



## Organ-Specific Phytochemical Distribution and Literature-Guided Metabolite Inference in the Peel, Pulp and Seed of *Carica papaya* L.

[Organisation phytochimique spécifique des tissus et inférence métabolique guidée par la littérature dans l'épluchure, la pulpe et les graines de *Carica papaya* L.]

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### Abstract

*Carica papaya* L. is a tropical fruit known for its nutritional benefits and content of biologically active compounds. Nevertheless, limited data exist concerning the tissue-specific partitioning of phytochemicals within fruit tissues. The present study examined the presence of different classes of secondary metabolites in the peel, pulp, and seeds of *C. papaya* via qualitative phytochemical analysis, together with biochemical inference based on data from literature sources. Secondary metabolite analyses revealed the unique presence of distinct phytochemical profiles in various fruit tissues. The pulp showed positive results for the presence of anthocyanins, leucoanthocyanins, alkaloids, quinones and terpenoids/sterols. Tannins, alkaloids, quinones, and terpenoids have been found in the peel, while the seed sample demonstrated the prevalence of flavonoids related to saponins, alkaloids, and terpenoids. Metabolites already described in *C. papaya* and associated with the mentioned fruit parts have been found using the LOTUS Natural Products Database and scientific literature. Nevertheless, these compounds were only used to interpret the presence of certain phytochemical groups without experimental confirmation in the studied samples. Based on data analysis, it can be suggested that alkaloids, shikimic acid-, and phenylpropanoid-related metabolites and terpenoids are the most abundant classes of metabolites in *C. papaya*. The findings indicate a tissue-dependent phytochemical localization within *C. papaya* fruits and illustrate the possible biochemical specificity in each tissue, such as the peel, pulp, and seeds. While the hypothesis on biochemical specificity still needs to be proven using advanced methods such as LC-MS/MS, GC-MS, NMR dereplication, and spatial metabolomics, this study will prove beneficial in determining the biochemical specificity of each tissue and may serve as a basis for valorizing the waste products of the papaya fruit.

**Keywords:** Phytochemical screening; tissue-specific phytochemistry; phytochemical compartmentalization; literature-guided biochemical inference; secondary metabolites; fruit by-products.

### Résumé

*Carica papaya* L. (la papaye). est un fruit tropical reconnu pour ses bienfaits nutritionnels et sa richesse en composés biologiquement actifs. Cependant, les données concernant la répartition spécifique des composés phytochimiques dans les différents tissus du fruit demeurent limitées. La présente étude a examiné la présence de diverses classes de métabolites secondaires dans l'épluchure, la pulpe et les graines de *C. papaya* à travers une analyse phytochimique qualitative, complétée par une interprétation biochimique fondée sur les données de la littérature scientifique. Les analyses des métabolites secondaires ont révélé des profils phytochimiques distincts selon les tissus du fruit. La pulpe a présenté des résultats positifs pour les anthocyanes, les leucoanthocyanes, les alcaloïdes, les quinones ainsi que les terpènes/stéroïdes. L'épluchure contenait des tanins, des alcaloïdes, des quinones et des terpènes, tandis que les graines se caractérisaient principalement par la présence de flavonoïdes, de saponines, d'alcaloïdes et de terpènes. Des métabolites déjà décrits chez *C. papaya* et associés aux différentes parties du fruit ont été identifiés à partir de la base de données LOTUS Natural Products Database ainsi que de la littérature scientifique. Toutefois, ces composés n'ont été utilisés que pour interpréter la présence de certains groupes phytochimiques et n'ont pas été confirmés expérimentalement dans les échantillons étudiés. L'analyse des données suggère que les alcaloïdes, les métabolites dérivés de l'acide shikimique et de la voie des phénylpropanoïdes, ainsi que les terpénoïdes, constituent les classes de métabolites les plus abondantes chez *C. papaya*. Ces résultats mettent en évidence une localisation tissulaire spécifique des composés phytochimiques dans les fruits de *C. papaya* et illustrent une possible spécificité biochimique propre à chaque tissu (l'épluchure, pulpe et graines). Bien que cette hypothèse de spécificité biochimique doive encore être validée par des approches analytiques avancées telles que la LC-MS/MS, la GC-MS, la déréplication par RMN et la métabolomique spatiale, cette étude fournit des informations utiles pour mieux comprendre la spécialisation biochimique des différents tissus du fruit et pourrait servir de base à la valorisation des sous-produits et déchets issus de *C. papaya*. La stratégie adoptée dans cette étude fournit des informations utiles sur la spécialisation métabolique dépendante des tissus ainsi que sur l'organisation métabolomique inférée des organes du fruit de *C. papaya*.

**Mots-clés :** Criblage phytochimique ; phytochimie spécifique aux tissus ; compartimentation phytochimique ; interprétation biochimique guidée par la littérature ; métabolites secondaires ; sous-produits de fruits.

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## 1. Introduction

*Carica papaya* (Caricaceae) is a species native to America and is distributed in tropical regions worldwide. Traditionally, the fruit has been used in folk medicine and cultivated for its edible fruits and latex, the latter containing papain, a cysteine protease (Koul et al., 2022; Ashutosh et al., 2020).

Previous studies have reported the presence of several secondary metabolites in different parts of this plant. *Papaya* fruit is a complex biochemical system comprising three specific organs (the peel, pulp, and seeds). The distribution of secondary metabolites is associated with specific physiological and ecological functions (Wang et al. 2024). Secondary metabolite accumulation is tissue-specific and represents a major feature of plant metabolism. Therefore, the biological activities of different fruit tissues may be associated with their specific secondary metabolite composition (Kumarasinghe et al., 2024; Zhou et al., 2021).

