Musa ornata (flowering banana) is one of more than 50 species of banana in the genus Musa of the family Musaceae. Based on the basic chromosome number and morphological descriptors, the genus Musa has been traditionally divided into four sections, including Eumusa, Rhodochlamys, Australimusa and Callimusa. And M. ornata is a member of Rhodochlamys (Cheesman, 1947). With the development of molecular marker technology, the genus Musa has been redivided into two sections, the Eumusa and Rhodochlamys were merged into the section Musa, and the Australimusa and Callimusa were merged into the section Callimusa (Häkkinen, 2013). As sources of resistance to pathogens exist in germplasm, M. ornata is one of the possible hybrid parents for ameliorate commercial banana varieties, which has been seriously threatened by the increasing range of fungal, viral, and insect diseases (Novák et al. 2014).

There are poor knowledge on genetic diversity of the genus Musa, considering that chloroplast DNA conservativity and its slow rate of nucleotide substitution make chloroplast DNA widely used in plant phylogeny (Sugiura, 1995). In this study, we report and characterize the complete chloroplast genome of M. ornata.

Musa ornata was obtained from CIRAD (Guadeloupe) as rooted plants. Plants were maintained in a greenhouse. Genomic DNA of M. ornata was isolated from healthy young leaf tissue (Zhang et al. 1995). Genome sequencing was performed using Roche/454, sequencing libraries were prepared by the GS Titanium library preparation kit (454 Life Sciences, a Roche company, Branford, USA). Roche/454 sequencing data were assembled using CLC Genomic Workbench v3.6 (http://www.clcbio.com). The chloroplast genome was annotated using DOGMA (Wyman et al. 2004) with manual correction. The complete chloroplast genome sequence together with gene annotations were submitted to the GenBank with the accession number of MH545183.

The complete size of the M. ornata chloroplast genome is 169,989 bp, which includes a pair of inverted repeat regions (IRs) of 35,426 bp separated by a large single-copy region (LSC) of 88,362 bp and a small single copy (SSC) region of 10,775 bp, similar to the previously reported Musaceae chloroplast genomes (Martin et al. 2013; Niu et al. 2018). The size of the M. ornata chloroplast genome is larger than M. acuminata and M. balbisiana. The base composition of the circular chloroplast genome is A (31.43%), G (18.16%), C (18.65%), and T (31.75%). GC content of 36.82% for the whole M. ornata chloroplast genome. A total of 113 genes were annotated in M. ornata chloroplast genome composed by 79 protein-coding genes, 4 ribosomal RNA (rRNA) genes and 30 transfer RNA (tRNA) genes. The M. ornata chloroplast genome has 18 different intron containing genes, two of these genes (ycf3 and cipP) exhibiting two introns and the rest of the genes contain a single intron.

Phylogenetic analysis based on complete plastome sequences was performed using species in Musaceae and Zingiberaceae, and Oryza sativa as the outgroup (Figure 1). A total of 10 selected complete plastome sequences were aligned using MAFFT (Katoh and Standley, 2013). Maximum-likelihood (ML) analysis was performed using MEGA7 (Kumar et al. 2016) with 1000 bootstrap replicates. The result shows that the phylogenetic relationship of M. ornata is close to M. acuminata.
In conclusion, the complete chloroplast genome sequence of *M. ornata* is decoded for the first time in this study. Moreover, this study will be useful for further phylogenetic and evolutionary analysis for Musaceae.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work was supported by The Technology Innovation Talents Project of Yunnan Province (Liu Jin); The Sci-Tech Innovation System Construction for Tropical Crops Grant of Yunnan Province (No.RF2018-8)

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