all isolates.

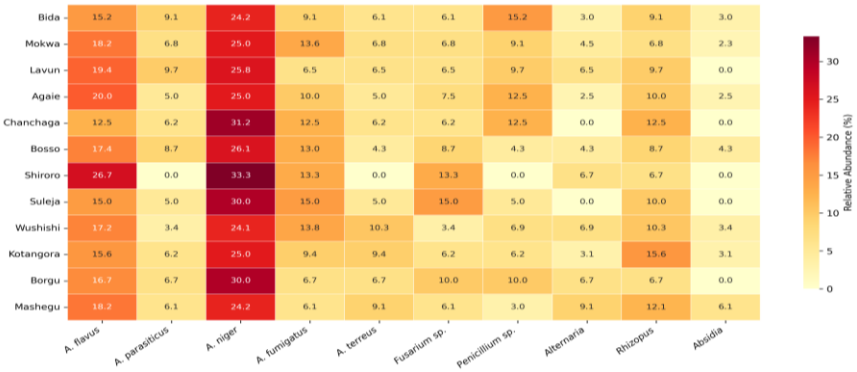

Figure 6: Heatmap of row-normalised relative fungal species abundance (%) per sample area. Colour intensity (yellow-orange-red) indicates proportional abundance. Italic column labels denote fungal taxa

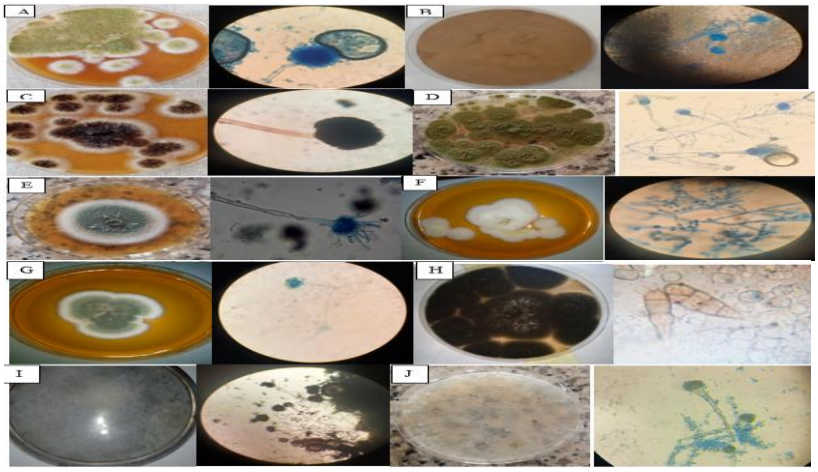

Figure 7: Pure cultures and photomicrographs of fungal isolates recovered from stored groundnut seeds

A. Pure culture and Photomicrograph of *Aspergillus flavus,*

B. Pure culture and Photomicrograph of *Aspergillus parasicus*
C. Pure culture and Photomicrograph of *Aspergillus terreus*
D. Pure culture and Photomicrograph of *Aspergillus niger*
E. Pure culture and Photomicrograph of *Aspergillus fumigatus*
F. Pure culture and Photomicrograph of *Penicillium crysogenum*
G. Pure culture and Photomicrograph of *Fusarium moniliforme,*
H. Pure culture and Photomicrograph of *Alternaria alternata*
I. Pure culture and Photomicrograph of *Rhizopus stolonifera*
J. Pure culture and Photomicrograph of *Absidia* species

Community Structure Across Storage Sites

PCA of the standardized 12 × 10 matrix yielded ten components; PC1 and PC2 together explained 70.40% of total variance (Table 1), which we adopted as an internal benchmark consistent with conventional community-ecology practice of retaining components jointly explaining ≥60% of variance (Robertson et al., 2023), and the scree plot supported a two-component ordination. Given the comparatively small 12 × 10 matrix, this two-component solution is best treated as a stable summary rather than an exhaustive description of community structure.

