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PHYTOCHEMICAL VARIATIONS OF PURPLE AND WHITE *DIOSCOREA ALATA* TUBERS UNDER AGROCLIMATIC CONDITIONS OF YOGYAKARTA, INDONESIA

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SUMMARY

Phytochemical traits in crop plants reflect both genetic characteristics and environmental conditions and could serve as useful markers for germplasm evaluation. This study compared the phytochemical profiles of purple and white *Dioscorea alata* L. tubers cultivated in Yogyakarta, Indonesia. Proximate analysis, Fourier Transform Infrared Spectroscopy (FTIR), and Gas Chromatography-Mass Spectrometry (GC-MS) were methods used to characterize biochemical composition in raw and steamed tubers. The results revealed clear phytochemical differences between the two tuber types, with purple tubers showing relatively higher carbohydrate levels and greatly abundant phenolic-related compounds. FTIR spectra indicated functional groups associated with carbohydrates, phenolics, and lipid derivatives, while the GC-MS analysis identified phenolic compounds and fatty acid ethyl esters as major constituents. The agroclimatic data describe the environmental conditions during tuber development and provide contextual background for interpreting the observed phytochemical profiles. These findings highlight the potential use of phytochemical traits as biochemical markers for *D. alata* germplasm characterization and will support the selection of nutritionally valuable yam varieties in breeding programs.

Keywords: *Dioscorea alata*, phytochemical variation, agroclimatic influence, germplasm characterization, FTIR, GC-MS, crop improvement

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Key findings: Purple and white *Dioscorea alata* L. exhibited distinct agroclimatic-driven phytochemical variations, with purple tubers consistently containing higher levels of phenolic compounds and fatty acid ethyl esters than white tubers. Favorable agroclimatic conditions, particularly stable temperatures and high solar radiation, enhanced secondary metabolite accumulation, supporting the use of these phytochemical traits as biochemical markers for *D. alata* germplasm evaluation and varietal selection.

INTRODUCTION

The *Dioscorea alata* L. (greater yam) is an important tuber crop widely cultivated in tropical and subtropical regions due to its adaptability, high carbohydrate content, and potential contribution to food security (Lebot, 2019). In many developing countries, *D. alata* serves not only as a staple food but also as a valuable genetic resource for crop diversification and nutritional improvement (Saint *et al*., 2019). The species exhibits substantial phenotypic diversity, including variation in tuber color, morphology, and biochemical composition, which is of interest for germplasm characterization and breeding programs (Mignouna *et al*., 2003).

Phytochemical traits, such as phenolic compounds, lipids, and other secondary metabolites, receive increasing recognition as vital phenotypic descriptors in crop plants because they reflect both genetic characteristics and environmental influences (Kliebenstein, 2004). In *D. alata*, previous studies have reported variability in nutritional composition and bioactive compounds among varieties, particularly between purple- and white-fleshed tubers (Polycarp *et al*., 2012). However, most existing studies have primarily focused on nutritional or ethnopharmacological properties, with limited attention to the role of phytochemical variation in germplasm characterization and crop improvement. Moreover, information linking phytochemical profiles of yam varieties with their agroclimatic growing conditions remains limited. Therefore, investigating phytochemical variation between different tuber types under specific agroclimatic contexts could provide useful insights for germplasm evaluation and breeding programs.

Environmental factors, such as temperature, solar radiation, and rainfall, usually strongly influence secondary metabolite biosynthesis in plants, leading to location-specific biochemical expression (Agostini-Costa *et al*., 2012; Moore *et al*., 2014). Despite this, the role of agroclimatic conditions in driving phytochemical variation in *D. alata* remains poorly documented, particularly using integrative analytical approaches that combine spectroscopic and chromatographic techniques. Moreover, information linking agroclimatically driven biochemical traits to their potential use in germplasm selection is scarce.

Therefore, the design of this study sought to evaluate phytochemical variation driven by agroclimatic conditions in purple and white *D. alata* L. cultivated in Yogyakarta, Indonesia. Proximate analysis, Fourier Transform Infrared Spectroscopy (FTIR), and Gas Chromatography-Mass Spectrometry (GC–MS), as employed, characterized biochemical diversity in relation to environmental conditions. By integrating phytochemical profiles with agroclimatic data, this research aimed to provide biochemical descriptors useful for germplasm characterization and support the selection of superior *D. alata* varieties for future breeding and crop improvement programs.

MATERIALS AND METHODS

Plant material and agroclimatic data

Purple- and white-fleshed *D. alata* L. tubers came from local cultivation sites in Bantul Regency, Special Region of Yogyakarta, Indonesia. The harvest of tubers took place at physiological maturity before selecting based on uniform size, shape, and absence of visible defects. Agroclimatic data, including temperature, rainfall, and solar radiation, upon obtaining from the Indonesian Agency for

Meteorology, Climatology, and Geophysics (BMKG DIY), aided in characterizing environmental conditions during the growing period. The obtained agroclimatic data were monthly means from the nearest BMKG stations during the tuber development period (January-June 2021).

