Unlocking Mango's Peptide Potential: Exploring Bioactive Peptides in Pulp, Peel and Seed

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Introduction

Mango (*Mangifera indica* L.), known as "the king of fruits" for its delectable taste and nutritional richness, belongs to the *Anacardiaceae* family and is a widely cherished tropical fruit. Throughout the process of mango processing, a significant portion of the fruit, ranging from 35-60%, is disposed of, often without any treatment, resulting in environmental challenges and financial setbacks. Peels and seeds, accounting for 40-50% of the fruit's weight, are typically discarded as by-products[1]. This waste holds potential for conversion into valuable resources. Although mango is known to have various bioactive compounds, the understanding of bioactive peptides within different mango tissues remains limited. This research aims to explore mango tissues to uncover potential bioactive peptide-encoding genes present in the pulp, peel, and seed using publicly available genomic data resources in combination with discovery proteomic.

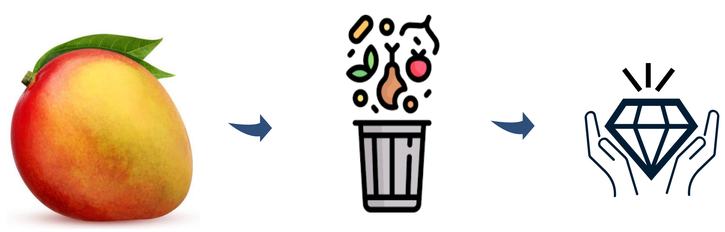

Figure 1: Mango fruit is a potential candidate for food waste valorisation.

Materials and Methods

Employing bioinformatics tools, we conducted an *in-silico* analysis of published mango genomic data[2]. We evaluated gene expression patterns and mapped an in-house bioactive database to translated gene models, identifying bioactive peptides and their corresponding coding genes. Then, we conducted proteomics and peptidomics experiments on two mango varieties, Kensington Pride (KP) and R2E2. Mango flesh, peel, and seed tissues from these varieties were prepared and proteins were extracted using different extraction protocols. In Protocol 1 we used a solvent mixture of acetonitrile, water, and formic acid (25:24:1) to extract native proteins and peptides. Protocol 2 involved the use of urea (8M) in Tris-HCl, followed by the application of trypsin enzyme for digestion. The samples were then subjected to discovery proteomics and bioactive peptide screening as shown in Figure 2.

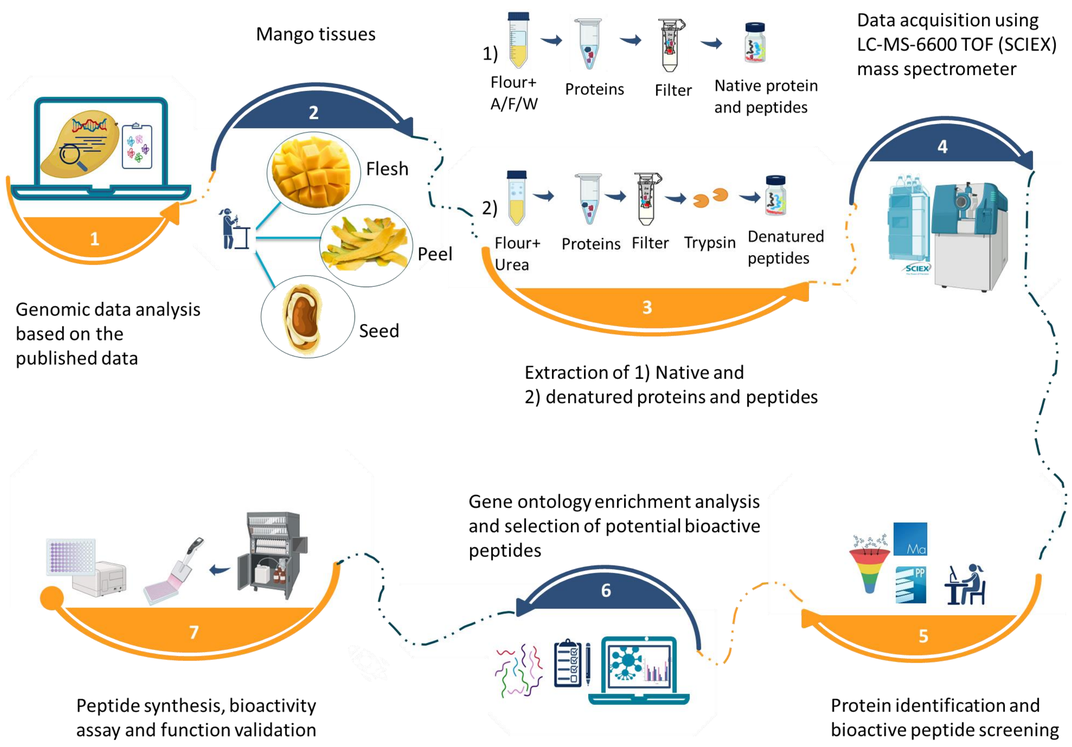

Figure 2: Workflow of protein and peptide extraction and identification of bioactive proteins and peptides in three different mango tissues using mass spectrometry-based techniques.

Results

As a result of the *in-silico* analysis, from the mango reference proteome (52,078 proteins), we identified 1,586 proteins with a 100% match mapped to regions of our in-house database of known bioactive peptides. Proteomic experiments were then conducted using two protocols (native and denaturing) to extract bioactive proteins and peptides from three different tissues (flesh, peel and seed). Across all tissues and varieties, 1,195 proteins were identified that produce bioactive peptides with >80% sequence similarity match to reported bioactive peptides (Table 1).