Table 1: PCA Eigenvalues and Cumulative Variance Explained for Fungal Community Data

Component	Eigenvalue	Variance (%)	Cumulative Variance (%)
PC1	5.331	53.31	53.31
PC2	1.709	17.09	70.40
PC3	0.887	8.87	79.27
PC4	0.793	7.93	87.20
PC5	0.528	5.28	92.49
PC6–PC10	0.752 (pooled)	7.51	100.00

All taxa loaded positively on PC1 (0.170–0.409), consistent with a general abundance gradient, while PC2 separated *Fusarium* and *Penicillium* (positive) from *Absidia*, *Alternaria*, and *Rhizopus* (negative) a split consistent with a moisture-availability gradient across storage sites. Ward-linkage clustering, validated against these PCA scores, resolved three storage-risk groupings (Table 2): Cluster I, four low-abundance LGAs; Cluster II, two high-abundance sites (Mokwa, Agaie); and Cluster III, six LGAs at intermediate-to-high abundance and near-maximal richness.

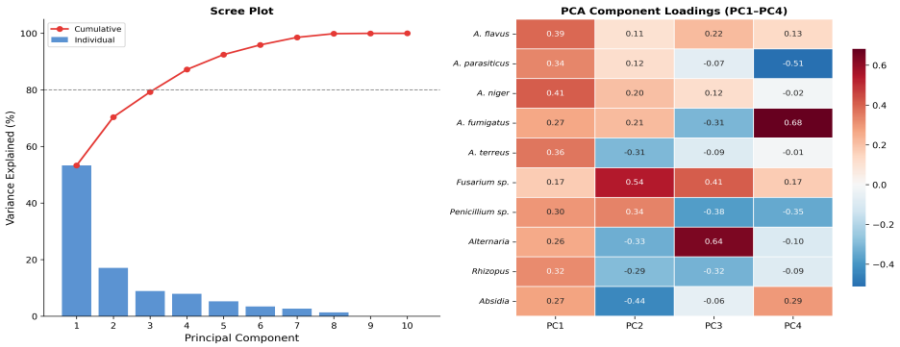

Figure 8: Left: Scree plot showing individual (bars) and cumulative (line) variance explained by each principal component. Dashed line indicates the 80% threshold. Right: Heatmap of PCA component loadings (PC1–PC4) for all ten fungal taxa

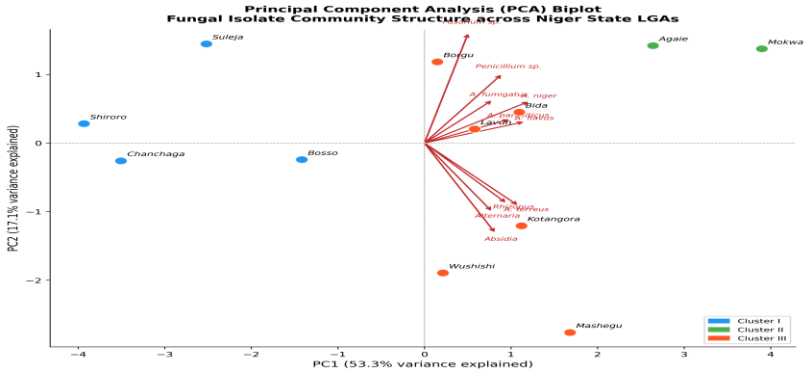

Figure 9: PCA biplot of fungal community structure across twelve Niger State LGAs. Site scores (circles, colour-coded by cluster) and species loading vectors (red arrows) are jointly projected onto the PC1-PC2 plane. Variance explained by each axis is indicated in parentheses.

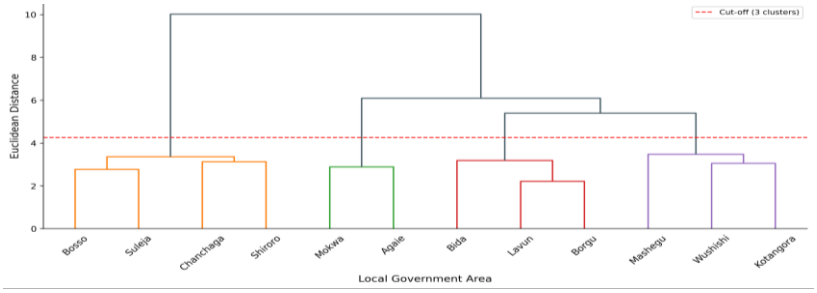

Figure 10: Hierarchical dendrogram (Ward linkage, Euclidean distance) depicting fungal community similarity among twelve Niger State LGAs. Red dashed line indicates the optimal cut-off for three-cluster delineation. Vertical axis represents Euclidean distance.