To date, phytochemical studies on papaya fruits have focused on their nutritional and phytochemical compositions and the biological activities of their extracts. However, Congolese species remain underexplored, and investigations on the fruit focusing on the organ-specific distribution of phytochemical classes are limited.

The phytochemical composition of specific tissues can vary greatly, considering that these tissues face different environmental and biological stimuli. It can be advanced that peels accumulate defense-related metabolites due to their exposure to external pressures. On the other hand, pulp, as an internal tissue, could present a phytochemical composition rich in pigments and antioxidant metabolites. Finally, seeds may contain metabolites with protective ecological roles (Reshi et al., 2023).

Moreover, the organ-specific distribution of phytochemicals can contribute to the valorization of fruit-by-products. Agricultural residues, such as fruit peels and seeds, are considered waste and discarded. However, recent studies suggest that they could be potential sources of interesting bioactive compounds (Rahim et al., 2024; Nirmal et al., 2023).

The objective of the present study was to investigate the tissue-specific distribution of phytochemicals in the peel, pulp, and seed tissues of *Carica papaya* through qualitative phytochemical screening. In addition, a literature-guided biochemical inference approach based on previously reported

metabolites was employed to provide a conceptual interpretation of the detected phytochemical classes. This approach does not constitute direct metabolite identification but rather provides a literature-supported framework for discussing potential biochemical organization within fruit tissues.

## 2. Material and methods

### 2.1. Plant Material

Two fresh mature fruits of *C. papaya* were collected from a single tree on October 13, 2023. The collected zone is an agricultural site locally known as “Bilanga ya ba Chinois. Located in the municipality of N’djili, Kinshasa, Democratic Republic of the Congo (4°21’50” S, 15°22’03” E), agricultural operations are conducted without the use of chemical fertilizers or pesticides.

A careful analysis of the collection site led to the selection of a tree that appeared to be healthy and growing under homogeneous environmental conditions. Since the objective of our study was to investigate tissue-specific phytochemical compartmentalization rather than interindividual variability, the use of fruits originating from the same tree minimized environmental and genetic variability and facilitated comparative biochemical interpretations among the peel, pulp, and seed tissues.

A sample specimen was authenticated by Mr. Boniface Landu Lukebakio on October 13, 2023 at the Herbarium of the Institut National des Etudes et de Recherches Agronomiques (INERA), Faculté des Sciences et Technologies, Université de Kinshasa. The plant material was authenticated by comparison with a herbarium specimen (voucher number Goossens 4495) and stored as Biocam-DMN-2023-Iza-CP in Biocam Laboratory at the Food Chemistry and Biochemistry Unit, Faculté des Sciences et Technologies, Mention Chimie et Industrie (D.R. Congo), the Université de Kinshasa.

The fruits were washed with deionized water and manually processed to separate the pulp, peels, and seeds. Each part was subsequently dried in a ventilated oven at 40°C. The seeds and peels were dried for four days, while the pulp was dried for seven days. The dried parts were finely ground using an electric grinder to obtain a homogeneous powder. The resulting powders were labeled and stored in airtight containers until further analysis.

## 2.2. Previously reported metabolites

A database of previously reported metabolites from *C. papaya* was derived from the LOTUS Natural Products Database (LOTUS), accessed on November 25, 2024, and a literature search. The LOTUS database is an open-access annotated database that provides information on the structures of natural products. The database also includes biological sources and literature references for recorded natural products. The LOTUS database uses information from various sources to provide detailed information on the metabolites synthesized by plants (Adriano et al., 2022). The metabolites retrieved from the LOTUS database and literature were not experimentally identified in the analyzed samples. These compounds were used exclusively as literature-supported biochemical references for interpreting the phytochemical groups detected during the qualitative screening.

## 2.3 Phytochemical Screening

The presence of secondary metabolites was confirmed by color reactions and precipitation in the test tubes. Flavonoids were identified using the Shinoda test, and tannins and polyphenols were detected using the ferric chloride test. The presence of terpenoids and steroids was confirmed by Liebermann-Burchard reaction. Saponins were detected using foam tests, and the presence of alkaloids was assessed using the Dragendorff test.

All tests were performed following the phytochemical screening protocols described by Bandiola (2018) (Bandiola et al., 2018 and Shaikh et al., 2020). All tests were performed in triplicate to ensure accuracy and reproducibility. The presence of secondary metabolites was assessed in both powdered fruit organ material and its extracts.

### 2.3.1. Preparation of extracts

The extracts were prepared by maceration using dichloromethane and a methanol-water mixture (80:20, v/v) as follows: 2 g of powdered organ was introduced into a flask containing 30 mL of dichloromethane and maintained under magnetic stirring for 48 h. The mixture was subsequently filtered through Whatman No. 1 filter paper. After drying, the residual plant material was re-extracted with 30 mL methanol-water (80:20, v/v) under magnetic stirring for 24 h.

### 2.3.2. Screening test

#### a) Detection of total polyphenols

Total polyphenols were detected using a 2% ferric chloride ( $\text{FeCl}_3$ ) solution. To 1 mL of the aqueous filtrate, three drops of 2%  $\text{FeCl}_3$  were added. The

intense dark coloration indicated the presence of polyphenolic compounds.

#### b) Detection of flavonoids

The Shinoda reaction was used to detect flavonoids. The Shinoda reagent consisted of a mixture of 95% ethanol, 12 N hydrochloric acid, distilled water (1:1:1). 1 mL of the reagent was added to a test tube containing 1 mL of the organic extract of the fruit organ and a few magnesium (Mg) chips. The appearance of a reddish or pink color indicated the presence of flavonoid compounds.

