

Accepted Manuscript

Genome-wide differential expression profiling in wild and cultivar genotypes of cardamom reveals regulation of key pathways in plant growth and development

F. Nadiya, N. Anjali, Jinu Thomas, A. Gangaprasad, K.K. Sabu

PII: S2352-2151(18)30006-0
DOI: doi:[10.1016/j.aggene.2018.03.002](https://doi.org/10.1016/j.aggene.2018.03.002)
Reference: AGGENE 67

To appear in:

Received date: 12 January 2018
Revised date: 18 March 2018
Accepted date: 21 March 2018

Please cite this article as: F. Nadiya, N. Anjali, Jinu Thomas, A. Gangaprasad, K.K. Sabu , Genome-wide differential expression profiling in wild and cultivar genotypes of cardamom reveals regulation of key pathways in plant growth and development. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Aggene(2018), doi:[10.1016/j.aggene.2018.03.002](https://doi.org/10.1016/j.aggene.2018.03.002)

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Genome-wide differential expression profiling in wild and cultivar genotypes of cardamom reveals regulation of key pathways in plant growth and development

F. Nadiya^{1*}, N. Anjali¹, Jinu Thomas¹, A. Gangaprasad² and K. K. Sabu¹

¹Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), Palode, Thiruvananthapuram 695562, India

²Department of Botany, University of Kerala, Thiruvananthapuram

*Corresponding author: nadiyashiyas@jntbgri.res.in

Abstract

Cardamom (*Elettaria cardamomum* Maton) is an economically valuable spice crop and the essential oil of cardamom possesses splendid medicinal properties. To get insight into the domestication related traits and varied gene regulation, differential expression profiling of wild and cultivar cardamom was performed by analyzing the transcriptome data available for cardamom. Functional annotation using seven different publicly available databases identified significant genes coding for enzymes participating in monoterpenoid biosynthesis. Differential expression profile of cultivar and wild genotypes of cardamom exhibited 132 unigenes as differentially expressed ($\log_2 > 4$) with 105 up regulated and 27 down regulated genes in cultivars comparing with its wild genotype. Expression analysis showed wild cardamom has increased drought stress tolerance, defense response, and various plant growth regulations. Most of the genes coding for enzymes participating in flavanoid biosynthesis were up regulated, while resistance related genes (cinnamoyl CoA reductase) and few genes involved in the monoterpenoid biosynthetic pathway were down regulated in cultivars when compared to its wild progenitor. Transcriptome data were validated and correlated using qPCR using 10 randomly selected differentially expressed genes. Our study is the first application of next generation RNA-seq to explore the genes involved in various metabolic pathways and quantification of transcript expression levels in cultivar and wild cardamom genotypes.

Keywords

Cardamom; Transcriptome; Differential expression; Up regulation, Down regulation, Essential oil biosynthesis

Download English Version:

<https://daneshyari.com/en/article/8634887>

Download Persian Version:

<https://daneshyari.com/article/8634887>

[Daneshyari.com](https://daneshyari.com)