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Comparative Phytochemical Composition and Interspecific Variation in Leaves of Plantain and Banana (*Musa* spp.) Genotypes

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ABSTRACT

Banana and plantain (*Musa spp*.) are among the important staple and cash crops, but their leaves remain a largely underexploited by-product with potential nutraceutical, ethnoveterinary and feed-industry value. This study compared leaf phytochemical composition across ten *Musa* genotypes (five bananas, five plantains) developed by NIHORT, analyzed for alkaloids, flavonoids, glycosides, saponins, terpenoids and tannins using standard spectrophotometric and titrimetric protocols. One-way ANOVA with Tukey's HSD test revealed significant genotype (cultivar) effects within both species for most of the phytochemicals ($p < 0.05$). Independent-samples t-tests showed that banana genotypes, as a group, carried significantly higher alkaloid, flavonoid, glycoside and tannin concentrations than plantain genotypes ($p < 0.05$), while terpenoid and saponin concentrations did not differ significantly ($p > 0.05$). Principal component analysis showed that genotypes did not cluster along species lines for glycosides, saponins and tannins, indicating that cultivar identity, rather than species, is the stronger determinant of leaf phytochemical profile. Steroids, free phenols and anthraquinones were undetected in all samples. High-tannin/high-saponin genotypes (VTS 107, VTS 102, BRS 102, ITC 1307-SH-3640) are identified as priority candidates for bioprospecting as antiparasitic, antimicrobial and rumen-modulating feed or nutraceutical resources, while requiring processing before livestock use owing to anti-nutritional potential at high concentration.

Keywords: Comparative phytochemistry, genotype variation, *Musa* spp., nutraceutical potential

INTRODUCTION

Banana and plantain (genus *Musa*, family Musaceae) are among the foremost important global food crops by gross production value and constitute a staple food and income source for more

than 500 million people across the tropics and subtropics [1]. Cultivated *Musa* accessions are derived from the wild diploid species *Musa acuminata* (A genome) and *Musa balbisiana* (B genome) and their interspecific hybrids, giving rise to the AA, AB, AAA, AAB and ABB genomic groups that are conventionally distinguished in commerce and local usage as "banana" (sweet, dessert types) and "plantain" (starchy, cooking types).

Nigeria is one of the leading producers of both crops in West Africa, and a wide range of local and introduced genotypes, including International *Musa* Transit Centre (ITC) accessions maintained under the Bioversity International/KU Leuven germplasm collection and nursery-propagated "VTS" and "BRS" lines, are actively evaluated for agronomic and post-harvest traits.

Beyond the fruit, the vegetative parts of the *Musa* plant - pseudostem, rhizome, bracts and leaves - are generated in very large quantities as field and processing residues and are increasingly recognized as a reservoir of bioactive secondary metabolites. Recent phytochemical surveys of banana leaf extracts have reported appreciable concentrations of polyphenols, flavonoids, tannins, terpenoids and fatty acids with demonstrable antioxidant, anti-inflammatory and antimicrobial activity [2, 3]. Similar classes of compounds - alkaloids, flavonoids, saponins, tannins and cardiac glycosides - have also been documented in banana pseudostem and pseudostem waste [4], and genotype-dependent variation in phenolics, flavonoids and tannins has been reported among plantain cultivars used in West African tissue-culture and improvement programmes [1]. These compounds are of direct relevance to animal science and veterinary practice: tannins and saponins in particular are well documented to modulate rumen fermentation, suppress gastrointestinal parasites and reduce enteric methane output in ruminants when present within an appropriate dosage range [5].