Sample preparation

The study gathered purple and white *D. alata* tubers from local farms in Bantul Regency, Yogyakarta, Indonesia. For each type of tuber, selecting these was according to uniform size (approximately similar weight), physiological maturity, and the absence of visible mechanical damage, pest infestation, or disease symptoms. Selected tubers received thorough washing with distilled water to remove adhering soil and debris before peeling manually and slicing into pieces of uniform thickness to ensure consistent processing. The sliced samples' dividing into two processing treatments comprised raw and steamed. The conduct of steaming was at approximately 100 °C for 30 min to simulate common household cooking conditions. After processing, the samples sustained oven-drying at ≤ 50 °C until reaching constant weight, then grinding into fine powder using a laboratory grinder, and thorough homogenization to minimize variability between subsamples. The powdered samples entailed storage in airtight containers at room temperature before chemical analyses.

Proximate analysis

Proximate composition determination included moisture, ash, crude protein, crude lipid, and carbohydrate content using standard Association of Official Analytical Chemists (AOAC) methods (AOAC International, 2020). All conducted analyses were in triplicate, with results expressed on a dry weight basis.

FTIR analysis

Using the Fourier Transform Infrared Spectroscopy (FTIR) served to identify functional groups present in tuber samples. Spectra recording used an FTIR spectrometer equipped with an attenuated total reflectance (ATR) accessory over a wavenumber range of 4000–400 cm^{-1}. Each sample scanned was in triplicate, processing the spectra using the instrument's proprietary software. This approach has reached wide application for the qualitative characterization of plant biomolecules and phytochemical functional groups (Coates, 2000; Stuart, 2004).

GC-MS analysis

The successful determination of bioactive compound profiles used Gas Chromatography-Mass Spectrometry (GC-MS) following solvent extraction of tuber powders. Briefly, extracting 1 g of dried tuber powder utilized 10 mL of n-hexane (1:10 w/v). The mixture, after shaking and allowing to stand at room temperature for 3 h, enabled the extraction of non-polar compounds. Then, the extract underwent filtration through Whatman No. 1 filter paper, with the filtrate used for GC-MS analysis after passing through a 0.22 µm syringe filter.

The study carried out GC-MS analysis using an HP-5MS capillary column (5% phenyl–95% dimethylpolysiloxane, 30 m length, 0.25 mm internal diameter, and 0.25 µm film thickness). Helium (He) served as the carrier gas at a constant flow rate. Compound ionization, as performed, used the Electron Impact (EI) method with an ionization energy of 70 eV. Compound identification depended on the comparison of resulting mass spectra with the NIST library and published databases (Adams, 2017), expressing the relative abundance of detected compounds as percentage peak area.

Experimental design and data analysis

The experiment followed a factorial design consisting of two tuber types (purple and white) and two processing treatments (raw and steamed), with three independent replicates for each treatment combination. Proximate composition data's analysis used two-way analysis of variance (ANOVA) to evaluate the effects of tuber type, processing treatment, and their interaction. Before ANOVA, the assumptions of normality and homogeneity of

variance obtained assessment using the Shapiro-Wilk test and Levene's test, respectively. When detecting significant differences ($p < 0.05$), mean comparisons between treatment groups continued using Tukey's honestly significant difference (HSD) test. No data transformation was necessary as the data met the assumptions of ANOVA. FTIR and GC-MS results underwent descriptive and comparative interpretations to evaluate phytochemical variations between tuber types and processing treatments. Statistical analyses and data visualization succeeded in using GraphPad Prism version 10.6.0 (GraphPad Software, San Diego, CA, USA). Agroclimatic data incorporation served as contextual environmental information to support the interpretation of phytochemical profiles.

RESULTS AND DISCUSSION

This study does not establish causal relationships, but it provides indicative evidence of an agroclimatic association with phytochemical expression (Moore *et al*., 2014; Qaderi *et al*., 2023).

Proximate composition of purple and white *D. alata*

The proximate composition of purple and white *D. alata* tubers has a summary in Table 1. Two-way ANOVA revealed that processing (raw vs. steamed) was the dominant factor influencing proximate composition, although varietal effects and interaction effects were also notable, depending on the parameter analyzed.

Previous literature indicated that *D. alata* tubers exhibit substantial variation in both major and bioactive constituents, underscoring the importance of proximate and phytochemical profiling across cultivars and processing treatments (Lebot *et al.*, 2023; Amedor *et al*., 2025). Additionally, recent studies employing spectroscopic and chromatographic techniques have demonstrated that phenolic and antioxidant components vary with genotypes and postharvest handling, reinforcing our finding that both variety and processing significantly influence biochemical composition.

Nevertheless, the presence of significant varietal effects for certain parameters suggests that genetic differences between purple and white *D. alata* contribute to baseline compositional variability, likely associated with differences in tuber physiology, storage compound allocation, and pigment-related metabolism. Previous studies have documented that pigmented yam varieties often exhibit distinct nutrient partitioning patterns compared with non-pigmented varieties, reflecting coordinated regulation between primary metabolism and secondary-metabolite biosynthesis (Ceci *et al*., 2022; Lu *et al*., 2022).