Table 2

Cluster	LGA Members	Abundance Range	Mean Richness	Ecological Characterization
I	Chanchaga, Bosso, Shiroro, Suleja	15–23	8.0	Low-abundance, reduced diversity
II	Mokwa, Agaie	40–44	10.0	High-abundance, maximal richness
III	Bida, Lavun, Wushishi, Kontagora, Borgu, Mashegu	29–33	9.7	Intermediate-high, stable community

Diversity Indices and Storage Risk

Shannon–Wiener H' ranged from 1.62 (Shiroro) to 2.13 (Mashegu), mean 2.02 ± 0.13; Shiroro's low value reflects both reduced richness (S = 6) and the absence of *A. parasiticus* and *Penicillium* at that site. Simpson's index (1-D) varied narrowly (0.829–0.893), indicating consistently high dominance resistance. Margalef's richness varied more widely (1.846–2.870), highest in Bosso and Wushishi. Pielou's evenness (J') remained uniformly high (0.903–0.934) across all sites, indicating no single species disproportionately dominated any community. Shannon H' correlated positively and significantly with total isolate counts (r = 0.628, 95% CI [0.084, 0.883], p = 0.029). Species richness (S) also correlated positively with total isolate counts (r = 0.729, 95% CI [0.267, 0.919], p = 0.007), and richness correlated more strongly with H' itself (r = 0.903, p < 0.0001) than either metric did with raw abundance, indicating that community richness, more than total isolate load per se, underlies the Shannon index values reported here.

A one-way ANOVA testing whether these metrics differed among the three hierarchical clusters (Section 3.4) showed that total isolate abundance (N) and Pielou's evenness (J') differed significantly by cluster (N: $F(2,9) = 53.52$, $p < 0.0001$, $\eta^2 = 0.92$; J': $F(2,9) = 10.24$, $p = 0.005$, $\eta^2 = 0.69$), with Cluster II showing significantly higher isolate totals (M = 42.00, SD = 2.83) but lower evenness (M = 0.89, SD = 0.01) than Clusters I and III. Shannon (H'), Simpson (1-D), and Margalef richness (D_Mg) did not differ significantly by cluster (H': $F(2,9) = 3.56$, $p = 0.073$; 1-D: $F(2,9) = 3.14$, $p = 0.092$; D_Mg: $F(2,9) = 0.29$, $p = 0.755$). The three-cluster zonation therefore reflects real differences in total fungal load and community evenness rather than in overall species diversity as such; H', 1-D, and D_Mg were comparable across clusters even where total abundance was not.

Table 3: Mycological Diversity Indices for Fungal Isolates Across Sampled Locations

LGA	N	S	H'	1-D	D_Mg	J'
Bida	33	10	2.12	0.89	2.57	0.92
Mokwa	44	10	2.11	0.88	2.38	0.91
Lavun	31	9	2.05	0.88	2.33	0.93
Agaie	40	10	2.07	0.87	2.44	0.90
Chanchaga	16	8	1.92	0.88	2.53	0.93
Bosso	23	10	2.10	0.89	2.87	0.91
Shiroro	15	6	1.62	0.82	1.85	0.90
Suleja	20	8	1.90	0.87	2.34	0.91
Wushishi	29	10	2.11	0.89	2.67	0.92
Kotangora	32	10	2.11	0.89	2.60	0.92
Borgu	30	9	2.02	0.87	2.35	0.92
Mashegu	33	10	2.13	0.89	2.57	0.93
Mean	28.8	9.2	2.021	0.88	2.46	0.92

GIS Spatial Distribution Mapping

High-abundance LGAs (Mokwa, Agaie) were visually concentrated in the south-western corridor, while Cluster III LGAs spanned the central and northern portions of the state, and Cluster I sites clustered in the eastern and peri-urban zones around Minna. Shiroro, the lowest-diversity site, occupied an isolated northern position, potentially reflecting distinct elevation and humidity conditions. Diversity hotspots (Mashegu, Kotangora, Wushishi) appeared visually consistent with the northern agricultural transition zones on the bubble maps, a pattern we interpret as suggestive of agro-ecological gradients such as rainfall variability and soil type; no formal spatial-autocorrelation statistic (e.g., Moran's I) was computed to test this pattern, so it should be read as a qualitative spatial observation pending confirmatory analysis.