Most of the existing literature on *Musa* phytochemistry is on the fruit pulp, peel and pseudostem, with few studies examining the leaf, and comparing banana and plantain genotypes against one another. Where genotype level comparisons exist, they are limited to qualitative screening or to descriptive mean ± SD reporting without formal inferential statistics, making it difficult to determine whether differences between genotypes, or between the banana and plantain species groups as a whole, are statistically significant or fall within the definition of common biological and analytical variation. This gap is significant because Nigerian breeding and germplasm conservation programmes evaluate genotypes such as PITA 24, Orishele, Agbagba and Obino l'Ewai for release. Any nutraceutical, ethnoveterinary or feed

industry valorisation strategy for *Musa* leaf biomass requires information in which phytochemical differences are genotype specific.

Although prior studies have established that *Musa* vegetative tissues contain bioactive alkaloids, flavonoids, tannins and saponins, and that phytochemical content varies among plantain cultivars, no study has statistically tested, within a single analytical framework, whether these differences are duly explained by specie identity (banana versus plantain) or by cultivar identity, which is the specific knowledge gap that the present study fills. This study addresses that gap by providing a genotype resolved analysis of leaf phytochemicals across ten banana and plantain accessions, comprising standard breeding lines and local cultivars, and by testing statistically whether secondary metabolites is dictated primarily by broad species grouping or by specific cultivar genetics. By bridging agronomy, livestock nutrition and the circular bioeconomy framework, these insights are intended to enable agronomists and germplasm managers to select and utilize *Musa* lines for dual purpose cropping systems, functional feeds, integrated crop and livestock farming.

The aim of this study is to statistically compare the leaf phytochemical composition of ten *Musa* genotypes and determine whether species identity or cultivar identity is the stronger determinant of secondary metabolite expression. The specific objectives are to: quantify six major classes of phytochemicals (alkaloids, flavonoids, glycosides, saponins, terpenoids and tannins) in the leaves of ten named *Musa* genotypes comprising five banana and five plantain accessions; test for significant within-species (inter-genotype/cultivar) variation in each phytochemical using one-way ANOVA with Tukey's HSD post-hoc grouping; test for significant between-species (interspecific, banana vs. plantain) differences in each phytochemical using independent-samples t-tests with appropriate correction for unequal variances; explore the multivariate structure of genotype phytochemical profiles using principal component analysis (PCA) to determine whether species identity or cultivar identity is the stronger organizing factor; and interpret the findings in the context of the nutraceutical, antimicrobial, and livestock feed/ethnoveterinary literature on *Musa* spp. and related tannin- and saponin-rich forages.

MATERIALS AND METHODS

Materials and Study Design

This study followed a comparative, laboratory-based analytical design in which leaf samples from ten *Musa* genotypes (five bananas and five plantains, treated as two independent groups) were subjected to standardized wet-chemistry phytochemical assays, each performed in triplicate, followed by within-species (genotype) and between-species (interspecific) statistical comparison. Ten *Musa* genotypes were included in the study, comprising five commonly classified as banana (dessert-type) - VTS 107, VTS 102 (*Caprishosa*), VTS 108 (*Paranata*), BRS 102 (*Caprichosa*) and BRS *Platina* - and five commonly classified as plantain (cooking-type) - VTS 111 (Cantebalon), ITC 1307-SH-3640, VTS 104 (PITA 24), ITC 0517 (Orishele) and VTS 101 (Oluokun). Genotype identities and accession codes follow the nomenclature supplied with the source nursery/germplasm material; ITC-prefixed accessions correspond to the International *Musa* Transit Centre naming convention used for *Musa* germplasm distribution. These varieties are improved tissue-culture banana and plantain hybrids developed by NIHORT. The varieties have high yielding ability, high suckering ability, tolerance to nematodes and weevils, long shelf life, and are well adapted to diverse agro-ecological zones in Nigeria. Vegetative tissue-culture selection was used in their development. Fully expanded, disease-free leaves were sampled from field-established mother stools at the Teaching and Research Farm of Babcock University, Ilishan-Remo, Ogun State, Nigeria, for each genotype, for comparative *Musa* phytochemical investigations.