Carbohydrate content

Carbohydrates constituted the major component in both *D. alata* tuber types, as shown in Table 1. Two-way ANOVA revealed a significant interaction between tuber color and processing treatment ($p < 0.0001$), indicating the response to steaming differed between purple and white tubers. Processing accounted for the largest proportion of the total variation (93.24% of the total sum of squares in the ANOVA model), with steamed samples exhibiting substantially lower carbohydrate content than raw samples ($p < 0.0001$). A considerable difference between the purple and white tubers was also evident ($p < 0.0001$), with purple tubers showing slightly higher mean carbohydrate content than white tubers. Recent studies have demonstrated that thermal processing, such as steaming, induces starch gelatinization and leaching of soluble carbohydrates in *Dioscorea* tubers, leading to reduced measurable carbohydrate content after cooking (Lebot, 2019; Amedor *et al*., 2025). In addition, varietal differences in starch structure and amylose–amylopectin ratios have had reports of influencing carbohydrate stability during heat treatment, supporting the observed interaction between genotype and processing effects in the presented study (Lu *et al*., 2022).

Table 1. Proximate composition of purple and white *D. alata* L. tubers under raw and steamed conditions (mean±SD).

No.	Samples	Percentage (%)					
		Water	Ash	Fat	Protein	Carbohydrate	Starch
1	white yam (Raw)	11.90±0.27	2.78±0.19	0.37±0.07	6.94±0.15	78.31±0.03	59.08±0.21
2	purple yam (Raw)	11.03±0.28	2.14±0.10	0.39±0.09	7.40±0.16	79.40±0.09	59.99±0.39
3	white yam (steamed)	14.63±0.12	2.59±0.11	0.15±0.01	6.67±0.10	75.96±0.07	57.23±0.14
4	purple yam (steamed)	14.91±0.06	2.42±0.05	0.16±0.01	6.99±0.22	75.52±0.11	52.55±0.13

Values are expressed as mean ± SD (n = 3) on a dry weight basis (% DW). Bold values indicate the highest result for each parameter. Statistical differences among varieties (purple vs white), processing treatments (raw vs steamed), and their interaction entailed evaluation using two-way ANOVA (α = 0.05).

Differences in carbohydrate retention between purple and white varieties may also reflect underlying physiological differences in starch granule microstructure and packing density, which determine susceptibility to hydrothermal disruption. Reports on pigmented *D. alata* varieties have detailed to possess more compact or partially modified granule morphologies associated with phenolic-starch interactions, potentially reducing leaching losses during cooking (Meng *et al*., 2022). Moreover, steaming-induced moisture redistribution can promote enzymatic or non-enzymatic breakdown of amorphous starch regions, a process that may progress at different rates, depending on varietal genotype and the local arrangement of crystalline domains (Selma-Gracia *et al*., 2020; Chakraborty *et al*., 2021). These combined factors could explain why carbohydrate content decreases sharply after steaming and why the magnitude of reduction differs between purple and white tubers.

Protein content

Protein content varied only slightly among treatments (Table 1). Two-way ANOVA indicated no significant interaction between tuber type and processing treatment, suggesting that steaming affected purple and white tubers similarly. Overall, purple tubers showed slightly higher protein levels than white tubers, while steaming resulted in lower protein content than with raw samples. These results indicate that protein variation in *D. alata* tubers reflects inherent differences between tuber types along with changes associated with thermal processing. Previous studies have reported that protein accumulation in yam tubers may vary among varieties due to differences in nitrogen uptake efficiency and storage protein synthesis during tuber development (Polycarp *et al*., 2012; Lebot *et al*., 2023).

The reduction in protein content following steaming is consistent with reports that thermal processing induces protein denaturation, aggregation, and leaching of soluble nitrogenous compounds into the cooking medium, resulting in lower measurable protein levels on a dry weight basis (Shitta *et al*., 2021; Amedor *et al*., 2025). Unlike carbohydrates, which undergo extensive structural transformation during heating, tuber proteins generally exhibit limited thermal reorganization, which may explain the relatively narrow range of protein variation and the lack of interaction between variety and processing (Adepoju *et al*., 2018).

From an applied perspective, the consistent differences observed between the purple and white tubers suggest the incorporation of nutritional and phytochemical traits could be possible into germplasm evaluation frameworks for *D. alata*. Varieties that maintain relatively higher protein levels or desirable phytochemical profiles across processing treatments could represent promising parental material for breeding programs targeting improved nutritional quality. In addition, phytochemical screening using techniques, such as FTIR and GC-MS, can assist breeders and agronomists in identifying superior yam cultivars that combine favorable biochemical traits with adaptation to local cultivation environments.

Lipid content

Lipid content represented the smallest fraction of the proximate composition, as shown in Table 1. Two-way ANOVA revealed no significant interaction between variety and processing ($p = 0.8839$), and no significant main effect of variety ($p = 0.6631$), indicating that lipid content did not differ substantially between purple and white tubers. In contrast, processing exerted a strong and remarkable effect ($p = 0.0001$), accounting for 84.83% of the total variation. Steamed tubers exhibited substantially lower lipid content than raw samples. This pronounced reduction suggests that lipid components are highly sensitive to thermal processing, likely due to melting, oxidation, or leaching during steaming.

Recent studies on *Dioscorea* and other root and tuber crops have shown that lipid fractions are particularly susceptible to thermal degradation, with significant losses attributed to heat-induced oxidation and migration into cooking media during steaming or boiling (Shitta *et al*., 2021; Amedor *et al*., 2025). Similar findings reported minimal varietal influence on total lipid content but emphasized processing as the primary determinant of lipid retention, supporting the dominant processing effect observed in this present study (Lebot *et al.,* 2023).

