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Short Communication

A Putative Curcumin Biosynthetic Pathway in *Musa textilis* Née (Abaca)

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ABSTRACT

Curcumin is a diarylheptanoid compound extensively documented in *Curcuma* species (Zingiberaceae) and valued for its diverse pharmacological properties. To date, curcumin has not been reported as a naturally occurring metabolite in members of the genus *Musa* (Musaceae). In this study, we investigated the potential for curcumin biosynthesis in *Musa textilis* (abaca) through integrative analysis of available genomic and transcriptomic datasets. Using KEGG-based pathway reconstruction, we identified putative homologs of key enzymes involved in diarylheptanoid biosynthesis, including Diketide-CoA Synthase (DCS) and Curcumin Synthase (CURS), in the genomes of *M. textilis* var. Abuab and *M. balbisiana*. Transcriptomic data further revealed the expression of diarylheptanoid-associated genes across multiple *M. textilis* genotypes. While direct chemical detection of curcumin was not performed, these findings provide molecular evidence suggesting the presence of a putative curcumin biosynthetic pathway in *M. textilis*. This work expands current understanding of secondary metabolism in abaca and highlights the need for targeted metabolomic validation.

Keywords: Abaca, Curcumin, Diarylheptanoid, *Musa textilis*, Secondary metabolism.

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INTRODUCTION

Musa textilis Née, commonly known as abaca or Manila hemp, is a fiber crop native to the Philippines and globally valued for producing one of the strongest natural fibers (Cheesman, 1949; Lobrigo, 2008; PhilFIDA, 2016). Research on abaca has historically focused on fiber yield, quality, and resistance to biotic stresses (Secretaria *et al*., 2012; Galvez *et al*., 2021), with limited attention given to its secondary metabolism. In contrast, several members of the genus *Musa* are known to synthesize diverse secondary metabolites, including phenolic compounds, flavonoids, terpenoids, and alkaloids, which contribute to reported antioxidant, anti-inflammatory, and medicinal properties (Hänsel *et al*., 1993; Evans, 2009; Lopes *et al*., 2020).

Curcumin is a phenolic diarylheptanoid best known as the principal bioactive compound of *Curcuma longa* and related *Curcuma* species (Hewlings & Kalman, 2017). It is biosynthesized via the phenylpropanoid pathway, with Diketide-CoA Synthase (DCS) and Curcumin Synthase (CURS) catalyzing key downstream steps (Ayer *et al*., 2020; Ganapathy *et al*., 2019). Despite extensive phytochemical studies on *Curcuma*, curcumin has not been reported from *Musa* species, and its biosynthetic machinery has not been explored in abaca (Ayoola-Oresanya *et al*., 2021).

Recent advances in *Musa* genomics and transcriptomics provide new opportunities to investigate secondary metabolic pathways in non-model plant species (Nadarajah, 2018). The availability of draft genome assemblies for *M. textilis* var. Abuab and *M. balbisiana*, together with RNA-seq datasets from multiple abaca genotypes, enables *in silico* reconstruction of putative biosynthetic pathways (Galvez *et al*., 2021; Ereful *et al*., 2022). This study aimed to determine whether genes associated with curcumin biosynthesis are present and expressed in *M. textilis*, thereby providing molecular evidence for a putative diarylheptanoid pathway in this economically important fiber crop.

MATERIALS AND METHODS

Genomic Data Sources

The assembled genome of *Musa textilis* var. Abuab was obtained from the Data Dryad Digital Repository as reported by Galvez *et al*., (2021). For comparative purposes, the genome assembly of *Musa balbisiana* cv. DH-PKW was retrieved from the National Center for Biotechnology Information (Wang *et al*., 2019).

KEGG-Based Pathway Assignment

Predicted protein sequences from both genomes were analyzed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) Mapper platform (Kanehisa *et al*., 2019). KEGG Orthology

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(KO) terms were assigned using the BlastKOALA/ASSIGN KO tool, with Musaceae (NCBI taxonomy ID 4637) specified as the reference group. Reconstructed pathways were visualized using the KEGG Reconstruct tool, with particular focus on phenylpropanoid and diarylheptanoid biosynthesis.