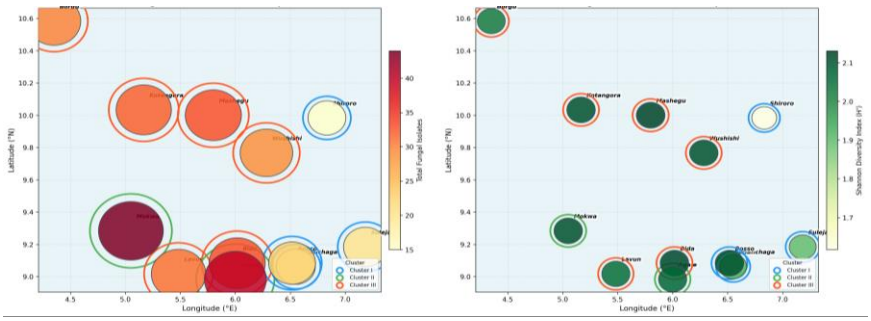

Figure 11: GIS bubble maps of total fungal isolate abundance (left) and Shannon diversity H' (right) across twelve Niger State LGAs. Symbol size proportional to metric magnitude; ring colour denotes cluster membership (blue = Cluster I; green = Cluster II; orange = Cluster III).

Qualitative Mycotoxin Screening

Fluorescence screening on CAM indicated putative toxigenic capability in seven of the ten identified taxa (Table 4).

Table 4: Qualitative Mycotoxin Screening of Isolated Fungal Species

S/N	Isolated Mycoflora	Reaction
1	*Aspergillus flavus*	Positive
2	*Aspergillus parasiticus*	Positive
3	*Aspergillus niger*	Negative
4	*Aspergillus fumigatus*	Negative
5	*Aspergillus terreus*	Positive
6	*Fusarium species*	Positive
7	*Penicillium chrysogenum*	Positive
8	*Alternaria alternata*	Positive
9	*Rhizopus stolonifera*	Positive
10	*Absidia species*	Negative

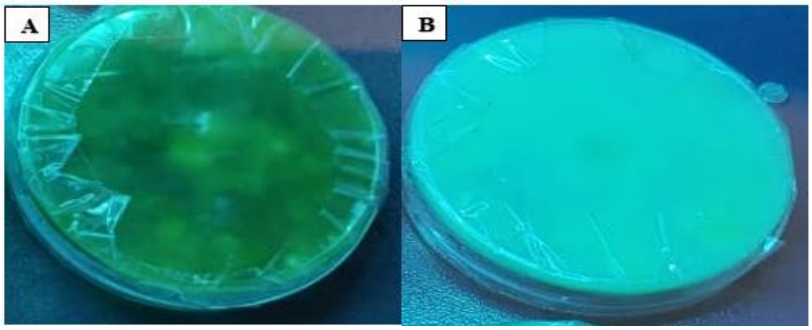

Figure 12: Fluorescence characteristics of fungal isolates on CAM under UV illumination (365 nm): A, positive; B, negative

Discussion

Beyond corroborating the established dominance of *Aspergillus* in Nigerian stored groundnut, this study's contribution is best characterized as a methodological translation rather than a methodological innovation: principal component analysis, hierarchical clustering, and GIS mapping are established community-ecology tools, and the contribution here lies in converting their output into an explicit storage-risk zonation, so that postharvest intervention can be targeted by ecological zone rather than applied uniformly or decided facility by facility. This distinguishes the present findings from prior isolate-frequency surveys, which have not translated community data into a spatial prioritization tool though that prioritization remains a hypothesis pending validation against independent, quantitative toxin data.