Starch content

Starch content exhibited pronounced variability influenced by both variety and processing, as illustrated in Table 1. Two-way ANOVA demonstrated significant main effects of variety and processing, as well as a highly significant interaction between the two factors ($p < 0.0001$). Processing accounted for the largest proportion of variation (64.17%), with steaming causing a marked reduction in starch content. Overall, white tubers displayed considerably higher starch content than purple tubers. The noteworthy interaction effect indicates the impact of steaming on starch content differs between varieties, suggesting varietal differences in starch composition, granule organization, or thermal stability.

Recent studies have stated starch content and thermal stability in *D. alata* are strongly genotype-dependent, with white-fleshed varieties often exhibiting higher starch concentration and more heat-stable granule structures than pigmented varieties (Meng *et al*., 2022; Lebot *et al*., 2023). Moreover, steaming has been shown to induce starch gelatinization and solubilization, leading to apparent starch losses that vary according to amylose-amylopectin ratios and granule crystallinity, supporting the significant interaction between varieties and processing observed in this study (Amedor *et al*., 2025).

FTIR functional group profiles

Fourier Transform Infrared (FTIR) spectra revealed the presence of major functional groups associated with carbohydrates, proteins, lipids, and secondary metabolites in both purple and white *D. alata* L. tubers under raw and steamed conditions (Table 2; Figures 1, 2, and 3). Although the overall spectral profiles were qualitatively similar among treatments, variations in band intensity and definition reflected the combined effects of varietal characteristics and thermal processing.

The broad absorption band at 3415–3275 cm^{-1}, corresponding to O–H stretching vibrations, was evident in all samples but exhibited stronger intensity in purple tubers than in white tubers. This band reached further enhancement after steaming, suggesting increased exposure or release of hydroxyl-containing compounds, such as phenolics, flavonoids, and proteins, following thermal treatment (Sutharsan *et al*., 2022; Nie *et al*., 2023). Reports on similar observations have come out on pigmented tuber crops, where higher phenolic content contributes to stronger O–H absorption signals (Thummajitsakul *et al*., 2023).

Table 2. Major FTIR absorption bands and their biochemical interpretation in purple and white *D. alata* L. tubers under raw and steamed conditions.

Wavenumber (cm^{-1})	Functional group (vibration)	Major source compounds	Observed spectral characteristics	Reference
3415–3275	O–H stretching	Phenols, flavonoids, proteins	Stronger absorption in purple tubers than in white tubers; band intensity increased after steaming, indicating enhanced exposure of hydroxyl-containing compounds	Sutharsan *et al*., 2022; Nie *et al*., 2023
2928–2925	Aliphatic C–H stretching	Proteins, lipids	Detected in all samples with comparable positions; slightly enhanced in steamed samples, suggesting structural modification of lipid–protein complexes	Nie *et al*., 2023
2149–2095	C≡C / C≡N stretching	Minor biomolecular components	Weak bands observed across all treatments; no marked varietal differentiation, consistent with minor functional groups	Coates, 2000
1732–1640	C=O stretching (amide I)	Carbohydrates, proteins	More pronounced absorption in purple tubers, particularly after steaming, indicates changes in protein secondary structure and carbohydrate-associated carbonyl groups	Ciursa *et al*., 2021
1560–1545	Aromatic C=C stretching	Phenolic compounds	Higher band intensity in purple tubers, reflecting greater phenolic-associated aromatic structures than with white tubers	Thummajitsakul *et al*., 2023
1420–1382	C–H bending	Carbohydrates	Present in all samples, with a slight reduction in sharpness after steaming, suggesting polysaccharide rearrangement	Rozenberg *et al*., 2019
1338–1243	C–N stretching (amide III)	Proteins	Consistently detected in all samples; relative intensity slightly reduced after steaming due to protein denaturation	Rozenberg *et al*., 2019
1158–1080	C–O–C stretching	Sucrose, polysaccharides	Broad bands observed in all samples; decreased band definition after steaming, indicating modification of glycosidic linkages	Ciursa *et al*., 2021
1023–995	C–O / C–OH stretching	Glucose, fructose	Strong bands in raw samples; partial attenuation after steaming due to thermal alteration of soluble sugars	Ciursa *et al*., 2021
931–858	β-glycosidic bond vibration	Glucose units	Detected in all samples; relatively stronger in raw tubers, consistent with intact starch structure	Hamid *et al*., 2019
764–710	Ring deformation	Polysaccharides	Weak-to-moderate bands across samples; no clear varietal separation	Coates, 2000
664–441	Skeletal vibrations	Complex biomolecules	Low-intensity bands common to all treatments, reflecting overall plant biomolecular matrix	Stuart, 2004

