

Abstract

Debregeasia hekouensis, which belongs to the nettle family (Urticaceae), is a local endemic species in Hekou County, Yunnan Province, China. To provide a basis for the development of effective molecular markers for its conservation, we sequenced the chloroplast (cp) genome of *D. hekouensis* in the present study. The total length of the chloroplast(cp) genome was 155,941 bp, and exhibited a typical quadripartite structure, with a pair of IRs (inverted repeats; 25,664 bp in length) being separated by a small single copy (SSC) region of 19,085 bp and a large single copy (LSC) region of 85,528 bp. The cp genome contained a total of 112 genes, including 78 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. The GC content of the entire cp genome, LSC region, SSC region, and IR region was 36.3%, 34.0%, 29.4%, and 42.7%, respectively. Phylogenetic analysis indicated that *D. hekouensis* is evolutionarily closer to *Debregeasia orientalis* and *Debregeasia squamata*