The elevated fungal loads recorded in Mokwa and Agaie, against markedly lower counts in Chanchaga, point to storage conditions rather than sampling artefact as the primary driver of contamination: both high-load LGAs sit within the wetter, more humid south-western storage belt of Niger State, where humidity, temperature, and water activity jointly favor rapid fungal proliferation during storage (Pitt and Hocking, 2022). This has direct, practical implications for postharvest management independent of toxin risk the fungal burden recorded here translates into reduced seed viability, accelerated spoilage, and economic loss along the storage chain, and the LGA-level variation observed suggests that drying and storage-infrastructure investment would deliver the greatest return if targeted at the south-western belt rather than applied uniformly across the state.

A key limitation of this study is that identification relied on morphological criteria alone, without ITS sequencing confirmation, and toxigenic assessment was qualitative (UV fluorescence) rather than quantitative. The reported proportions of toxigenic isolates should therefore be read as

screening-level risk estimates suitable for prioritizing storage interventions, not as confirmed toxin loads; combining this fluorescence screen with molecular detection of biosynthetic genes and chromatographic quantification would sharpen surveillance accuracy in any follow-on monitoring program (Koudokpon et al., 2024; Martínez-Culebras et al., 2021).

The community-structure analysis clarifies why a uniform storage policy would be inefficient. PC1 captured a general abundance gradient and PC2 separated Fusarium and Penicillium, which favor higher humidity, from the comparatively xerotolerant Absidia and Alternaria (Pitt and Hocking, 2022) a split that mapped onto the wetter south-western LGAs versus the rest of the state. This moisture-gradient reading is a hypothesis generated by the loading pattern and its geographic correspondence, not a directly tested relationship, since humidity, temperature, and residue load were not measured at each site; it should be confirmed with direct environmental data before being used to justify intervention spending. The resulting three-cluster solution is, on the same basis, a working storage-risk zonation rather than a validated one: Cluster I (low-abundance, peri-urban fringe) likely reflects comparatively better existing storage infrastructure and shorter grain transit times; Cluster II (high-abundance, agricultural belt: Mokwa, Agaie) reflects elevated crop-residue loads, higher humidity, and extended on-farm storage periods, making it the clearest candidate priority for intervention; and Cluster III represents an intermediate, comparatively stable group of LGAs where seasonal drying and traditional storage practice appear to be moderating fungal buildup. With only twelve sites split unevenly across the three clusters (four, two, and six members), and with Mojena's stopping rule and Ward's linkage both known to be sensitive to small sample sizes, this zonation should guide where monitoring resources are deployed first, not where drying or storage-infrastructure capital is committed, until it is checked against independent toxin data.

The genera recovered *Aspergillus*, *Fusarium*, and *Penicillium* dominant among them match prior Nigerian surveys of stored groundnut and groundnut products, including reports from Rivers State (Tobin-West and Baraka, 2018) and from within Niger State itself (Odeniyi et al., 2019), and are consistent with *Aspergillus* being the dominant genus colonizing tropical oilseeds in storage generally (Atehnkeng et al., 2021). Their co-occurrence raises a realistic possibility of multi-mycotoxin contamination in postharvest kernels, since *Aspergillus*, *Penicillium*, and *Fusarium* are associated respectively with aflatoxins, ochratoxins, and fumonisins (Awuchi et al., 2023; Darwish et al., 2020), a pattern also reported for Zaria-area markets in Kaduna State (Gambo et al., 2025) and consistent with the broader observation that these toxin classes frequently co-occur in the same food matrix with potentially additive effects (Gbashi et al., 2020). *A. flavus* and *A. parasiticus* warrant particular monitoring priority given their conserved aflatoxin biosynthetic pathways (Adeleke et al., 2023; Ezekiel et al., 2022), and fluorescence intensity was highest precisely in the highest-load LGAs Mokwa, Bida, and Borgu reinforcing that storage-load hotspots and toxigenic-risk hotspots substantially overlap in this dataset.

