MORPHOLOGICAL AND PHYLOGENETIC RELATIONSHIPS OF THE GENUS *TRICHOTOSIA* BLUME (ORCHIDACEAE) IN SABAH

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ABSTRACT

MORPHOLOGICAL AND PHYLOGENETIC RELATIONSHIPS OF THE GENUS *TRICHOTOSIA* BLUME (ORCHIDACEAE) IN SABAH

A study on the genus *Trichotosia* (Orchidaceae) in Sabah was carried out to determine useful morphological characters for its classification and to generate a phylogenetic relationship between its species in Sabah. Samples were collected from eight localities within Sabah, namely Mount Kinabalu, Mount Trus Madi, Mount Lumaku, Tawau Hills Park, Mount Tambuyukon, Mount Alab, Minduk Sirung, and Imbak Canyon Conservation Area. Morphological characteristics in the living plants were examined to determine informative characters for the genus classification. Subsequently, DNA was extracted from fresh leaves of *Trichotosia* using the cetyltrimethyl-ammonium bromide (CTAB) method. Molecular phylogenetic analysis using nuclear DNA sequence data from the internal transcribed spacer region (ITS1, ITS4) and the 5.8S gene for 20 taxa was conducted to examine the phylogenetic relationship of the genus. Descriptions of 16 flowering species based on morphological characteristics were presented. Out of these, one is a new record for Sabah, namely *Trichotosia teysmannii* (J.J. Sm.) Kraenzl., and *Trichotosia poculata* (Ridl.) Kraenzl. is new to Sabah and Borneo. An identification key for the 16 species of *Trichotosia* was presented. Hairs distribution, the positions of flower attachment to bract, inflorescences length and flower numbers are good morphological characters in identification. The strict consensus tree (Length=356; CI=0.8511; RI=0.800; RC=0.6809) obtained from parsimony analysis of the ITS sequence data showed that *Trichotosia* is divided into four groups (BS-98%). Two of the groups, however, were not fully resolved morphologically. The phylogenetic tree can be improved in the future by increasing the number of *Trichotosia* samples and using more markers, such as *rbcl, trnL-F* and *matK.* The ITS sequences provide supporting data for inferring relationships within *Trichotosia* that will be valuable for future classification.

ABSTRAK

Satu kajian ke atas genus Trichotosia (Orchidaceae) telah dijalankan untuk menentukan ciri morfologi yang penting untuk pengelasan dan hipotesis terhadap hubungan filogenetik di antara spesies Trichotosia di Sabah. Sampel telah dikutip dari lapan kawasan di Sabah, iaitu Gunung Kinabalu, Gunung Trus Madi, Gunung Lumaku, Gunung Tambuyokon, Taman Bukit Tawau, Gunung Alab, Minduk Sirung, dan Kawasan Konservasi Kanyon Imbak. Ciri-ciri morfologi pada tumbuhan hidup telah diperiksa untuk mendapatkan ciri-ciri berinformasi untuk pengelasan genus tersebut. Ekstrak DNA daripada daun segar Trichotosia dijalankan dengan menggunakan kaedah cetyltrimethyl-ammonium bromide (CTAB). Analisis filogenetik molekul menggunakan data jujukan DNA, pada kawasan internal transcribed spacer (ITS1, ITS4) dan gen 5.8S bagi 20 takson telah dijalankan untuk mengkaji status filogenetik genus tersebut. Pencirian 16 spesies berbunga berdasarkan ciri morfologi telah disediakan. Selain daripada ini, satu adalah rekod baru bagi Sabah, bernama Trichotosia teysmannii (J.J. Sm.) Kraenzl., dan Trichotosia poculata (Ridl.) Kraenzl. adalah baru kepada Sabah dan Borneo. Satu kekunci pengecaman bagi 16 spesies Trichotosia disediakan. Pokok strict consensus (Panjang = 356; Indeks kestabilan= 0.8511; Indeks penahanan= 0.800; Indeks terskala= 0.6809) yang diperolehi daripada analisis parsimoni data jujukan ITS menunjukkan empat kumpulan terbentuk (BS-98%), bagaimana pun, dua kumpulan tidak terbahagi secara morfologi sepenuhnya. Taburan bulu, kedudukan bunga pada pelepah, panjang gugusan bunga dan jenis bunga merupakan ciri yang baik untuk digunakan dalam proses pengecaman. Pokok filogenetik boleh diperbaiki di masa hadapan dengan menambah bilangan sampel Trichotosia dan menggunakan lebih banyak penanda genetik seperti rbcl, trnL-F, dan matK. Jujukan ITS memberikan data sokongan dalam andaian hubungan di antara Trichotosia yang bernilai untuk pengelasan di masa hadapan.