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Data article

Transcription profile data of phorbol esters biosynthetic genes during developmental stages in Jatropha curcas

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ABSTRACT

Jatropha curcas is currently known as an alternative source for biodiesel production. Beside its high free fatty acid content, J. curcas also contains typical diterpenoid-toxic compounds of Euphorbiaceae plant namely phorbol esters. This article present the transcription profile data of genes involved in the biosynthesis of phorbol esters at different developmental stages of leaves, fruit, and seed in Jatropha curcas. Transcriptional profiles were analyzed using reverse transcription-polymerase chain reaction (RT-PCR). We used two genes including GGPPS (Geranylgeranyl diphospate synthase), which is responsible for the formation of common diterpenoid precursor (GGPP) and CS (Casbene Synthase), which functions in the synthesis of casbene. Meanwhile, J. curcas Actin (ACT) was used as internal standard. We demonstrated dynamic of GGPPS and CS expression among different stage of development of leaves, fruit and seed in Jatropha.

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Specifications Table

Subject area Biology More specific Molecular plant biology, plant physiology subject area Type of data Figures and text How data was cDNA synthesis, RT-PCR and image analysis acquired Data format Analyzed Experimental Genes involved in the biosynthesis of phorbol esters were GGPPS and CS. The factors expression of each gene was analyzed using reverese-transcriptase PCR (RT-PCR). Samples consisted of three plant organs including leaves, endosperm and fruit Experimental (pericarp) in two different developmental stages (young and mature stages). All features samples were subjected to total RNA extraction followed by cDNA synthesis. The cDNA obtained was then amplified using specific GGPPS and CS primers. ACT (actin) was used as internal standard. Department of Biology, Institut Teknologi Sepuluh Nopember, Surabaya, Indonesia Data source location Data accessibility The data are available with this article

Value of the data

- The transcription profile of *JcGGPPS* and *JcCS* data of the *J. curcas* demonstrate the dynamic expression of the genes in different plant organs at distinct developmental stages.
- The data are useful to be combined with biochemical analysis to determine in which part of plant organ the phorbol esters are accumulated.
- Determination of the expression of both genes might contribute for further study to understand the relationship between phorbol esters biosynthesis and plant development.

1. Data

Jatropha curcas - a species of Euphorbiaceae family - is generally found in the tropical asian countries [1]. Jatropha is currently cultivated and is importantly used for alternative biodiesel development throughout those regions. Like other Euphorbiaceae plants, *J. curcas* is characterized by the presence of toxic compounds, including phorbol esters [2]. Here, we demonstrate the transcription profile of *GGPPS* and *CS* as key genes involved in the biosynthesis of phorbol esters [3]. The profile was analyzed semi quantitatively using Reverese Transcription-Polymerase Chain Reaction (RT-PCR) at different stages of leaves, seeds (endosperm) and fruit (exocarp) development (young and matured organs). Young fruit and seed were collected at 29 days after pollination (dap). Meanwhile, the matured exocarp and seed were at 35 and 41 dap, respectively. Fig. 1 shows different DNA fragments with varying sizes representing *JcGGPPS*, *JcCS* and *JcACT* (577 bp, 956 bp and 554 bp, respectively). Figs. 2 and 3 demonstrate the transcription profile of *JcGGPPS* dan *JcCS* genes in different organs and developmental stages of *J. curcas*.

2. Experimental design, materials, and methods

2.1. Collection of plant materials

Fruits (exocarp), seeds (endosperm) and leaves of *J. curcas* were obtained from Purwodadi-Botanical Garden, The Indonesian Institute of Science (LIPI), Indonesia. No specific regulations were

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