Evenness values above 0.90 at every site indicate no single species monopolized any community, a notably more balanced structure than reported for drier Sahelian storage zones such as northern Kano State, where A. flavus alone can exceed 60% relative abundance (Atehnkeng et al., 2021) likely reflecting Niger State's comparatively mesic Guinea Savanna climate. *A. niger's* occurrence across a wide range of moisture conditions confirms its established xerotolerance; although fluorescence was not observed for *A. niger* isolates here, the species has previously been implicated in ochratoxin contamination elsewhere (Kortei et al., 2022), so a negative CAM screen alone should not be read as ruling out its toxigenic relevance in storage-monitoring programs.

CONCLUSION

Fungal load and community composition in stored groundnut across Niger State track storage conditions rather than location alone, with the wetter south-western LGAs (Mokwa, Agaie) carrying both the highest fungal burden and the highest concentration of toxigenic isolates. The co-occurrence of *Aspergillus*, *Penicillium*, and *Fusarium* indicates a realistic risk of multi-mycotoxin contamination in the region's groundnut storage chain. The three-zone storage-risk classification proposed here is a working hypothesis, not a validated decision rule; it should guide the sequencing of monitoring effort prioritizing CAM-based screening in Cluster II and the high-PC2 LGAs identified in this study while confirmatory molecular and chromatographic testing, and independent environmental measurement, determine whether infrastructure investment should follow the same zonation.

Acknowledgements

The authors gratefully acknowledge the technical support of the Mycology Laboratory, Department of Plant Biology, Federal University of Technology, Minna, Nigeria.

Data Availability Statement

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

REFERENCES

Abdullahi, M. A., Yusuf, A. U., & Ibrahim, S. (2023). Postharvest fungal contamination of oilseed crops in northern Nigeria. *Journal of Stored Products Research, 104*, Article 102145. https://doi.org/10.1016/j.jspr.2023.102145

Abdullahi, N., & Dandago, M. A. (2022). Aflatoxins In Food Grains: Contamination, Dangers And Control. *FUDMA Journal of Sciences, 5*(4), 22–29. https://doi.org/10.33003/fjs-2021-0504-776

Adebiyi, J. A., Atehnkeng, J., & Katerere, D. (2024). Emerging concerns of aflatoxin contamination in staple foods in West Africa. *Food Control, 158*, Article 110245. https://doi.org/10.1016/j.foodcont.2024.110245

Adebola, M. O., Bello, T. S., Oyelade, M. J., Aremu, M. B., Egubagi, M. & Umar, S. M. (2020). Fungicidal activities of methanolic plant extracts on mycelia growth of *Fusarium oxysporum* associated with sweet orange (*Citrus sinensis* (L.) Osbeck). *Bioscience Research Journal, 32*(1), 1–8.

Adeleke, R. A., Babalola, O. O., & Ogunjobi, A. A. (2023). Prevalence and molecular characterization of aflatoxigenic *Aspergillus* species in Nigerian groundnuts. *Journal of Food Safety, 43*(2), Article e12987. https://doi.org/10.1111/jfs.12987

Adetunji, C., Akinola, M., Nleya, S. N., & Mulunda, M. (2021). Nutrient composition and aflatoxin contamination of African sourced peanuts and cashew nuts: Its implications on health. In *Mycotoxins – Detection methods, management, public health and agricultural economy*. IntechOpen. https://doi.org/10.5772/intechopen.95082

Amaechi, C. N., Atanda, O. O., & Ezekiel, C. N. (2021). Distribution of aflatoxigenic fungi and aflatoxins in groundnut-based products in Nigerian markets. *Journal of Food Safety, 41*(3), Article e12899. https://doi.org/10.1111/jfs.12899

Atehnkeng, J., Donner, M., Ojiambo, P. S., & Bandyopadhyay, R. (2021). Distribution and toxigenicity of *Aspergillus* species associated with groundnut storage in sub-Saharan Africa. *Mycopathologia, 186*(4), 567–581. https://doi.org/10.1007/s11046-021-00567-z

Awuchi, C. G., Nwankwo, E. O., Eze, C. U., & Okeke, C. E. (2023). Occurrence and health risks of mycotoxin in foods in Africa. *Food Control, 147*, Article 109537. https://doi.org/10.1016/j.foodcont.2023.109537

