Diospyros blancoi A. DC. is commonly referred to as velvet apple. It is a widely cultivated tropical Asian fruit that originated in Philippine (Kim 2011). But, this is a rare plant in wild population. The fruit and stem of this species is used for both food and timber. Diospyros blancoi belongs to the family Ebenaceae of Ericales (Byng et al. 2016). Ericales consist of twenty-two families (Byng et al. 2016). Ericaceae consist of four genera and approximately 800 species (Christenhusz & Byng 2016). Most of them belong to the genus Diospyros. The recent studies reported a few plastome from Diospyrus, but no sequence data was released from the NCBI so far (Turner et al. 2016; Fu et al. 2016). Furthermore, the two studies did not include the D. blancoi. The complete plastome sequence of D. blancoi will aid us in developing molecular markers for the identification and improvement of cultivars of this economically important tropical fruit species.

The leaves of D. blancoi used in this study were collected from the Korea University greenhouse, where we grew the plants from the seeds that were originally collected from the Philippines. The plants flowered and fruited in the greenhouse. A voucher specimen was deposited in the Korea University Herbarium (KUS acc. no. 2014-0240). Fresh leaves were ground into powder in liquid nitrogen and total DNAs were extracted using the CTAB method (Doyle & Doyle 1987). The DNAs were further purified by ultracentrifugation and dialysis (Palmer 1986). The genomic DNAs are deposited in the Plant DNA Bank in Korea (PDBK acc. no. 2014-0240). The complete plastome sequence was generated using an Illumina HiSeq 2000 system (Illumina, Inc., San Diego, CA). Annotations were performed using the National Center for Biotechnology Information (NCBI) BLAST, DOGMA (Wyman et al. 2004), and tRNAscan-SE programs (Lowe & Eddy 1997).
and 4 rRNA genes from the 25 taxa using RAxML v. 7.7.1 (Stamatakis et al. 2008). The 80 gene sequences (81,895 bp in length) were aligned with the MUSCLE program using Geneious v. 6.1.8 (Biomatters Ltd.). As a result, *D. blancoi* form a clade with Primulaceae with a 100% bootstrap value (Figure 1). This results are similar to the recent updated phylogeny of the group (www.mobot.org/MOBOT/APweb/). However, the results are somewhat different from other data (Fu et al. 2016). Fu et al. (2016) data suggested that Primulaceae is the basal family of the Ericales, and Ebenaceae is the sister group to other members of Ebenales. Our complete plastome sequence of *D. blancoi* will be helpful to resolve not only the interfamilial relationships of Ericales, but also the species relationship within a *Diospyros* (Ebenaceae).

**Disclosure statement**

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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