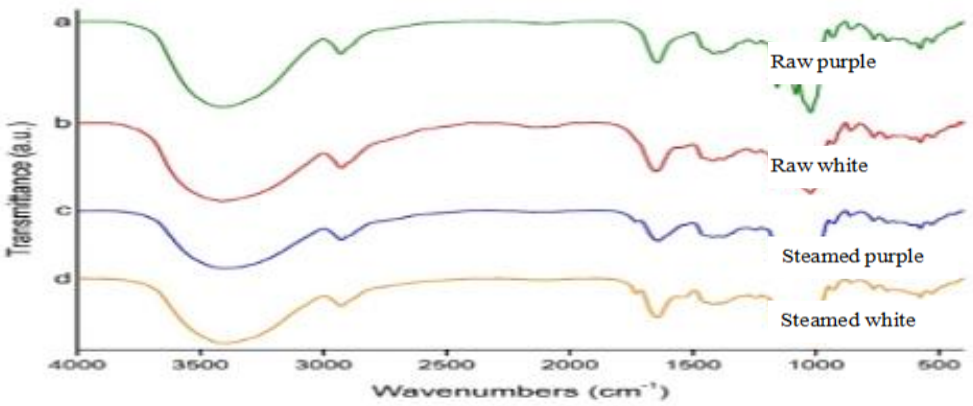

Figure 1. Overlay of FTIR spectra (transmittance) of *Dioscorea alata* tubers under four conditions: (a) raw purple variety, (b) raw white variety, (c) steamed purple variety, and (d) steamed white variety.

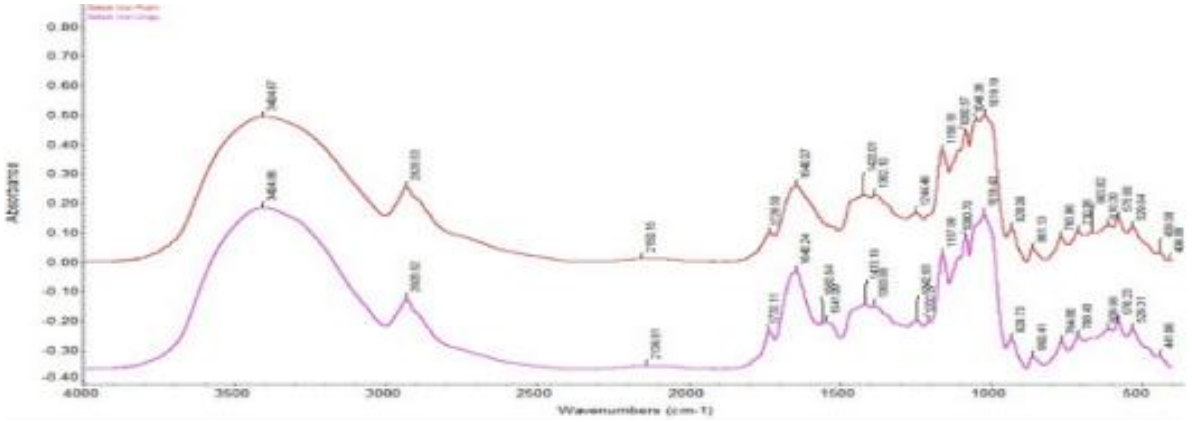

Figure 2. Overlay of FTIR spectra (absorbance mode) of raw *Dioscorea alata* tubers: comparison of raw white and raw purple varieties.

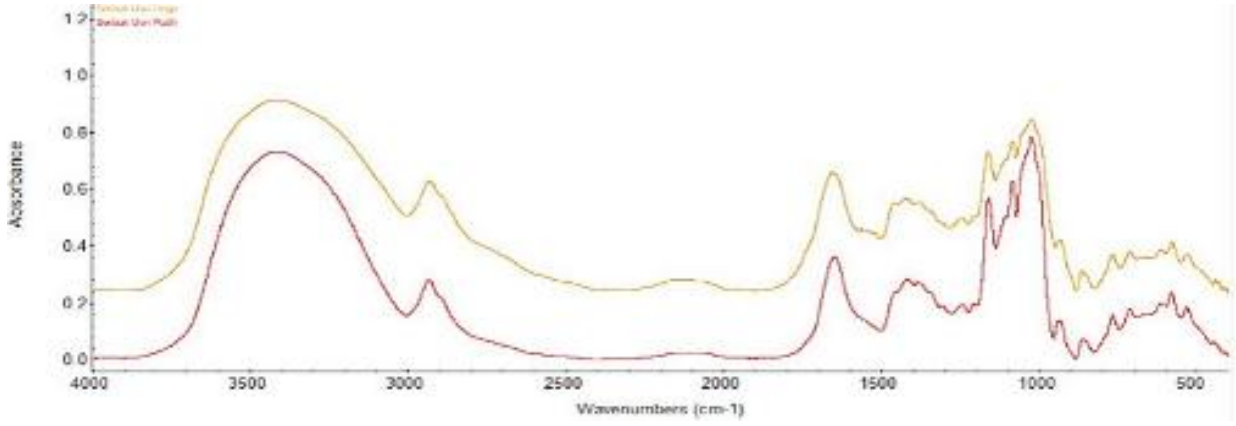

Figure 3. Overlay of FTIR spectra (absorbance mode) of steamed *Dioscorea alata* tubers: comparison of steamed white and steamed purple varieties.

Absorption bands at 2928–2925 cm^{-1}, attributed to aliphatic C–H stretching, succeeded in consistent detection across all samples, indicating the presence of lipid- and protein-associated structures. Slight enhancement of this band in steamed samples suggests thermal modification of lipid-protein complexes, a phenomenon commonly reported following hydrothermal processing of root and tuber crops (Nie *et al*., 2023). Minor bands in the region of 2149–2095 cm^{-1} were weak and showed no clear varietal differentiation, consistent with vibrations originating from minor biomolecular components (Coates, 2000).