Bakoye, O., Baoua, I., Sitou, L., Moctar, M. R., Amadou, L., Njoroge, A. W., Murdock, L. L., & Baributsa, D. (2019). Groundnut production and storage in the Sahel: Challenges and opportunities in the Maradi and Zinder regions of Niger. *Journal of Agricultural Science, 11*(4), 25–38. https://doi.org/10.5539/jas.v11n4p25

Çiftçi, S., & Suna, G. (2022). Functional components of peanuts (*Arachis hypogaea* L.) and health benefits: A review. *Future Foods, 5*, Article 100140. https://doi.org/10.1016/j.fufo.2022.100140

Darwish, W. S., Ikenaka, Y., Nakayama, S. M. M., & Ishizuka, M. (2020). An overview on mycotoxin contamination of foods in Africa. *Journal of Veterinary Medical Science, 82*(5), 671–684. https://doi.org/10.1292/jvms.19-0567

Ezekiel, C. N., Sulyok, M., Warth, B., & Krska, R. (2022). Mycotoxin risks in groundnut value chain in West Africa. *World Mycotoxin Journal, 15*(1), 45–60. https://doi.org/10.3920/WMJ2021.2719

Gambo, U., Obansa, A., & Whong, C. (2025). Detection of aflatoxigenic molds and aflatoxin levels in groundnuts marketed in Zaria, Kaduna State, Nigeria. *Research Square*. https://doi.org/10.21203/rs.3.rs-7290071/v1

Gbashi, S., Njobeh, P. B., Madala, N. E., De Boevre, M., Kagot, V., & De Saeger, S. (2020). Parallel validation of a green-solvent extraction method and quantitative estimation of multi-mycotoxins in staple cereals using LC-MS/MS. *Scientific Reports, 10*(1), Article 10334. https://doi.org/10.1038/s41598-020-66787-z

Gide, S., Abdulkarim, S. M., & Danjuma, L. (2025). Screening for Aflatoxigenic Fungi in Stored and Open Market Grains in Potiskum, Northeast Nigeria. *FUDMA Journal of Sciences, 9*(1), 106–117. https://doi.org/10.33003/fjs-2025-0901-2916

International Agency for Research on Cancer. (2023). *Aflatoxins*. IARC Monographs on the Evaluation of Carcinogenic Risks to Humans. https://monographs.iarc.who.int/monographs-available

Kortei, N. K., Tetteh, R. A., Wiafe-Kwagyan, M., Amon, D. N. K., Odamtten, G. T. (2022). Mycobiota profile, phenology, and potential toxicogenic and pathogenic species associated with stored groundnuts (*Arachis hypogaea* L.) from the Volta Region, Ghana. *Food Science & Nutrition, 10*(3), 888–902. https://doi.org/10.1002/fsn3.2719

Koudokpon, H., Lègba, B., Sintondji, K., Kissira, I., Kounou, A., Guindo, I., Koné, K. M., Abdou, M., Koné, A., Sambou, C., Bankolé, H., Yadouleton, A., & Dougnon, V. (2024). Empowering public health: Building advanced molecular surveillance in resource-limited settings through collaboration and capacity-building. *Frontiers in Health Services, 4*, Article 1289394. https://doi.org/10.3389/frhs.2024.1289394

Kumar, P., Mahato, D. K., Kamle, M., Mohanta, T. K., & Kang, S. G. (2022). Aflatoxins: A global concern for food safety, human health and their management. *Frontiers in Microbiology, 13*, Article 897345. https://doi.org/10.3389/fmicb.2022.897345

Mahato, D. K., Lee, K. E., Kamle, M., Devi, S., Dewangan, K. N., Kumar, P., & Kang, S. G. (2019). Aflatoxins in food and feed: An overview on prevalence, detection and control strategies. *Frontiers in Microbiology, 10*, Article 2266. https://doi.org/10.3389/fmicb.2019.02266

Martínez-Culebras, P. V., Gandía, M., Garrigues, S., Marcos, J. F., & Manzanares, P. (2021). Antifungal peptides and proteins to control toxigenic fungi and mycotoxin biosynthesis. *International Journal of Molecular Sciences, 22*(24), Article 13261. https://doi.org/10.3390/ijms222413261

