The complete plastome sequence of the endangered orchid
*Kuhlhasseltia nakaiana* (Orchidaceae)

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**ABSTRACT**

In this study, we report the complete plastome sequence of *Kuhlhasseltia nakaiana* (F.Maek.) Ormerod (Orchidaceae) (NCBI acc. no. KY354041), an endangered plant species protected by the national law of Korea. The gene order and number in the *K. nakaiana* plastome were similar to a typical orchid plastome. The complete plastome was 147,614 bp in length and consisted of a large single copy region of 81,617 bp and a small single copy region of 13,673 bp, separated by two inverted repeats of 26,162 bp. The plastome contained 103 genes, of which 69 were protein-coding genes, 30 were tRNA genes, and four were rRNA genes. Fourteen genes contained one intron and two genes (*clpP* and *ycf3*) had two introns. The AT content of the plastome was 60.5%. A total of 74 simple sequence repeat regions were identified from the plastome. Phylogenetic analysis determined that *K. nakaiana* was a member of the tribe Cranichideae and revealed the sister group relationship between *K. nakaiana* and *Ludisia discolor* within the tribe Cranichidac.</p>
the development of genetic markers among \textit{K. nakaiana} populations.

Phylogenetic analyses were performed on a dataset that included 78 protein-coding genes (excluding \textit{ycf1}) and four rRNA genes extracted from 38 taxa in the NCBI database and \textit{Cymbidium macrorhizon} (KY354040) and \textit{K. nakaiana} (KY354041). \textit{Fritillaria hupehensis} and \textit{F. taipaiensis}, representing the sister order Liliales, were used as outgroups. The gaps for lost genes were treated as missing bases. The 82 gene sequences were aligned with MUSCLE in Geneious 6.1.8; the
aligned data matrix consisted of a total of 70,620 bp. This alignment is used for phylogenetic analysis using RAxML v. 7.7.1 (Stamatakis et al. 2008). An ML tree was obtained with an ML estimation value of \(-302818.486357\). The sister group relationship between \(K. \text{nakaiana}\) and \(Ludisia \text{discolor}\) was confirmed with 100% bootstrap value support (Figure 1). Both species occurred in the tribe Cranichideae within Orchidoideae.

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Disclosure statement
The authors report no conflicts of interest, and are independently responsible for the content and writing of the paper.

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