The carbonyl-related region (1732–1640 cm^{-1}), associated with C=O stretching of carbohydrates and amide I vibrations of proteins, showed more pronounced absorption in purple tubers, particularly after steaming. This pattern indicates varietal differences in protein structure and carbohydrate-associated carbonyl groups, as well as processing-induced conformational changes (Ciursa *et al*., 2021). Enhanced aromatic C=C stretching bands at 1560–1545 cm^{-1} were also more evident in purple tubers, reflecting a higher contribution of phenolic-associated aromatic structures relative to white tubers (Thummajitsakul *et al*., 2023).

Bands related to carbohydrate structures, including C–H bending (1420–1382 cm^{-1}), C–N stretching of amide III (1338–1243 cm^{-1}), and C–O–C stretching of polysaccharides (1158–1080 cm^{-1}), were present in all samples but displayed reduced sharpness following steaming. These changes indicate partial disruption or rearrangement of polysaccharide and protein matrices during thermal processing (Rozenberg *et al*., 2019; Ciursa *et al*., 2021). Similarly, absorption bands at 1023–995 cm^{-1}, associated with C–O and C–OH stretching of glucose and fructose units, suffered attenuation in steamed samples, suggesting modification of soluble sugars and starch components.

The region at 931–858 cm^{-1}, corresponding to β-glycosidic bond vibrations, entailed detection in all treatments but appeared relatively stronger in raw samples, consistent with the preservation of intact starch structures before steaming (Hamid *et al*., 2019). Lower wavenumber regions (764–710 cm^{-1} and 664–441 cm^{-1}) showed weak skeletal vibrations common to all samples, reflecting the complex biomolecular matrix of yam tubers rather than treatment-specific features (Coates, 2000; Stuart, 2004).

Overall, the FTIR analysis demonstrated that while the major functional groups prevailed across varieties and processing treatments, differences in spectral intensity and band definition provided evidence of varietal biochemical differentiation and processing-induced structural modification. The stronger phenolic-associated signals observed in purple *D. alata* tubers, together with their responsiveness to agroclimatic and thermal conditions, support the potential use of FTIR-derived traits as complementary biochemical descriptors for germplasm characterization and selection in yam breeding programs.

GC-MS identification of bioactive compounds

GC-MS analysis identified a diverse range of phytochemical constituents across all samples, with phenolic derivatives and fatty acid ethyl esters (FAEEs) predominating in the profiles (Table 2). Purple tubers exhibited higher relative intensity/abundance and greater diversity of these compounds than white tubers. The increased presence of FAEEs in steamed samples suggests that thermal treatment may facilitate the release or transformation of lipid-related compounds. Variation in secondary metabolite composition among varieties supports previous observations that biochemical diversity in tuber crops received influences from both genotype and environmental conditions (Moore *et al*., 2014; Badal *et al*., 2024).

The higher abundance of phenolic derivatives in purple *D. alata* tubers is consistent with the role of pigmentation-associated metabolic pathways, particularly those linked to the phenylpropanoid route, which contributes to both color expression and antioxidant capacity. Recent studies have shown that pigmented yam varieties accumulate a broader spectrum of phenolic

compounds due to coordinated regulation of secondary metabolism, reinforcing the varietal differentiation observed in the present GC-MS profiles (Meng *et al*., 2022).

The prominence of fatty acid ethyl esters in steamed samples may reflect heat-induced lipid hydrolysis followed by esterification reactions or increased extractability of bound lipid fractions during thermal processing. Similar increases in esterified lipid derivatives after cooking have come out on root and tuber crops, suggesting that processing alters not only the quantity but also the chemical form of lipid-associated metabolites (Li *et al*., 2023; Amedor *et al*., 2025). Such processing-related shifts in metabolite composition are particularly relevant when evaluating biochemical traits intended as markers for germplasm characterization.

Agroclimatic influence on phytochemical expression

A summary of agroclimatic conditions during the tuber development period (January-June 2021) in Yogyakarta, Indonesia, appears in Table 3. The study area experienced relatively stable air temperatures, with mean values of 26.4 °C and a narrow range between 26.0 °C and 27.1 °C. Sunshine duration showed moderate to high variability, with an average of 58.6%, indicating increasing solar radiation toward the dry season. Monthly rainfall exhibited a strong seasonal decline, with mean values of 201.5 mm and a wide range from 0 to 402 mm, accompanied by a decrease in the number of rainy days.

These environmental conditions characterize the general growing environment where the cultivation of the purple and white *D. alata* tubers took place. All collected samples came from the same location and growing period; hence, the presented study does not directly evaluate the effects of agroclimatic variation on phytochemical composition. Instead, the study provided the agroclimatic information to provide environmental context for the cultivation conditions of sampled tubers. The observed differences in phytochemical profiles between purple and white *D. alata* tubers, therefore, primarily reflect varietal variation rather than differences in environmental conditions.

Previous studies have reported that agroclimatic factors, such as temperature, solar radiation, and rainfall, may influence carbohydrate metabolism and secondary metabolite biosynthesis in root and tuber crops, including *Dioscorea* species (Lebot *et al*., 2023; Saravanan and Gutam, 2023). Similarly, reduced rainfall or moderate environmental stress has shown an association with increased accumulation of phenolic compounds in several crop species (Moore *et al*., 2014; Nahuelcura *et al*., 2023; Qaderi *et al*., 2023). Although this study does not directly test these relationships, the agroclimatic data provide useful background information on the environmental conditions under which the sampled yam varieties grew.