Reagents and Sample Extraction

Analytical-grade reagents were used. For alkaloid, tannin and glycoside determination, powdered leaf samples were extracted with dilute acetic acid/aqueous solvents; for flavonoid determination, samples were extracted with 80% aqueous methanol; and for saponin determination, samples were extracted with 20% aqueous ethanol under heated agitation [6–11]. All determinations were performed in triplicate for each genotype, and results are expressed as mean ± standard deviation (SD) in milligrams per 100 g of dry leaf extract (mg/100 g).

Phytochemical Determination

Alkaloid content was determined gravimetrically following the method of Harborne [6]. Flavonoid content was determined following the method of Bohm and Kocipai-Abyazan [7].

Saponin, free phenol and glycoside contents were determined following the methods of Obadoni and Ochuko [8]. Tannin content was determined by the titrimetric method of Onwuka [9]. Terpenoid, steroid and anthraquinone contents were determined spectrophotometrically following the Association of Official Analytical Chemists [10] and Okwu and Okwu [11] protocols. Qualitative intensity of each phytochemical was additionally scored on the standard three-point scale used in the source laboratory report: (+++) present in high amount, (++) present in moderate amount, (+) present, and (−) not detected.

Statistical Analysis

The reports provided mean ± SD values (based on triplicate determinations) for each genotype, rather than raw individual replicate readings. To enable formal inferential statistics, a pseudo-replicate dataset (n = 3 per genotype × phytochemical combination) was reconstructed algebraically such that x_1 = mean − SD, x_2 = mean, and x_3 = mean + SD; this construction reproduces both the reported sample mean and the reported sample standard deviation (n − 1 denominator) for every genotype × phytochemical cell. This is conceptually analogous to established summary-data reconstruction approaches used in meta-analysis when only means, SDs and sample sizes are available [12]. All inferential statistics are based on this reconstructed dataset and are interpreted as indicative of the pattern of variation implied by the laboratory's reported means and SDs.

Within species (inter-genotype/cultivar) differences were tested separately for the five banana genotypes and the five plantain genotypes using one-way analysis of variance (ANOVA), with Tukey's honestly significant difference (HSD) test applied post hoc where the overall F-test was significant ($p < 0.05$); genotypes sharing a letter within a species/phytochemical combination were not significantly different. Between-species (interspecific) differences were tested for each phytochemical using an independent-samples t-test on the pooled reconstructed values for all banana genotypes (n = 15) versus all plantain genotypes (n = 15); Levene's test was used to check the assumption of equal variances, with Welch's correction applied where variances differed significantly ($p < 0.05$). Effect size was expressed as Cohen's d.

Principal component analysis was performed on standardised (z-scored) genotype-level mean concentrations across all six phytochemicals to visualise multivariate clustering. All

analyses were performed in Python 3 using SciPy and statsmodels, with statistical significance set at $p < 0.05$.

RESULTS AND DISCUSSION

Descriptive concentrations of the six quantified phytochemicals across all ten genotypes are presented in Table 1, together with Tukey HSD grouping letters computed separately within each species. Within the banana group, genotype (cultivar) differences were statistically significant ($p < 0.05$) for all six phytochemicals, including a striking split between high-glycoside/high-saponin/high-tannin genotypes (VTS 107, VTS 102, BRS 102) and comparatively low-glycoside/low-saponin genotypes (VTS 108, BRS Platina), despite all five being classified as banana. Within the plantain group, genotype differences were similarly significant for five of six phytochemicals (all except alkaloids, $F(4,10) = 0.75$, $p = 0.580$), with ITC 1307-SH-3640 standing out as an outlier with saponin and tannin concentrations several-fold higher than the other four plantain genotypes (Table 1, Table 3).

