

## BUKTI KORESPONDENSI ARTIKEL JURNAL

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# Phylogenetic Relationship of *Cymbidium Mosaic Virus* from the Native Orchids of South Kalimantan, Indonesia

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**Abstract.** Information on viral genetics, including their phylogenetic relationship, is valuable in controlling viral infection and screening for the development of virus-resistant cultivars in the future. The objectives of this study were to detect and characterize the *Cymbidium mosaic virus* (CymMV) from the native orchids of South Kalimantan, Indonesia, by the RT-PCR method. Also, to determine their phylogenetic relationship based on a partial genome of RdRp by the ML and PCA methods. Following RT-PCR analysis, one of 10 samples of native orchids used was positively infected by CymMV. In early detection, the RdRp region of CymMV has approximately 530 bp in size. After being sequenced and aligned with other isolates, this region has 121 polymorphic or mutation sites, a GC content of 45.21%, a transition/transversion bias value of 3.52, and nucleotide diversity (0.0415). The phylogenetic analysis revealed that CymMV from South Kalimantan, Indonesia, has closest related to similar isolates from Korea Type 2 (AF016914.1), Niigata, Japan (AB197937.1), Hawaii (EF125180.1), and Taiwan M2 (EU314803.1), with the coefficient divergence of 0.025. But, it has very distantly related to Hawaii 18-1 (EF125178.1) with a coefficient of 0.142. The results provide urgent information in supporting the native orchid's conservation and breeding efforts, locally and globally, including mitigating or controlling the viral infection and screening for the development of virus-free or resistant cultivars in the future.

**Keywords:** Breeding and conservation; mosaic virus; orchids; plant protection; RT-PCR.

**How to Cite:** Mursyidin, D. H., Saputra, A. W. (2023). Phylogenetic Relationship of *Cymbidium Mosaic Virus* from the Native Orchids of South Kalimantan, Indonesia. *Biosaintifika: Journal of Biology & Biology Education*, 15(2), 185-193.

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## INTRODUCTION

The native orchids are valuable germplasm for

period until six months (Mursyidin et al., 2021).

However, due to many human impacts, like illegal logging and trading, including natural



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Authors	Dindin Hidayatul Mursyidin, Ahmad Winarto Saputra
Title	Phylogenetic Relationship of Cymbidium Mosaic Virus from the Native Orchids of South Kalimantan, Indonesia
Original file	41842-106952-1-SM.DOCX 2023-01-08
Supp. files	None
Submitter	Dindin Hidayatul Mursyidin
Date submitted	January 8, 2023 - 11:12 AM
Section	Articles
Editor	Priyantini Widyaningrum
Abstract Views	243

**Status**

Status	Published Vol 15, No 2 (2023): August 2023
Initiated	2023-06-03
Last modified	2023-08-30

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**Authors**

Name: Dindin Hidayatul Mursyidin  
Affiliation: Laboratory of Genetics and Molecular Biology, Faculty of Mathematics and Natural Sciences, Universitas Lambung Mangkurat, Jl. A. Yani Km. 36 Banjarbaru, South Kalimantan, Indonesia.  
Country: Indonesia  
Bio Statement: —  
Principal contact for editorial correspondence.

Name: Ahmad Winarto Saputra  
Affiliation: Laboratory of Genetics and Molecular Biology, Faculty of Mathematics and Natural Sciences, Universitas Lambung Mangkurat, Jl. A. Yani Km. 36 Banjarbaru, South Kalimantan, Indonesia.  
Country: Indonesia  
Bio Statement: —

**Title and Abstract**

Title: Phylogenetic Relationship of Cymbidium Mosaic Virus from the Native Orchids of South Kalimantan, Indonesia  
Abstract: Information on viral genetics, including their phylogenetic relationship, is valuable in controlling viral infection and screening for the development of virus-resistant cultivars in the future. The objectives of this study were to detect and characterize the *Cymbidium mosaic virus* (CymMV) from the native orchids of South Kalimantan, Indonesia, by the RT-PCR method. Also, to determine their phylogenetic relationship based on a partial genome of RdRp by the ML and PCA methods. Following RT-PCR analysis, one of 10 samples of native orchids used was positively infected by CymMV. In early detection, the RdRp region of CymMV has approximately 530 bp in size. After being sequenced and aligned with other isolates, this region has 121 polymorphic or mutation sites, a GC content of 45.21%, a transition/transversion bias value of 3.52, and nucleotide diversity (0.0415). The phylogenetic analysis revealed that CymMV from South Kalimantan, Indonesia, has closest related to similar isolates from Korea Type 2 (AF016914.1), Niigata, Japan (AB197937.1), Hawaii (EF125180.1), and Taiwan M2 (EU314803.1), with the coefficient divergence of 0.025. But, it has very distantly relate to Hawaii 18-1 (EF125178.1) with a coefficient of 0.142. The results provide urgent information in supporting the native orchid's conservation and breeding efforts, locally and globally, including mitigating or controlling the viral infection and screening for the development of virus-free or resistant cultivars in the future.

**Indexing**

Keywords: Breeding and conservation; mosaic virus; orchids; plant protection; RT-PCR

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