Table 3. Agroclimatic conditions of the study area (Yogyakarta, Indonesia) during the tuber development period in 2021 (BMKG data).

Parameter	Location (Station)	Jan-June Mean	Range	Interpretation
Air temperature (°C)	Sleman (Staklim and Stageof)	26.4	26.0–27.1	Stable thermal condition
Sunshine duration (%)	Sleman (Staklim and Stageof)	58.6	33–74	Increasing solar radiation
Rainfall (mm/month)	Bantul (BPP Imogiri and SDA Siluk)	201.5	0–402	Strong seasonal decline
Rainy days (days/month)	Bantul (BPP Imogiri and SDA Siluk)	11.6	1–27	Transition to dry period

Germplasm characterization, breeding, and study limitations

The combined results demonstrate that phytochemical traits, through FTIR and GC-MS profiles, provide informative biochemical descriptors for differentiating *D. alata* varieties. These traits could serve as useful indicators for identifying promising germplasm with desirable nutritional and biochemical characteristics. Incorporating such biochemical markers into germplasm characterization frameworks may enhance the efficiency of future *D. alata* breeding and crop improvement programs. Overall, the integration of proximate composition, FTIR spectral features, and GC-MS profiles provides complementary evidence of agroclimatic-associated biochemical variation between purple and white *D. alata* tubers.

Recent breeding-oriented studies have emphasized that metabolite- and spectroscopy-based markers can serve as valuable tools for germplasm evaluation, particularly in clonally propagated crops, such as yams, where conventional phenotypic selection may be insufficient (Lebot *et al.*, 2023; Saravanan and Gutam, 2023). Additionally, integrating biochemical fingerprints with environmental information has reached proposing as a promising approach for identifying nutritionally improved and climate-resilient root and tuber varieties (Moore *et al*., 2014; Nahuelcura *et al*., 2023; Qaderi *et al*., 2023).

However, several limitations of this study should receive attention. The samples collected came from a single cultivation location and growing period, which limits the ability to directly evaluate the influence of agroclimatic variation on phytochemical composition. Consequently, the observed differences primarily reflect varietal variation between purple and white *D. alata* tubers rather than environmental effects. Moreover, multivariate statistical approaches, such as principal component analysis (PCA), could further assist in visualizing overall variation and relationships among samples based on their phytochemical profiles. Future studies involving larger datasets and broader germplasm collections may therefore benefit from applying PCA or other multivariate analyses to better characterize biochemical diversity and genotype-environment interactions in *Dioscorea* species.

CONCLUSIONS

This study demonstrates that phytochemical and proximate traits of purple and white *D. alata* tubers vary in association with agroclimatic conditions and processing treatments. Thermal processing, particularly steaming, succeeded in its identification as the dominant factor affecting carbohydrate, protein, lipid, and starch contents, while varietal differences independently contributed to baseline compositional variation. FTIR and GC-MS analyses revealed clear varietal differentiation, with purple tubers exhibiting a higher abundance of phenolic-associated functional groups and secondary metabolites. Agroclimatic conditions characterized by stable temperatures, increasing solar radiation, and reduced rainfall during tuber development showed an association with enhanced expression of secondary metabolites. Although this study does not establish direct causal relationships, the observed patterns indicate that agroclimatically responsive phytochemical traits can serve as informative biochemical descriptors for *D. alata* germplasm characterization. These findings support the integration of phytochemical profiling into yam breeding programs aimed at selecting nutritionally superior and agroclimate-adapted varieties, with further multi-location studies recommended to validate these associations across diverse environments.

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REFERENCES

Adams RP (2017). Identification of Essential Oil Components by Gas Chromatography/Mass Spectrometry. 4th Ed. Allured Publ. Corp., Carol Stream, IL, USA.

Adepoju OT, Boyejo O, Adeniji PO (2018). Effects of processing methods on nutrient and antinutrient composition of yellow yam (*Dioscorea cayenensis*) products. *Food Chem.* 238: 160–165. doi:10.1016/j.foodchem.2016.10.071.

Agostini-Costa TS, Vieira RF, Bizzo HR, Silveira D, Gimenes MA (2012). Secondary metabolites. In: B. Sasikumar (Ed.). Chromatography and its Applications. Vol. 1. InTech, pp. 131–164.

Amedor EN, Sarpong F, Bordoh PK, Boateng EF, Owusu-Kwarteng J (2025). Impact of pretreatment and drying on the chemical composition and sensory quality of fried yam (*Dioscorea rotundata*) chips. *Explor. Foods Foodomics* 3: 101095. doi:10.37349/eff.2025.101095.

AOAC International (2020). Official methods of analysis of AOAC International. 21st Ed. AOAC Int., Gaithersburg, MD, USA.

Badal S, Delgoda R, Efferth T (2024). Evolutionary perspectives on the role of plant secondary metabolites. In: S. Badal and R. Delgoda (Eds.). Pharmacognosy. Academic Press, pp. 93–101.

Ceci AT, Franceschi P, Serni E, Perenzoni D, Oberhuber M, Robatscher P, Mattivi F (2022). Metabolomic characterization of pigmented and non-pigmented potato cultivars using joint and individual variation explained analysis. *Foods* 11(12): 1708. doi:10.3390/foods11121708.