Table 1: Mean ± SD phytochemical concentrations (mg/100 g) by genotype, with Tukey HSD grouping letters computed within each species

Genotype	Alkaloids	Flavonoids	Glycosides	Saponins	Terpenoids	Tannins
Banana						
BRS 102 Caprichosa (Banana)	0.28±0.02a	0.35±0.02a	5.33±0.01a	7.24±0.03a	0.50±0.02a	7.52±0.04a
BRS Platina (Banana)	0.30±0.02a	0.38±0.02a	0.44±0.01b	0.46±0.03b	0.50±0.02a	0.54±0.04b
VTS 102 Caprishosa (Banana)	0.30±0.02a	0.37±0.02a	5.22±0.01c	8.20±0.03c	0.48±0.02a	8.55±0.04c
VTS 107 (Banana)	0.50±0.05b	0.28±0.02b	5.02±0.01d	8.30±0.02d	0.60±0.02b	5.25±0.05d

VTS 108 Paranata (Banana)	0.40±0.03c	0.36±0.02a	0.22±0.01e	0.42±0.02b	0.55±0.02b	0.48±0.05b
Plantain						
ITC 0517 Orishele (Plantain)	0.42±0.03a	0.40±0.02a	0.28±0.01a	0.44±0.02a	0.55±0.02a	0.50±0.05a
ITC 1307-SH-3640 (Plantain)	0.44±0.05a	0.28±0.02b	5.10±0.01b	10.20±0.02b	0.52±0.02a	6.32±0.05b
VTS 101 Oluokun (Plantain)	0.40±0.03a	0.47±0.02c	0.33±0.01c	0.42±0.02a	0.45±0.02b	0.52±0.05a
VTS 104 PITA 24 (Plantain)	0.44±0.02a	0.49±0.02c	0.28±0.01a	0.40±0.03a	0.50±0.02a	0.52±0.04a
VTS 111 Cantebalon (Plantain)	0.42±0.03a	0.46±0.02c	0.25±0.01d	0.40±0.02a	0.55±0.02a	0.60±0.05a

* *Means sharing a letter within the same species and phytochemical column are not significantly different ($p > 0.05$).*

Note. Steroids, free phenols and anthraquinones were not detected (mean = 0.00) in any of the ten genotypes and are omitted from the table.

Table 2: Independent-samples t-test comparing pooled banana (n = 15) and plantain (n = 15) reconstructed leaf phytochemical concentrations.

Phytochemical	Banana mean ± SD	Plantain mean ± SD	t	df	p-value	Cohen's d
Alkaloids	0.36 ± 0.09	0.42 ± 0.03	-2.75	17.5	**0.013***	-1.01
Flavonoids	0.35 ± 0.04	0.42 ± 0.08	-3.09	28.0	**0.004***	-1.13

Glycosides	3.25 ± 2.47	1.25 ± 1.99	2.44	28.0	**0.021***	0.89
Saponins	4.92 ± 3.81	2.37 ± 4.05	1.78	28.0	0.086	0.65
Terpenoids	0.53 ± 0.05	0.51 ± 0.04	0.73	28.0	0.474	0.27
Tannins	4.47 ± 3.52	1.69 ± 2.40	2.52	24.7	**0.018***	0.92

Note. Positive t-values indicate higher concentration in banana; negative t-values indicate higher concentration in plantain. Degrees of freedom are non-integer where Welch's correction for unequal variances was applied.

Table 3: Within species one-way ANOVA (genotype/cultivar effect) for each phytochemical.

Phytochemical	Banana genotypes: F(4,10); p-value	Plantain genotypes: F(4,10); p-value
Alkaloids	F=28.30; p=<0.0001*	F=0.75; p=0.5801 (ns)
Flavonoids	F=11.78; p=0.0008*	F=54.38; p=<0.0001*
Glycosides	F=213128.40; p=<0.0001*	F=139130.10; p=<0.0001*
Saponins	F=72542.91; p=<0.0001*	F=114897.12; p=<0.0001*
Terpenoids	F=17.85; p=0.0002*	F=12.97; p=0.0006*
Tannins	F=22164.14; p=<0.0001*	F=8656.97; p=<0.0001*