#### c) Detection of anthocyanins

The presence of anthocyanins was assessed using hydrochloric acid. The aqueous organ extract (2 mL) was mixed with 2 mL of 2 N HCl, followed by the addition of a few milliliters of ammonia solution. The shift to blue-violet coloration after ammonia addition indicates the presence of anthocyanins.

#### d) Detection of tannins

They were detected in the aqueous filtrate (1 mL) by adding 1 mL of distilled water and one to two drops of 10% ferric chloride ( $\text{FeCl}_3$ ) solution. The appearance of a dark green or blue-black coloration indicated that the sample contained tannins. Tannins were further characterized using the Stiasny reagent, prepared from 30% formaldehyde ( $\text{CH}_2\text{O}$ ) and 12 N hydrochloric acid (HCl) in a 20:1 (v/v) ratio.

#### e) Detection of free quinones

Free quinones were directly detected from powdered material of the different organs. The powder (1g) was mixed with petroleum ether (20 mL) and agitated for 24 h. The mixture was left for two hours and then filtered using a filter paper. The filtrate was concentrated under vacuum, and a few drops of 0.1 N sodium hydroxide (NaOH) were added. The appearance of yellow, red, or violet coloration in the aqueous phase confirmed the presence of free quinones.

#### f) Detection of bound quinones

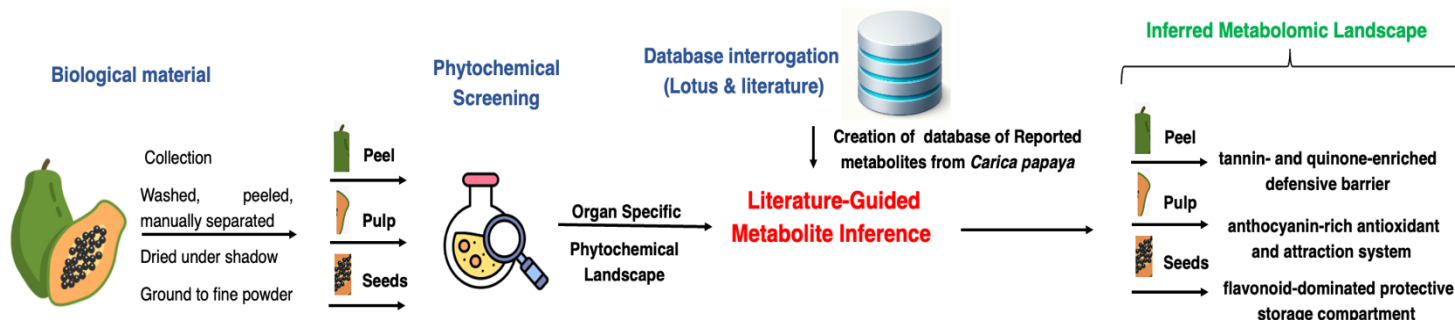
Bound quinones were detected using a modified Bornträger reaction. The organic extract of the fruit organs was treated with 5% hydrochloric acid (HCl). The mixture was heated in a water bath for a few minutes. After cooling, the mixture was extracted using chloroform. The appearance of yellow, red, or violet coloration upon the addition of 10% sodium hydroxide (NaOH) solution indicated the presence of bound quinones.

#### g) Detection of Coumarins

Coumarins were detected in the organic extracts. The extract (5 mL) was evaporated in a test tube. A

solution was obtained by dissolving the residue in 2 mL of hot water. The solution was divided into two parts, one of which was treated with 0.5 mL of 25%

literature-guided metabolite inference using reported metabolite databases. With this approach, an inferred metabolomic landscape could be devised, and



**Figure 1.** Conceptual workflow illustrating qualitative phytochemical screening and literature-guided biochemical inferences. The inferred metabolomic organization presented in this study represents a conceptual interpretation based on previously reported metabolites and does not correspond to direct metabolite identification in the analyzed tissues.

coumarins was indicated by fluorescence under ultraviolet light at 366 nm.

#### h) Detection of Saponins

Saponins were screened using a foam test. The aqueous extract was vigorously shaken in a test tube for 30–45 seconds. The formation of stable and persistent foam indicates the presence of saponins.

#### i) Detection of Terpenoids and Steroids

Terpenoids and steroids were detected using the Liebermann–Burchard reaction method. The organic extract (1 mL) was dissolved in 2 mL of acetic anhydride, followed by the careful addition of 0.5 mL concentrated sulfuric acid. The appearance of a violet coloration gradually changing from blue to green or the formation of a brownish-red ring at the interface of the two liquids indicated the presence of terpenoid and steroidal compounds.

#### j) Detection of Alkaloids

Alkaloids were detected using Dragendorff's reagent, which was prepared from 0.85 g of bismuth nitrate ( $\text{BiNO}_3$ ), 10 mL of glacial acetic acid, and 40 mL of distilled water. Briefly, 1 g of powdered material or 1 mL of extract was introduced into 50 mL of 0.1 M sulfuric acid ( $\text{H}_2\text{SO}_4$ ) solution. After agitation, five drops of Dragendorff's reagent were added to 1 mL of the solution. The formation of an orange precipitate indicated the presence of alkaloids in the extract.

### 2.4. Conceptual framework of the study

The methodological strategy adopted in this study is illustrated in [figure 1](#). This workflow combines tissue-specific phytochemical screening with

dependent metabolic specialization could be deduced for *C. papaya* fruit organs.