Chakraborty I, Govindaraju I, Rongpipi S, Mahato KK, Mazumder N (2021). Effects of hydrothermal treatments on physicochemical properties and in vitro digestion of starch. *Food Biophys.* 16(4): 544–554. doi:10.1007/s11483-021-09687-7.

Ciursa P, Pauliuc D, Dranca F, Ropciuc S, Oroian M (2021). Detection of honey adulterated with agave, corn, inverted sugar, maple, and rice syrups using FTIR analysis. *Food Control* 130: 108266. doi:10.1016/j.foodcont.2021.108266.

Coates J (2000). Interpretation of infrared spectra, a practical approach. In: R.A. Meyers (Ed.). Encycl. Anal. Chem. John Wiley and Sons, Chichester, UK, pp. 10815–10837.

Hamid ZAA, Idris MHM, Arzami NAAB, Ramle SFM (2019). Investigation on the chemical composition of *Dioscorea hispida* Dennst. (Ubi Gadong). *AIP Conf. Proc.* 2068: 020041. doi:10.1063/1.5089340.

Kliebenstein DJ (2004). Secondary metabolites and plant/environment interactions: A view through *Arabidopsis thaliana* tinged glasses. *Plant Cell Environ.* 27(6): 675–684. doi:10.1111/j.1365-3040.2004.01180.x

Lebot V (2019). Tropical Root and Tuber Crops: Cassava, Sweet Potato, Yams and Aroids. CABI, Wallingford, UK.

Lebot V, Lawac F, Legendre L (2023). The greater yam (*Dioscorea alata* L.): A review of its phytochemical content and potential for processed products and biofortification. *J. Food Compos. Anal.* 115: 104987. doi:10.1016/j.jfca.2022.104987.

Lu K, Li X, Yu J, Wang S (2022). Structure and functional properties of purple yam (*Dioscorea alata* L.) starch from China. *Starch–Stärke* 74(5–6): 2100233. doi:10.1002/star.202100233.

Meng YY, Wang N, Si CC (2022). The application of nitrogen source in regulating lignin biosynthesis, storage root development and yield of sweet potato. *Agronomy* 12(10): 2317. doi:10.3390/agronomy12102317.

Mignouna HD, Abang MM, Asiedu R (2003). Harnessing modern biotechnology for tropical tuber crop improvement: Yam (*Dioscorea* spp.) molecular breeding. *Afr. J. Biotechnol.* 2(12): 478–485.

Moore BD, Andrew RL, Külheim C, Foley WJ (2014). Explaining intraspecific diversity in plant secondary metabolites in an ecological context. *New Phytol.* 201(3): 733–750. doi:10.1111/nph.12526.

Nie H, Dong H, Chen Y, Hao M, Chen J, Tang Z, Liu Q, Li J, Xu X, Xue Y (2023). Effects of spray drying and freeze drying on the structure and emulsifying properties of yam soluble protein: A study by experiment and molecular dynamics simulation. *Food Chem.* 409: 135238. doi:10.1016/j.foodchem.2022.135238.

Polycarp D, Afoakwa EO, Budu AS, Otoo E (2012). Characterization of chemical composition and anti-nutritional factors in seven species within the Ghanaian yam (*Dioscorea*)

germplasm. *Int. Food Res. J.* 19(3): 985–992.

Qaderi MM, Martel AB, Strugnell CA (2023). Environmental factors regulate plant secondary metabolites. *Plants* 12(3): 447. doi:10.3390/plants12030447.

Rozenberg M, Lansky S, Shoham Y, Shoham G (2019). Spectroscopic FTIR and NMR study of the interactions of sugars with proteins. *Spectrochim. Acta A Mol. Biomol. Spectrosc.* 222: 116861. doi:10.1016/j.saa. 2019.02.085.

Saravanan R, Gutam S (2023). Climate change impacts on tuber crops: Vulnerabilities and adaptation strategies. *J. Hortic. Sci.* 18(1): 1–18. doi:10.24154/jhs.v18i1.2129.

Selma-Gracia R, López-Jiménez MJ, Hernández-Cruz MC (2020). Potential beneficial effect of hydrothermal treatment of starches from various sources on in vitro digestion. *Food Hydrocoll.* 103: 105687. doi:10.1016/j.foodhyd.2020.105687.

Shitta NS, Adewumi AA, Gbadegesin WA, Adebayo TA (2021). A review on the cooking attributes of African yam bean (*Sphenostylis stenocarpa*). *Legume Res.* 44(9): 1029–1037. doi:10.18805/LR-620.

Stuart BH (2004). Infrared spectroscopy: Fundamentals and applications. John Wiley and Sons, Chichester, UK.

Sutharsan J, Boyer CA, Zhao J (2022). Physicochemical properties of chitosan edible films incorporated with different classes of flavonoids. *Carbohydr. Polym. Technol. Appl.* 4: 100232. doi:10.1016/j.carpta.2022.100232.

Thummajitsakul S, Paensanit P, Saeieo T, Sirirat J, Silprasit K (2023). FTIR and multivariate analysis of total phenolic content, antioxidant and anti-amylase activities of extracts and milk of *Glycine max* L. and *Phaseolus vulgaris* L. *Electron. J. Biotechnol.* 64: 69–75. doi:10.1016/j.ejbt.2023.04.001.