Figure 1 summarizes the interspecific comparison graphically. Banana leaves carried significantly higher mean concentrations of alkaloids ($t(17.5) = -2.76$, $p = 0.013$), flavonoids ($t(28) = -3.09$, $p = 0.004$), glycosides ($t(28) = 2.44$, $p = 0.021$) and tannins ($t(24.7) = 2.52$, $p = 0.018$) than plantain leaves, while terpenoid concentrations did not differ significantly ($t(28) = 0.73$, $p = 0.474$) and saponin concentrations showed only a non-significant trend toward higher banana values ($t(28) = 1.78$, $p = 0.086$). Effect sizes (Cohen's d) ranged from small (terpenoids, $d = 0.27$) to large (alkaloids, $d = -1.01$; flavonoids, $d = -1.13$; tannins, $d = 0.92$), indicating that where interspecific differences were statistically significant, they were also of substantial practical magnitude.

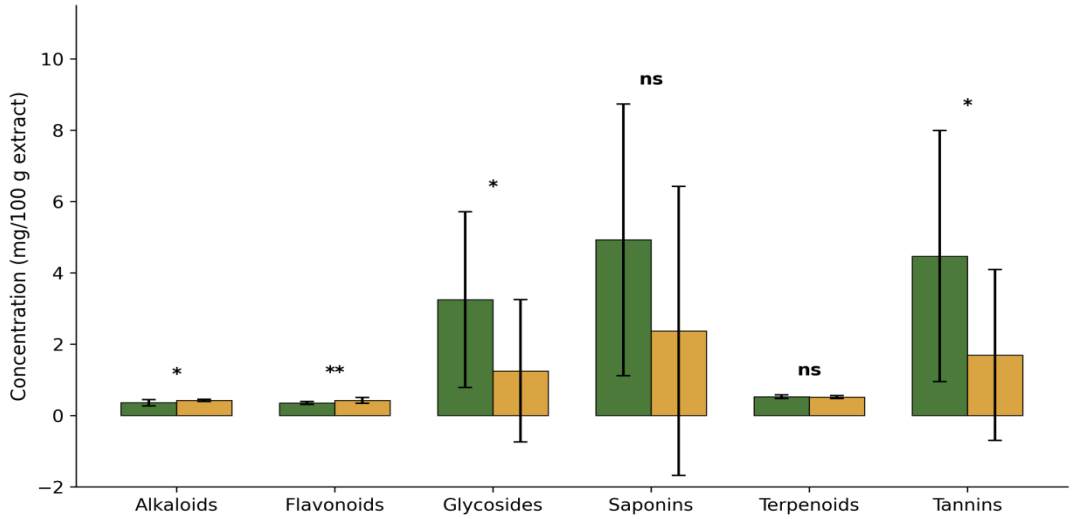

Figure 1: Mean ± SD leaf phytochemical concentration (mg/100 g) in banana versus plantain, pooled across five genotypes per species. Asterisks denote significance from independent t-tests: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, ns = not significant.

The genotype level heatmap (Figure 2) illustrates that the six phytochemicals do not vary in a coordinated, species-consistent fashion. Alkaloid and flavonoid concentrations were broadly similar across genotypes regardless of species, whereas glycoside, saponin and tannin concentrations showed a bimodal pattern that cut across the banana/plantain boundary: VTS 107, VTS 102, BRS 102 (all banana) and ITC 1307-SH-3640 (plantain) formed a distinct "high-glycoside/high-saponin/high-tannin" cluster, while VTS 108, BRS Platina (both banana) and all four remaining plantain genotypes formed a "low" cluster.