Transcriptomic Data and Differential Expression Analysis

RNA-seq datasets previously generated from five *M. textilis* genotypes (Abuab, Inosa, Tangongon, and two *M. textilis* × *M. balbisiana* hybrids) were used in this study (Ereful *et al.*, 2022), with samples collected from pseudostem tissues of three-month-old plants and sequenced using the Illumina NovaSeq 6000 platform. Available Pairwise Differential Expression (PDE) and Non-Differential Expression (NDE) datasets were reviewed to identify transcripts associated with secondary metabolite biosynthesis.

Identification of Secondary Metabolism-Related Transcripts

Differentially expressed transcripts were mapped onto KEGG-derived pathways to identify genes involved in phenylpropanoid and diarylheptanoid metabolism. Particular attention was given to transcripts encoding enzymes known to participate in curcumin biosynthesis, including 4-coumarate–CoA ligase (4CL), DCS, and CURS (Ayer *et al.*, 2020).

RESULTS

Reconstruction of Putative Diarylheptanoid Biosynthesis Pathway

KEGG-based analysis revealed the presence of putative homologs of diarylheptanoid biosynthesis enzymes in both *Musa textilis* and *M. balbisiana*. Specifically, sequences corresponding to diketide-CoA synthase (EC 2.3.1.218) and curcumin synthase (EC 2.3.1.217) were identified, enzymes previously characterized in *Curcuma longa* and related species (Ganapathy *et al.*, 2019; Ayer *et al.*, 2020). These enzymes are predicted to catalyze the conversion of p-coumaroyl-CoA and feruloyl-CoA into curcumin via intermediate diarylheptanoid compounds (Figure 1).

Expression of Phenylpropanoid-Associated Genes

Available transcriptomic data showed consistent expression of phenylpropanoid pathway genes across all examined *M. textilis* genotypes. Two transcripts, annotated as hydroxymethylglutaryl-CoA synthase and 4-coumarate–CoA ligase-like 7, were commonly upregulated. The latter enzyme plays a rate-limiting role in channeling phenylpropanoid intermediates toward downstream specialized metabolites (Chen *et al.*, 2019).

Curcumin Synthase-Related Transcripts

Putative curcumin synthase transcripts were detected in the available RNA-seq datasets, suggesting transcriptional activity of genes associated with diarylheptanoid biosynthesis. Similar genes have previously been reported in *M. acuminata* and *M. balbisiana* (Pothiraj *et al.*, 2021), supporting the hypothesis that *Musa* genomes harbor conserved enzymatic machinery potentially capable of curcumin-like compound synthesis (Table 1).

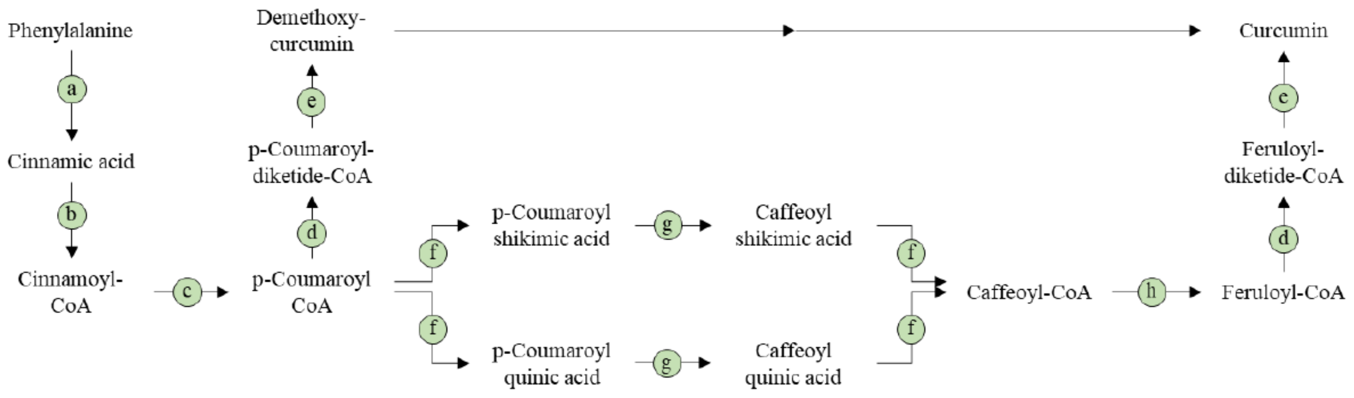
DISCUSSION

The identification of putative DCS and CURS homologs in *M. textilis* provides novel molecular evidence for the presence of a diarylheptanoid biosynthetic framework in abaca. While curcumin is traditionally considered unique to *Curcuma* species (Hewlings & Kalman, 2017), increasing evidence suggests that components of its biosynthetic pathway may be more widely distributed among monocot plants (Pothiraj *et al.*, 2021).

