

BUKTI KORESPONDENSI ARTIKEL JURNAL

Biosaintifika 13 (2) (2021): 212-221
Journal of Biology & Biology Education

p-ISSN 2085-191X | e-ISSN 2338-7610
<https://journal.unnes.ac.id/nju/index.php/biosaintifika>

Genetic Diversity and Relationships of *Phalaenopsis* Based on the *rbcL* and *trnL-F* Markers: *In Silico* Approach

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Submitted: 2021-04-19. Revised: 2021-05-06. Accepted: 2021-08-09

Abstract. *In silico* is the more comprehensive and applicable approach in supporting, both conservation and breeding programs of germplasm. The study aimed to analyze and determine the genetic diversity and relationships of 24 species of *Phalaenopsis* using two DNA barcoding markers, namely the *rbcL* and *trnL-F*, by *in silico* approach. All sequences of these markers were collected randomly from the NCBI website and analyzed using several softwares and methods, such as ClustalW and MultAlin for multiple sequence alignments and MEGA-X to determine its genetic diversity and relationships. Specifically, the genetic diversity was determined using a nucleotide diversity index and their relationships by the Maximum Likelihood method. The results showed that *Phalaenopsis* has a low genetic diversity of 0.24, 0.32, and 0.19, respectively. The phylogenetic analysis revealed that this orchid separated into five (for the *rbcL*), six (*trnL-F*), and seven clades (a combined one), where the closest relationship is shown by *P. amboinensis* vs. *P. venosa*, whereas the farthest by *P. gibbosa* vs. *P. doweryensis*, *P. stuartiana* vs. *P. micholitzii*, and *P. celebensis* vs. *P. pulchra*. The results have novel information on the diversity and relationships of *Phalaenopsis* on the *in silico* approach. Thus, our findings might be used in supporting the conservation and breeding program of *Phalaenopsis*, both locally and globally.

Key words: DNA barcoding; genetic diversity; *in silico*; *Phalaenopsis*; phylogenetic analysis

How to Cite: Mursyidin, D. H., Ahyar, G. M. Z., Saputra, A. W., & Hidayat, A. (2021). Genetic Diversity and Relationships of *Phalaenopsis* Based on the *rbcL* and *trnL-F* Markers: *In Silico* Approach. *Biosaintifika: Journal of Biology & Biology Education*, 13(2), 212-221.

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 Title: Genetic Diversity and Relationships of Phalaeopsis Based on the rbcL and trnL-F Markers: In Silico Approach
 Original file: 29904-76321-1-SM.DOCK 2021-04-19
 Supp. files: 29904-76323-1-SP.DOCK 2021-04-19
 Submitter: Dindin Hidayatul Mursyidin
 Date submitted: April 19, 2021 - 06:20 PM
 Section: Articles
 Editor: Sri Wahyuni
 Abstract Views: 358

Status

Status: Published Vol 13, No 2 (2021): August 2021
 Initiated: 2021-09-09

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 Title: Genetic Diversity and Relationships of Phalaenopsis Based on the rbcL and trnL-F Markers: In Silico Approach
 Section: Articles
 Editor: Sri Wahyuni

Peer Review

Round 1

Review Version: 29904-76324-1-RV.DOCK 2021-04-19
 Initiated: 2021-05-06
 Last modified: 2021-05-06
 Uploaded file: None

Editor Decision

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#29904 Editing

https://journal.unnes.acid/nju/index.php/biosaintifika/author/submissionEditing/29904

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Authors: Dindin Hidayatul Mursyidin, Gusti Muhammad Zainal Ahyar, Ahmad Winarto Saputra, Aminoor Hidayat
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