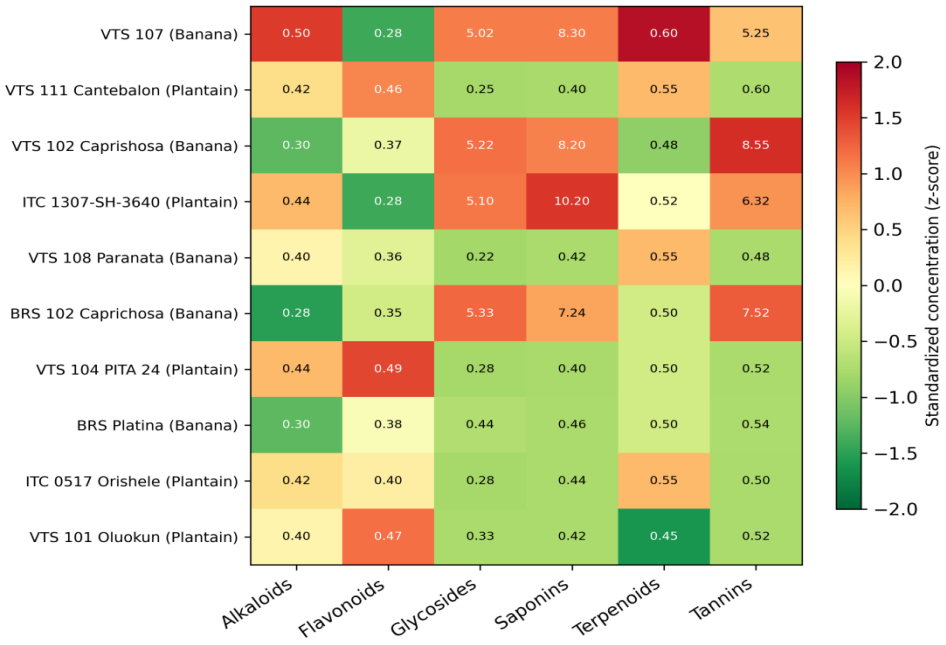

Figure 2: Heatmap of genotype-level mean phytochemical concentrations (mg/100 g). Colour intensity reflects the within-column (within-phytochemical) z-score; cell values show the actual concentration.

Principal component analysis reinforced this pattern: PC1 (explaining 59.8% of total variance) was driven primarily by glycosides, saponins and tannins (loadings of 0.52, 0.52 and 0.50, respectively) and separated the four "high" genotypes (VTS 107, VTS 102, BRS 102, ITC 1307-SH-3640) from the remaining six irrespective of species, while PC2 (29.1% of variance) was driven by terpenoids and alkaloids and further separated genotypes within each PC1 cluster (Figure 3). No clean species-based separation was evident along either axis, corroborating the Table 3 finding that cultivar/genotype identity, rather than species assignment alone, is the dominant source of variation for the glycoside/saponin/tannin compound group.

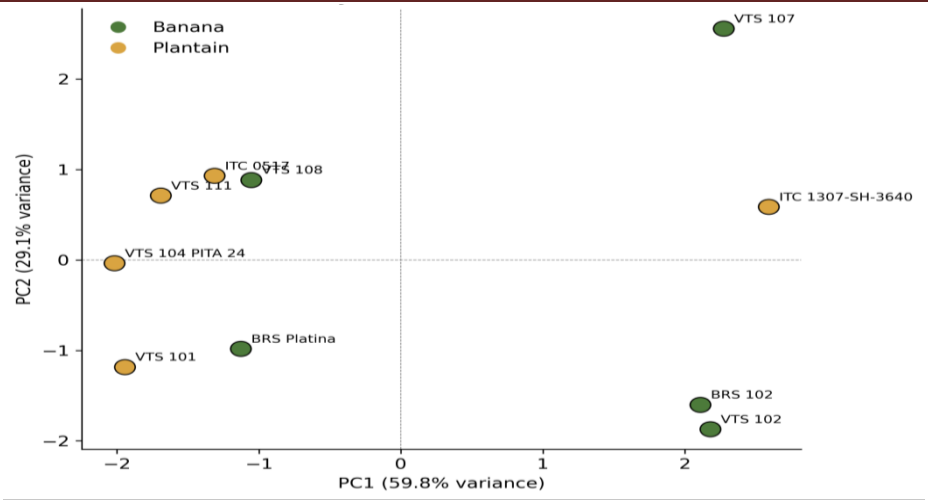

Figure 3: Principal component analysis of standardised genotype level phytochemical profiles. PC1 and PC2 together explain 88.9% of total variance.