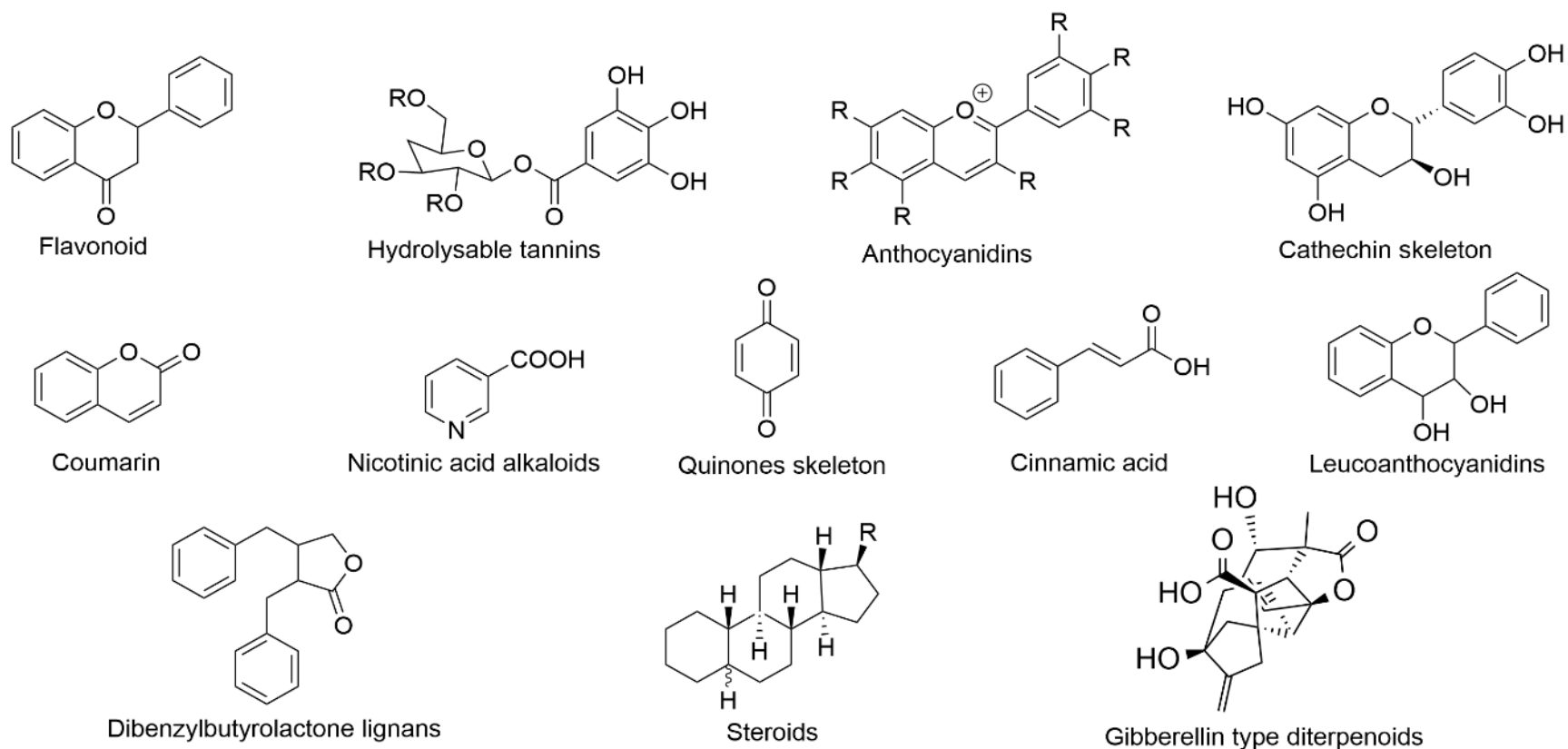
## 3. Results

### 3.1. Reported metabolites

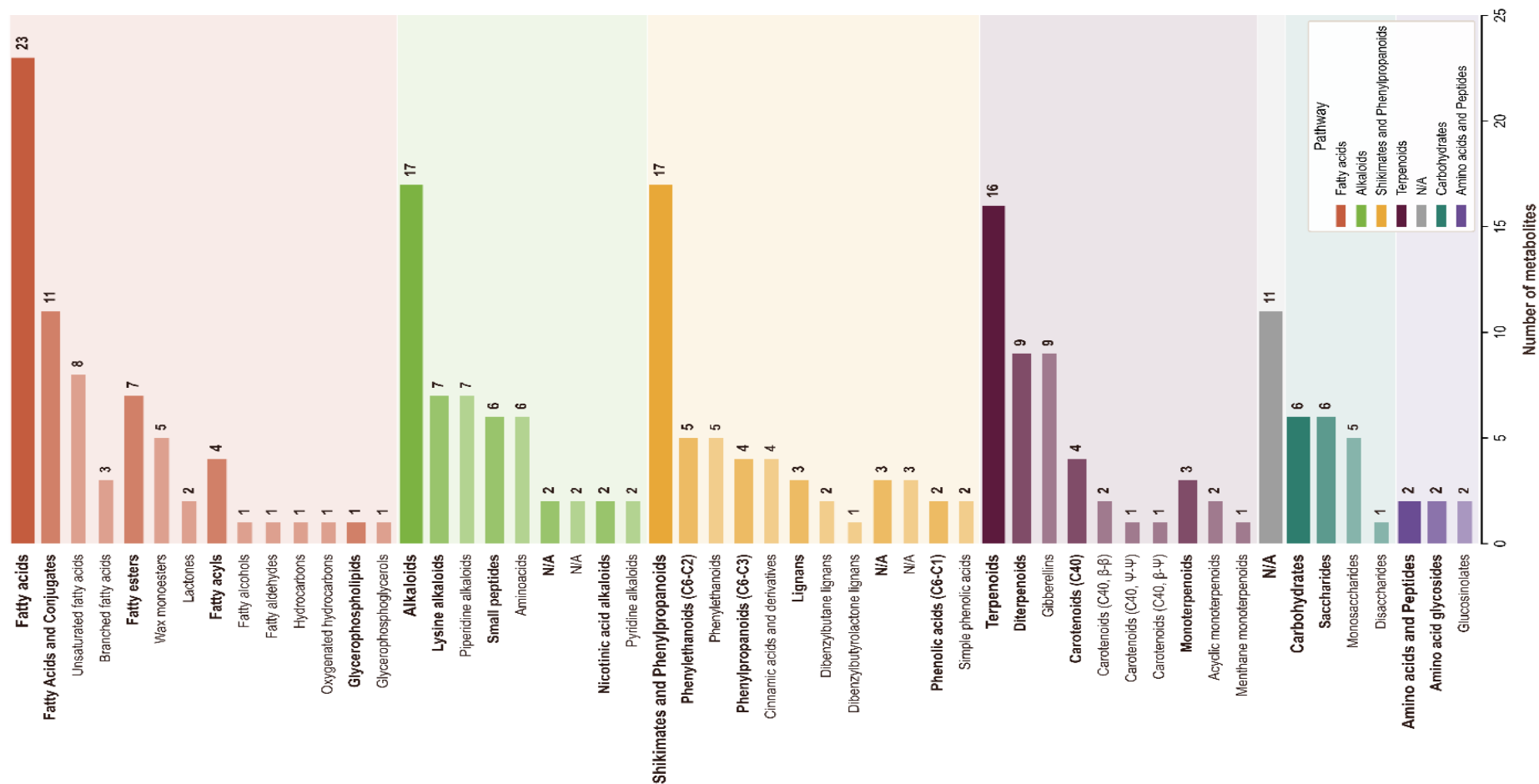
A literature survey was conducted using the Lotus Natural Products database and other literature sources to compile metabolites that have been previously reported in *Carica papaya*. Although these metabolites were not experimentally detected in the present investigation, they were used to support the biochemical interpretation of the phytochemical classes identified through qualitative screening. Ninety-two metabolites were retrieved and organized into a database according to their biosynthetic pathways, chemical superclasses, and metabolite classes.

Analysis of the dataset indicated the presence of chemically diverse phytochemicals, including fatty acid derivatives, alkaloids, shikimate and phenylpropanoid compounds,

terpenoids, carbohydrates, and amino acid-related metabolites. Further classification revealed the presence of diterpenoids, carotenoids, lignans, phenylethanoids, lysine alkaloids, and saccharides ([figure 2](#)). These structures represent the fundamental molecular frameworks from which numerous derivatives reported in the species are derived. [Figure 3](#) shows the hierarchical classification of metabolites reported in *C. papaya*.



**Figure 2.** The figure represents the structural skeletons of the major metabolite groups reported in *C. papaya*. The main skeletons associated with the phytochemical classes identified through screening analyses are presented. These representative skeletons provide a simplified structural overview of the inferred metabolomic diversities. In addition, it illustrates the biosynthetic organization of this species. Representative molecular skeletons were selected because they correspond to major chemical classes previously reported in *Carica papaya* and are associated with the phytochemical groups detected during screening