It is important to note that the presence and expression of biosynthetic genes do not necessarily confirm the accumulation of curcumin itself (Weber & Kim, 2016). The detected enzymes may participate in the synthesis of structurally related phenolic

Table 1: Putative genes involved in diarylheptanoid (curcumin) biosynthesis identified in *Musa textilis* based on genomic and transcriptomic analyses.

Enzyme	EC Number	Putative Gene/ Transcript ID	Data Source	Putative Function
4-Coumarate–CoA ligase-like 7 (4CL)	EC 6.2.1.12	LOCUS_011529-RA	RNA-seq	Activation of hydroxycinnamic acids for phenylpropanoid metabolism
Diketide-CoA Synthase (DCS)	EC 2.3.1.218	Mt unigene	Genome / RNA-seq	Condensation of hydroxycinnamoyl-CoA substrates
Curcumin Synthase (CURS)	EC 2.3.1.217	Mt unigene	Genome / RNA-seq	Formation of diarylheptanoid backbone
Hydroxymethylglutaryl-CoA synthase	EC 2.3.3.10	LOCUS_016809-RA	RNA-seq	Precursor supply for isoprenoid and secondary metabolism



LEGEND

Code	Enzyme		No. of Unigenes	
	Symbol	**Description**	***M. textilis***	***M. balbisiana***
a	PAL	phenylalanine ammonia-lyase	10	8
b	4CL	4-coumarate--CoA ligase	17	13
c	CYP73A	trans-cinnamate 4-monooxygenase	8	7
d	DCS	phenylpropanoylacetyl-CoA synthase	1	1
e	CURS1_2	curcumin synthase	2	1
f	HCT	shikimate O-hydroxycinnamoyltransferase	10	12
g	CYP98A, C3'H	5-O-(4-coumaroyl)-D-quinate 3'-monooxygenase	4	1
h	E2.1.1.104	caffeoyl-CoA O-methyltransferase	4	5

Figure 1: Schematic diagram of the putative biosynthetic pathway of curcumin in *M. textilis* var. Abuab and *M. balbisiana* cv DH-PKW. Enzymes in green color were identified in both plants.

compounds or serve alternative metabolic functions. Nonetheless, the coordinated presence of phenylpropanoid pathway enzymes and curcumin synthase homologs strengthens the plausibility of curcumin or curcumin-like metabolite production in *M. textilis*.

From an applied perspective, uncovering novel secondary metabolic pathways in abaca could expand its value beyond fiber production. Curcumin and related diarylheptanoids possess well-documented antioxidant, anti-inflammatory, and anticancer properties (Hewlings & Kalman, 2017; Rattis *et al.*, 2021), highlighting the importance of follow-up metabolomic and biochemical studies to validate these genomic predictions.

CONCLUSION

This study presents the first integrative genomic and transcriptomic evidence suggesting the existence of a putative curcumin biosynthetic pathway in *Musa textilis*. Although direct metabolite detection is required for confirmation, the identification and reported expression of key biosynthetic enzymes indicate that abaca possesses the molecular capacity for diarylheptanoid biosynthesis. These findings broaden current understanding of secondary metabolism in *Musa* species and provide a foundation for future phytochemical and functional studies.

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ABBREVIATIONS

4CL: 4-coumarate–CoA ligase; **CURS:** Curcumin synthase; **DCS:** Diketide-CoA synthase; **DOST-ASTHRDP:** Department of Science and Technology – Accelerated Science and Technology Human Resource Development Program; **EC:** Enzyme Commission; **HCT:** Shikimate O-hydroxycinnamoyltransferase; **KEGG:** Kyoto Encyclopedia of Genes and Genomes; **KO:** KEGG Orthology; **NDE:** Non-differential expression; **PAL:** Phenylalanine ammonia-lyase; **PDE:** Pairwise differential expression.

CONFLICT OF INTEREST

The author declares that there is no conflict of interest.

AUTHOR'S CONTRIBUTIONS

The author performed the data analysis and interpretation, conducted the literature review, and wrote the manuscript. The author approved the final version of the manuscript and takes full responsibility for its content.

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