The present findings show that *Musa* leaf tissue is a phytochemically rich, genotype-variable resource. The concentrations are consistent with those reported for related *Musa* tissues. Akpabio et al. [4] reported tannin concentrations of 6.55–7.99 mg/100 g and detected flavonoids, saponins and alkaloids (with steroids absent) in banana and plantain pseudostem waste, that were close to the tannin concentration range (0.48–8.55 mg/100 g) observed here; steroids were likewise absent across all ten leaf genotypes in the present study. Similarly, Jekayinoluwa et al. [1] reported genotype-dependent variation in total phenolics, flavonoids and tannins among West African plantain cultivars including Orishele, a finding corroborated by the significant within-species variation observed in this study, in which four of five plantain phytochemicals varied significantly among cultivars.

The interspecific comparison showed that banana leaves contained higher alkaloid, flavonoid, glycoside and tannin concentrations than plantain leaves on average, which is a less consistent pattern than reports for banana and plantain fruit pulp, where tannin has sometimes been described as present in plantain but absent in ripe banana pulp. This divergence is not unexpected: fruit-pulp phytochemistry is strongly influenced by ripening stage starch-to-sugar conversion and associated changes in secondary metabolism, whereas leaf tissue phytochemistry is governed more directly by photosynthetic and structural-defence physiology, and the two tissue types need not track one another [13].

The large effect sizes for alkaloids and flavonoids ($|d| > 1.0$) indicate that, in spite of the wide within species genotype variation observed in this study, the species level signal for these two compounds likely reflects a biologically meaningful difference between the A- and B-genome-influenced physiology typical of many banana versus plantain genotypes.

In contrast, the absence of a significant species effect for terpenoids and saponins, combined with the PCA result showing that glycoside/saponin/tannin-"high" genotypes cut across the species boundary (VTS 107, VTS 102 and BRS 102 among banana; ITC 1307-SH-3640 among plantain), demonstrates that for these three compound classes cultivar identity is a stronger organizing variable than the coarse banana/plantain dichotomy. This mirrors the broader *Musa* genetic diversity literature, in which phenotypic and biochemical trait variation among West African plantain landraces and hybrids has repeatedly been shown to reflect fine-grained cultivar pedigree rather than simple taxonomic grouping [1]. This means that phytochemical bioprospecting or feed-formulation decisions based on the species label alone ("use banana leaf" or "use plantain leaf") risk substantially under- or over-estimating the target compound's concentration; genotype specific screening, as performed here, is necessary for reliable downstream application.

The implication of the high tannin and saponin genotype cluster is noteworthy as reported in the literature [5]. Condensed tannins, when supplied within an appropriate low to moderate dietary inclusion range, bind dietary protein in the rumen to increase bypass protein supply, suppress methanogen activity and thereby reduce enteric methane emission per unit of feed, and exert anthelmintic activity against gastrointestinal nematodes [5]. Saponins act through complementary mechanisms, including defaunation of rumen protozoa and antiparasitic activity.

The tannin concentrations recorded here for VTS 102, BRS 102 and ITC 1307-SH-3640 (6.3–8.6 mg/100 g) fall in a range that, on a whole-diet inclusion basis, would be broadly consistent with the low-to-moderate dietary tannin levels associated with beneficial rather than toxic effects in the literature, suggesting these genotypes merit direct evaluation as functional feed or forage-additive candidates, an application directly relevant to the wider goal of methane-mitigating feed-additive development in Nigerian ruminant systems. Conversely, the same compounds are well established anti-nutritional factors at high concentration, depressing voluntary feed intake and fibre digestibility and, in the case of some glycosides, posing a cyanogenic risk; unprocessed feeding of the highest-tannin/saponin genotypes identified here

should therefore be approached cautiously and ideally validated with in vitro or in vivo digestibility and toxicity trials before field recommendation.