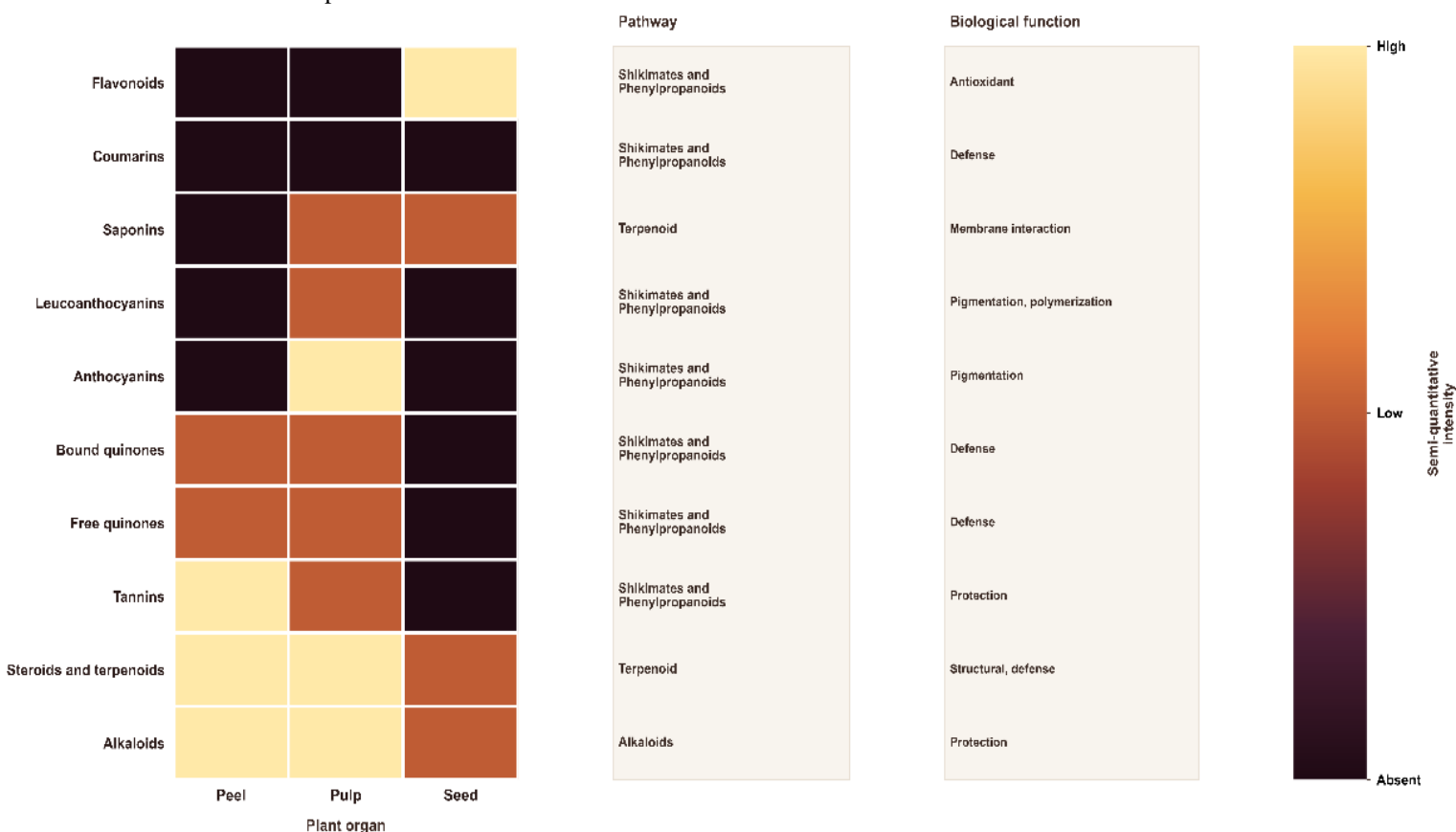
**Figure 3.** This figure represents the hierarchical classification of reported metabolites from *C. papaya* derived from the Lotus natural product database and literature search. Metabolites were organized according to biosynthetic pathway, chemical superclass, and metabolite class. Fatty acid derivatives, alkaloids, shikimate and phenylpropanoid compounds, and terpenoids were the dominant metabolite groups identified. Metabolite diversity reflects the extensive biochemical diversity and inferred metabolomic architecture of a species. Hierarchical classification was performed using literature-reported metabolites organized according to biosynthetic pathways, chemical superclasses, and metabolite classes.

### 3.2. Phytochemical screening

Differences in phytochemical composition were observed among the matrices studied upon analysis of the screening results. A heatmap diagram was designed and developed to provide an overview of the findings (figure 4). The heatmap diagram demonstrates the composition and putative biological roles of the predominant phytochemical groups. High alkaloid and steroid/terpenoid intensities were observed in both the peel and pulp tissues. Flavonoids were present in significant amounts only in seeds. Anthocyanins and leucoanthocyanins were primarily localized in pulp. In turn, a high abundance of tannins and quinones was observed in the peels.

hypothesized that such compounds constitute a protective layer preventing infection, herbivorous attack, UV irradiation, and oxidative stress.

Seeds: Flavonoids are highly enriched in seeds and are involved in oxidative protection, dormancy, and environmental stress responses.



**Figure 4.** Heatmap showing the organ-specific distribution, associated biosynthetic pathways, and inferred biological functions of the detected phytochemical classes. Color intensity represents the relative occurrence inferred from qualitative phytochemical screening. The figure highlights tissue-dependent biochemical compartmentalization and the differential allocation of metabolites associated with antioxidant activity, pigmentation, structural defense, membrane interactions, and other protective functions.

**Pulp:** The presence of anthocyanins and terpenoids/steroids implies that these compounds may contribute to pigmentogenesis, oxidative homeostasis, and signal transduction. These molecules are believed to play roles in fruit ripening and dispersal.