Mojena, R. (1977). Hierarchical grouping methods and stopping rules: An evaluation. *Computer Journal, 20*(4), 359–363. https://doi.org/10.1093/comjnl/20.4.359

Mwanza, M., Nyirenda, H., & Mlalazi, B. (2021). Mycotoxin contamination in legumes and oilseeds: Public health implications and management strategies. *Toxins, 13*(11), Article 812. https://doi.org/10.3390/toxins13110812

Najjar, A. A. (2023). Managing major foodborne mycotoxins: A therapeutic approach for safety and health. *World Journal of Environmental Biosciences, 12*(4), 46–53. https://doi.org/10.51847/fhNKVgnWUR

Naveen, K. H., & Vidyasagar, G. M. (2021). A coconut agar medium for rapid detection of aflatoxin production by *Aspergillus* spp. *Journal of Mycology and Plant Pathology, 51*(2), 164–172.

Odeniyi, O., Ojo, C., Adebayo-Tayo, B., & Olasehinde, K. (2019). Mycological, toxigenic, and nutritional characteristics of some vended groundnut and groundnut products from three northern Nigerian ecological zones. *African Journal of Biomedical Research, 22*, 65–71.

Olukosi, J., & Yusuf, A. (2021). Challenges and opportunities in groundnut production in Nigeria: A review. *Nigerian Journal of Economic and Social Studies, 63*(1), 15–30.

Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, E. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research, 12*, 2825–2830.

Pedro, A., Aleruchi, C., John, M., Bashir, S., Hannah, E. N., & Victor, K. F. (2022). Fungal biodiversity associated with groundnuts stored in Nasarawa State. *GSC Biological and Pharmaceutical Sciences*, *18*(3), 023–029. https://doi.org/10.30574/gscbps.2022.18.3.0087

Pitt, J. I., & Hocking, A. D. (2022). Ecology of fungal food spoilage. In *Fungi and food spoilage* (pp. 1–25). Springer.
Robertson, K. M., Simonson, E., Ramirez-Bullon, N. R., & others. (2023). Effects of spatial resolution, mapping window size, and spectral species clustering on remote sensing of plant beta diversity using biodivMapR and hyperspectral imagery. *Journal of Geophysical Research: Biogeosciences*, *128*(7), Article e2022JG007350. https://doi.org/10.1029/2022JG007350

Saleh, I., Zeidan, R., & Abu-Dieyeh, M. (2024). The characteristics, occurrence, and toxicological effects of alternariol: A mycotoxin. *Archives of Toxicology*, *98*(6), 1659–1683. https://doi.org/10.1007/s00204-024-03743-0

Sarah, K., Catriona, H., Helen, A., & David, E. (2016). *Descriptions of medical fungi* (3rd ed., revised November 2016). http://www.mycology.adelaide.edu.au

Sowmya, K. L., & Ramalingappa, B. (2024). Rapid detection of aflatoxin production by *Aspergillus flavus* using coconut agar medium. *Food Science & Nutrition Technology*, *9*(3), 000352–000357. https://doi.org/10.29328/journal.fsnut.1001035

Suleiman, M. N., & Atehnkeng, J. (2022). Occurrence of aflatoxigenic fungi in stored grains and nuts in Nigeria. *African Journal of Microbiology Research*, *16*(7), 301–312. https://doi.org/10.5897/AJMR.2022.9501

Tobin-West, M. D., & Baraka, R. E. (2018). Effects of methods of processing groundnut (*Arachis hypogaea* L.) on the nutritional composition and storage life of the seed. *International Journal of Agriculture and Earth Science*, *6*, 2489–0081.

Ward, J. H. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association*, *58*(301), 236–244. https://doi.org/10.1080/01621459.1963.10500845

Yakubu, M. N., Ladan, M. A., & Deba, F. A. (2022). Biodiversity and virulence characterization of entomopathogenic fungi isolated from soils in different regions of Nigeria. *Egyptian Journal of Biological Pest Control*, *32*, Article 93. https://doi.org/10.1186/s41938-022-00593-9