The high flavonoid and alkaloid content across genotypes, together with the antioxidant, anti-inflammatory and antimicrobial activities reported for banana leaf extracts by Ha et al. [3] and for banana byproduct extracts by Widoyanti et al. [2], supports the nutraceutical potential of *Musa* leaf biomass generally, independent of the species/cultivar distinctions driving the tannin/saponin/glycoside axis. The absence of steroids, free phenols (as measured by the ferric chloride type assay used here) and anthraquinones across all ten genotypes is consistent with prior *Musa* pseudostem findings [4] and suggests either a biosynthetic absence of these compounds in *Musa* vegetative tissue or a detection limit effect of the assay used, a distinction that could be resolved with more sensitive chromatographic profiling in future work.

Several limitations are acknowledged. First, the inferential statistics reported here relied on a reconstruction of pseudo-replicate values from laboratory-reported means and SDs rather than on original raw instrument readings, because only summary values were provided by the laboratory; while this reconstruction reproduces the reported means and SDs which is analogous to accepted meta-analytic practice [12]. Independent biological replication (multiple field-grown plants per genotype, analysed and reported as raw individual values) is recommended to confirm the conclusions drawn here. Second, phytochemical concentrations in *Musa* leaf tissue are known to vary with leaf position, plant age, season and agroecological conditions, none of which were experimentally controlled or varied in the present single time point laboratory analysis. Third, the present study quantified compounds by wet chemistry assay rather than individual compound identity, chromatographic fingerprinting would allow the specific bioactive constituents responsible for the observed genotype differences to be identified and would strengthen any subsequent bioactivity or feed trial.

This study provides a genotype-resolved, statistically tested comparison of banana and plantain leaf phytochemistry across ten *Musa* accessions. Banana leaves, as a specie, carried significantly higher alkaloid, flavonoid, glycoside and tannin concentrations than plantain leaves, with large effect sizes for alkaloids and flavonoids in particular, while terpenoid and saponin concentrations did not differ significantly by species. Within species genotype (cultivar) variation was statistically significant for most of the phytochemicals. Multivariate analysis showed that for glycosides, saponins and tannins, cultivar identity - rather than the

banana/plantain species boundary - was the dominant source of variation, with VTS 107, VTS 102 Caprishosa, BRS 102 Caprichosa and ITC 1307-SH-3640 forming a distinct high-concentration cluster regardless of species.

These results indicate against treating "banana" and "plantain" leaf as interchangeable, undifferentiated categories for phytochemical or nutraceutical purposes, and instead support genotype targeted bioprospecting, feed formulation and germplasm selection strategies. Given the reported rumen modulating and antiparasitic activity of tannins and saponins at appropriate dosage, the high-tannin/high saponin genotypes identified here are recommended for direct evaluation as functional feed additive or nutraceutical candidates, subject to dose response digestibility and safety testing. Chromatographic profiling is recommended to resolve the specific bioactive constituents underlying the observed genotype level differences.

CONCLUSION

This study demonstrates that *Musa* leaf is a cultivar. For agronomists, crop breeders, and agricultural extension specialists, incorporating foliar phytochemical profiling alongside conventional yield and post-harvest criteria offers a modern approach to germplasm evaluation. The findings from this study could serve as a guide for selection of clonal materials for purposeful cultivation. High tannin and high saponin accessions (VTS 107, VTS 102, BRS 102, and ITC 1307-SH-3640) may be prioritized for development into bio-based feed additives and livestock supplements. Farmers utilizing *Musa* foliage as raw livestock feed are informed on cultivar differences to balance nutritional intake and mitigate anti-nutritional risks.

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