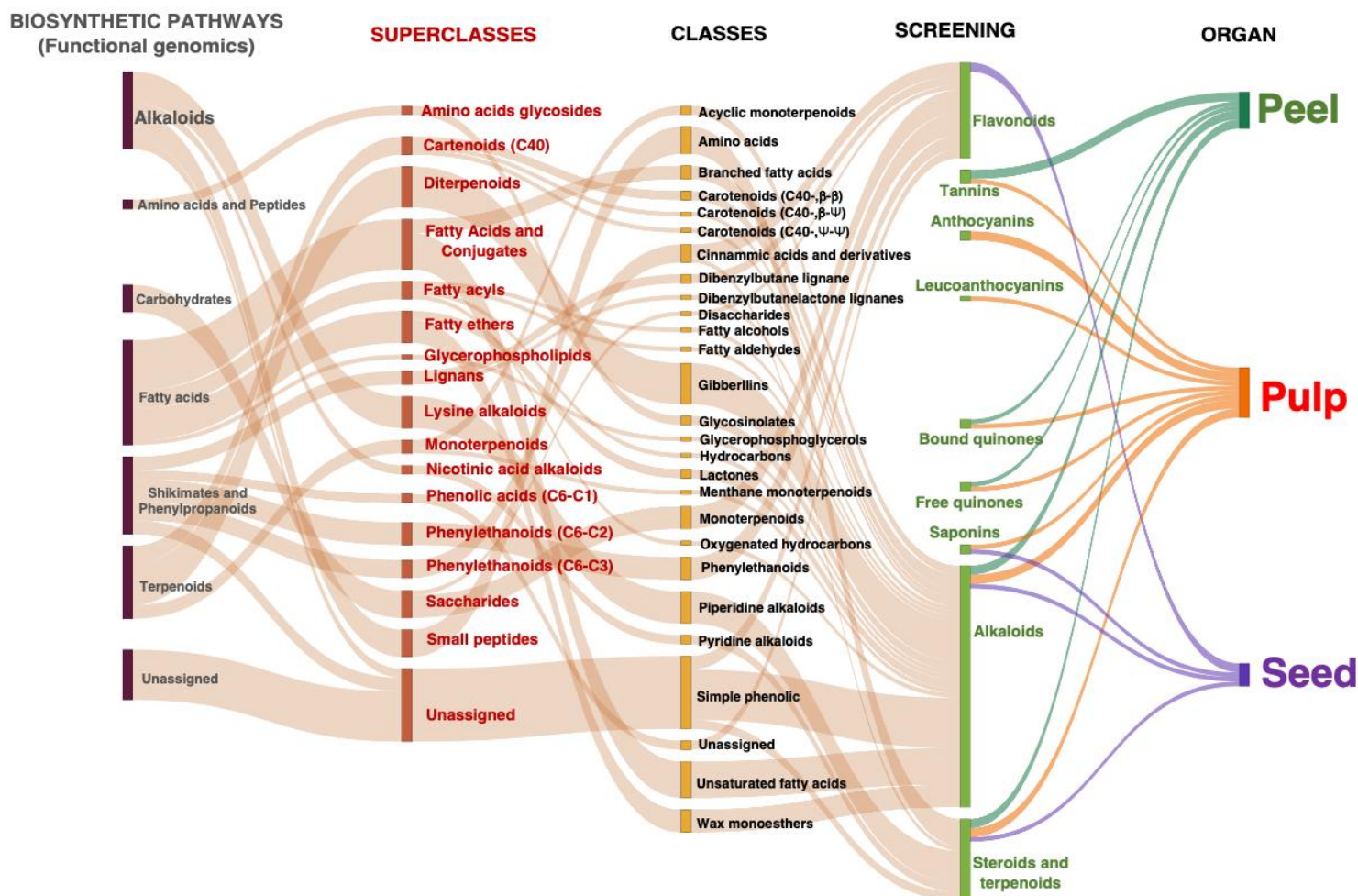
**Peel:** The peel contains tannins, quinones, alkaloids, and terpenoids/steroids. It can be

## 4. Discussion

Phytochemical screening of tissue-specific organs of *C. papaya* fruit revealed phytochemical compartmentalization in the organs. The observed patterns indicate that specific organs of the fruit represent specialized biochemical compartments. Each compartment has specific ecological and physiological

roles in the plant kingdom. Phytochemicals identified in fruit organs include diterpenoids, carotenoids, lignans, phenylethanoids, lysine alkaloids and saccharides. Such a composition demonstrates the high level of biochemical complexity of this fruit.

to specific pathways, chemical superclasses, and metabolite classes in the phytochemical groups detected in the fruit compartments is shown in the Sankey diagram (figure 5).



**Figure 5.** An integrative Sankey diagram was developed to show the relationships among biosynthetic pathways, chemical superclasses, metabolite classes, phytochemical screening results, and tissue-specific distribution in *C. papaya*. The reported metabolites compiled from the Lotus natural products database were hierarchically organized according to the pathway, superclass, and metabolite class. These were associated with the phytochemical screening groups detected in different tissues. The diagram highlights the predominance of fatty acids, alkaloids, phenylpropanoid-related compounds, and terpenoids, as well as the pronounced biochemical compartmentalization of metabolites in fruit organs. The associations illustrated in this diagram are inferred from literature-reported metabolites and do not represent direct metabolite identification in the analyzed tissues.

The obtained data offer a unique metabolomics map that could be further utilized to interpret the screening results and reveal tissue-specific biochemical compartmentalization in fruit organs. A literature-guided approach was used to infer metabolites for interpreting the phytochemical screening results. The hierarchical organization of the compounds belonging

The results obtained from the phytochemical screening in relation to the metabolites previously described in the literature are presented in Figure 5. The figure illustrates the relationships among biosynthetic pathways, chemical superclasses, metabolite classes, phytochemical screening results, and tissue-specific distribution in papayas.

According to the results obtained during phytochemical screening, alkaloids and steroids/terpenoids were present in all fruit organs. High concentrations of alkaloids and steroids/terpenoids are present in the pulp and peels. It was observed that tissues are biochemically specialized in various ways. The Sankey diagram shows that the peels are rich in tannins, quinones, alkaloids, and terpenoids. This pattern of biochemical content is associated with the protective role of the tissues (Iqbal & Poór, 2025; Punet et al., 2025; Khan et al., 2025).

The defense role is represented by antimicrobial activity, oxidative resistance, and herbivory prevention. Phytochemical screening of the pulp revealed the presence of anthocyanins, leucoanthocyanins, alkaloids, and terpenoids in the pulp. These metabolites are important for pigmentation, antioxidative activity, maturation, and attracting and dispersing agents (Sadowska & Bartosz, 2024; Kapoor et al., 2022). In particular, the tissue specificity of anthocyanin accumulation reveals that the shikimate-phenylpropanoid pathway is oriented toward the synthesis of pigment antioxidants. The phytochemistry of seeds includes flavonoids, alkaloids, saponins, and terpenoids. These phytochemicals play important roles in seed development, including seed viability, oxidative defense, embryo retention, and ultraviolet (UV) defense (Pirredda et al., 2024; Das & Majee, 2026). This indicates that seeds may constitute a biochemical reservoir associated with reproductive protection and storage.