Table 1: Proteomic and peptidomic results using two protocols and two mango varieties and three different tissues.

Protocol	Variety	Tissue	# of identified proteins	# of Peptide >95% conf	# Bioactive peptide (>80%)	# of Bioactive peptides (Normalised)
P1	KP	F	226	598	277	0.46
P1	KP	P	142	329	163	0.49
P1	KP	S	57	289	105	0.36
P1	R2E2	F	226	599	105	0.17
P1	R2E2	P	174	294	210	0.71
P1	R2E2	S	50	383	73	0.19
P2	KP	F	1455	6074	1617	0.26
P2	KP	P	911	2822	997	0.35
P2	KP	S	178	506	218	0.43
P2	R2E2	F	1506	6386	1634	0.25
P2	R2E2	P	887	2756	917	0.25
P2	R2E2	S	204	777	234	0.30

We performed gene ontology enrichment analysis on the identified proteins with bioactive peptides common to both varieties in each tissue (flesh, peel and seed) (Figure 3).

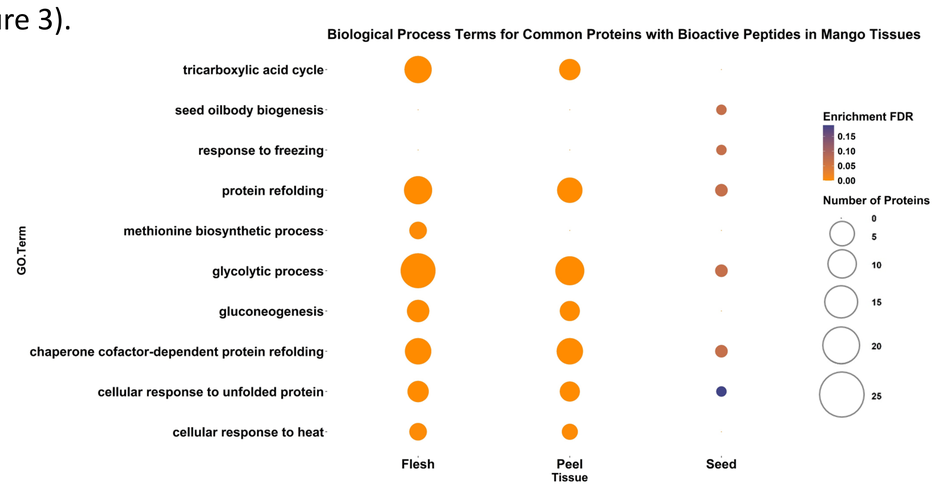

Figure 3: Gene ontology enrichment analysis of common proteins with bioactive peptides in flesh, peel, and seed of two mango varieties (KP and R2E2) based on the results of protocol 2.

Distribution of bioactive peptides across both varieties and three different tissues showed that in R2E2 variety, protocol 1 extracted more bioactive peptides from peel (compared to the flesh) in all six bioactive functions (Figure 4). In protocol 2, the highest number of bioactive peptides was found in flesh, followed by peel, and seed, with antimicrobial, antibacterial functions being most represented.

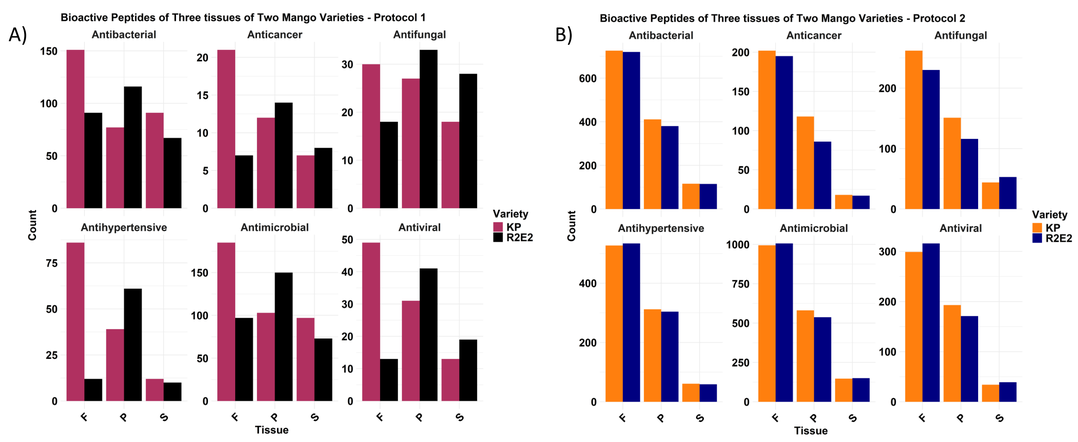

Figure 4: Distribution of bioactive peptides in two varieties and three different tissues based on their functions in protocol 1 (A) and 2 (B).

Next step

In the subsequent phase of this analysis, bioactive peptides will be quantified using targeted proteomics. Selected peptides will be synthesized and then tested in bioactivity assays to evaluate their functions and effects.

FOR FURTHER INFORMATION

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REFERENCES

[1] Owino, W. O., & Ambuko, J. L. (2021). Mango fruit processing: Options for small-scale processors in developing countries. Agriculture, 11(11), 1105.
[2] NCBI BioProject: PRJNA983966

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COLLABORATORS