These findings are supported by previous knowledge of the metabolomic complexity of plant species. As shown in figure 5, the metabolic compartments vary in fruits. This reveals how metabolites formed through the same biosynthesis processes are differently distributed (Martinez & Fernie, 2024; Hao et al., 2025). These compartments are linked through the phenylpropanoid biosynthesis pathway and work together to achieve fruit adaptation, protection, and function.

Organic compounds adapt to environmental events or stimuli. Thus, the spatial organization of organic molecules is required. The issue of metabolic compartmentalization has received considerable interest in recent studies on plant metabolomics and phytofunctional chemistry (Hao et al., 2025; Li et al., 2025). In fruits, the distribution of organic compounds in different organs may one of the factors affect nutritional properties and postharvest stability. The

findings of this study indicate that papaya by-products are promising sources of bioactive compounds.

Tannins and quinones, which possess known antioxidant and antimicrobial properties, are abundant in peel tissues. In addition, seed tissues, the only organ rich in flavonoids, might have nutraceutical value. The strategy employed in the current study was a combination of phytochemical screening and inference from the existing literature on metabolite profiling of papaya fruits. This is the primary strength of this study. Despite the absence of metabolite identification, the pathway-based strategy yielded significant information about the inferred metabolomic profiles of papaya fruits. Future directions of this study will confirm the findings with more data, including LC-MS/MS metabolomics, NMR dereplication, and analysis of biosynthetic gene clusters in *C. papaya*.

### **Strengths, Limitations, and Future Perspectives**

#### **Strengths of the Study**

The strategy adopted in this study provides an integrative approach combining classical phytochemical screening with literature-guided metabolite inference to investigate tissue-specific phytochemical organization in *C. papaya* fruit organs. A key strength of this work lies in the comparative evaluation of peel, pulp, and seed tissues within the same biological system. This way would minimize the environmental and genetic variability. Therefore, the interpretation of tissue-dependent phytochemical compartmentalization was facilitated. An additional important strength of this analysis is the integration of phytochemical screening data with reported metabolites compiled from the LOTUS natural products database. This approach has the merit of constructing a literature-supported biochemical framework that has been used to provide indications of the inferred phytochemical organization of the fruit tissues. Finally, the use of pathway-oriented and hierarchical metabolite classification has contributed to a system-level interpretation of tissue-specific metabolic specializations. These findings provide insights into the potential valorization of fruit by-products as sources of bioactive compounds.

#### **Study Limitations**

This study relied on qualitative phytochemical screening, and the detected groups were not assessed quantitatively. In addition, the metabolites discussed in this study were not directly identified in the analyzed samples but were inferred from literature-reported compounds and metabolite databases. The sampling strategy of this study only included fruits from one tree.

This strategy was adopted to conduct an exploratory tissue-comparative investigation. Biological variability and other environmental factors were not evaluated. Therefore, the findings do not provide a definitive metabolomic characterization. The lack of integration of data from analytical techniques such as LC-MS/MS, NMR dereplication, or spatial metabolomics prevents the direct validation of the inferred metabolomic landscape proposed in this study.

#### **Future Perspectives**

The findings of this study pave the way for future investigations that require the integration of advanced analytical techniques, such as LC-MS/MS, GC-MS, NMR dereplication, or spatial metabolomics, for the direct validation of the inferred metabolomic landscape proposed in this study. This study could be extended to include multiple cultivars, diverse ecological conditions, developmental stages, and biological replicates to better understand the metabolic variability and tissue specialization in *C. papaya*. Finally, the valorization potential of peel and seed tissues deserves further investigation because of their apparent enrichment in defense-related and antioxidant metabolites. These by-products may represent an interesting natural source of bioactive compounds for nutraceutical, pharmaceutical, cosmetic, and food industry applications.

## **5. Conclusion**

The present study provides a literature-supported interpretation of tissue-specific phytochemical compartmentalization in *Carica papaya* fruits based on qualitative phytochemical screening and biochemical inferences derived from previously reported metabolites. Distinct phytochemical distributions were observed among the peel, pulp, and seed tissues, suggesting potential tissue-dependent biochemical specialization. However, the inferred metabolomic organization proposed in this work does not constitute direct metabolite identification and requires confirmation through advanced analytical approaches such as LC-MS/MS, GC-MS, NMR dereplication, and spatial metabolomics. Nevertheless, these findings contribute to the understanding of phytochemical compartmentalization in papaya fruits and support the potential valorization of fruit by-products as promising sources of bioactive compounds.

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## **Conflict of interest**

The authors declare no conflict of interest.

## **Ethical considerations**

The database of previously reported metabolites from *C. papaya* generated during this study is available from the corresponding author, upon request.

## **Author contributions**

Conceptualization, D.F.D.; T. N. and J.N.K.M.; methodology, B.M.K. and I.M. D.F.D.; T. N. and J.N.K.M.; software, D.F.D.; T. N. and J. N. K. M.; validation, D. F. D.; T. N. and J.N.K.M.; formal analysis, I.M. and B.M.K.; investigation, I.M. and B.M.K.; resources, S. L. and J.N.K.M.; data curation, D.F.D.; T.N and J.N.K.M. and J.N.K.M.; writing-original draft preparation, I.M., and J.N.K.M.; writing-review and editing, D.F.D.; T. N. and J.N.K.M.; visualization, D.F.D. and T. N.; supervision, J.N.K.M.. Project administration: D.F.D.; T. N. and J. N. K. M.; funding acquisition; S. L., T. N., and J.N.K.M. All authors have read and agreed to the published version of this manuscript.

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