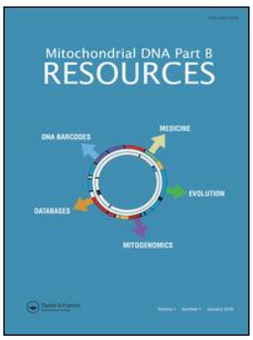

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MITOGENOME ANNOUNCEMENT

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Characterization of the complete plastid genome of an important Chinese Old Rose *Rosa odorata* var. *pseudindica*

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ABSTRACT

Rosa odorata var. *pseudindica* is a world-famous Chinese Old Rose endemic to the northwest of Yunnan province (China). In this study, the complete plastid genome of *R. odorata* var. *pseudindica* was characterized and assembled using a high-throughput sequencing method. The complete plastid genome is a typical quadripartite circular molecule of 156,652 bp length, including a large single-copy region of 85,785 bp and a small single-copy region of 18,761 bp separated by two inverted repeat regions of 26,053 bp. Totally 130 genes were identified, including 85 protein-coding genes (PCG), 37 transfer RNA genes, and 8 ribosomal RNA genes. The phylogenetic analysis revealed that *R. odorata* var. *pseudindica* and *R. odorata* var. *gigantea* formed an independent clade with a 100% bootstrap support.

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KEYWORDS
Rosa odorata var. *pseudindica*; plastid genome; phylogenetic analysis

Rosa odorata (Andrew) Sweet is one of the seven major wild ancestors of modern roses, mainly contributing excellent traits of large flower and unique tea scent (Wylie 1954). In the 1800s, four 'Stud Chinas' were introduced from China into Europe, and two of which were tea roses derived from *R. odorata* (Hurst 1941). *Rosa odorata* has been listed as a Class III protected plant (Fu 1992), rare and endangered species in Chinese Rare and Endangered Protective Plants List (The National Environment Protection Agency, Institute of Botany CAS 1987). *Rosa odorata* contains four varieties: *R. odorata* var. *odorata*, *R. odorata* var. *erubescens* (Focke) T. T. Yu & T. C. Ku, *R. odorata* var. *pseudindica* (Lindley) Rehder, and *R. odorata* var. *gigantea* (Crépin) Rehder & E. H. Wilson (Ku and Robertson 2003). *Rosa odorata* var. *pseudindica* is identified with double flowers, yellow or orange petals, and rich tea-scented fragrance endemic to northwest Yunnan (China) as an important Chinese Old Rose (Wang 2015). In this paper, the complete plastid genome of *R. odorata* var. *pseudindica* (GenBank Accession Number: MK116518) was characterized based on the Illumina next-generation sequencing techniques. The complete plastid genome research about this important germplasm resource will facilitate the conservation and breeding of modern roses, and will also be useful for the phylogenetic study of this plant and the genus *Rosa*.

Fresh leaves of *R. odorata* var. *pseudindica* were collected from Lijiang (Yunnan, China; 27°16′002″ N, 99°28′45″ E). Voucher specimen was deposited at the Herbarium of KUN. Total genomic DNA was extracted using the modified CTAB method (Doyle and Doyle 1987). Reads of the plastid genome were assembled using CLC Genomic Workbench v10 (CLC Bio., Aarhus, Denmark). All the contigs were checked against the reference genome of *R. chinensis* var. *spontanea* (MG523859) using BLAST (https://blast.ncbi.nlm.nih.gov/) and aligned contigs were oriented according to the reference genome. The complete plastid genomes were then constructed using Geneious v4.8.5 (Biomatters Ltd., Auckland, New Zealand) and was automatically annotated using DOGMA (http://dogma.ccbb.utexas.edu/). To identifying the phylogenetic position of *R. odorata* var. *pseudindica*, 11 plastid genomes of Rosaceae were aligned using the online program MAFFT (https://mafft.cbrc.jp/alignment/server/index/index.html), and the maximum likelihood (ML) tree was then conducted by MEGA v7.0 (Kumar et al. 2016).

The complete plastid genome of *R. odorata* var. *pseudindica* represents a typical quadripartite circular molecule with 156,652 bp in length. It is composed by a large single-copy (LSC) region of 85,785 bp, a small single-copy region of 18,761 bp, and a pair of IR regions of 26,053 bp. The genome encodes 130 genes, including 85 PCG genes, 37 tRNA genes, and 8 rRNA genes. Fourteen genes contain one intron and two genes contain two introns. Gene *inf*A was identified in the LSC region, and ψ*ycf*15 pseudogene was present in the IR regions due to the presence of seven stop codons in the gene sequence. The overall GC content of *R. odorata* var. *pseudindica* plastid genome is 37.2%.

To investigate the phylogenetic position of *R. odorata* var. *pseudindica*, eight published plastid genomes of the genus *Rosa* were used to construct a phylogeny tree, using

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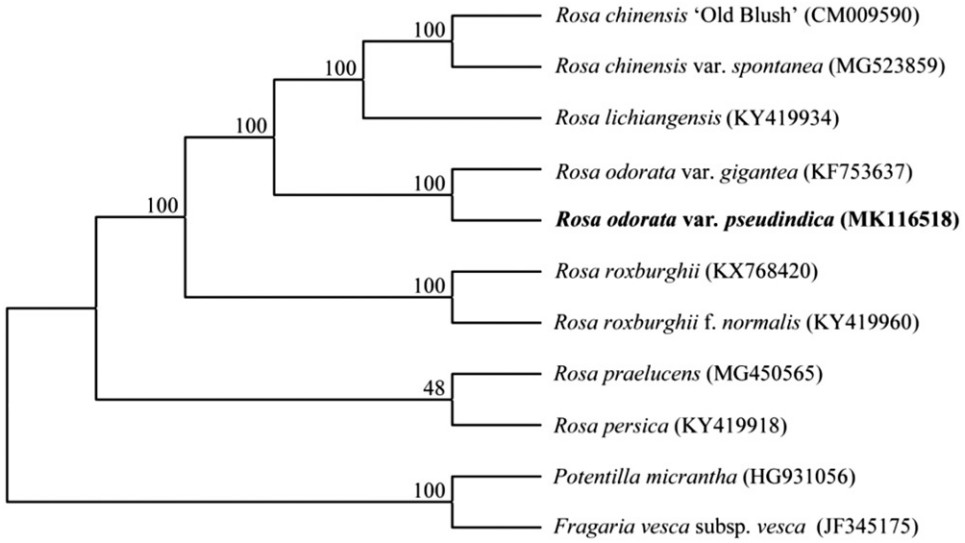

Figure 1. Phylogenetic relationship among *Rosa* species based on the maximum likelihood (ML) analysis of the complete plastid genome sequences. Bootstrap support values (%) are indicated in each node.

Potentilla micrantha (HG931056) and *Fragaria vesca* subsp. *vesca* (JF345175) in Rosaceae as the outgroups. The results showed that *R. odorata* var. *pseudindica* and *R. odorata* var. *gigantea* formed an independent clade with a 100% bootstrap support, which was in accordance with the previous result that *R. odorata* var. *gigantea* was the maternal parent of the other three double-petals varieties of *R. odorata* (Figure 1) (Meng et al. 2011).

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Disclosure statement

No potential conflict of interest was reported by the authors.

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References

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Fu LG. 1992. China plant red data book: rare and endangered plants. Beijing: Science Press.

Hurst CC. 1941. Notes on the origin and evolution of our garden roses. J Roy Hort Soc. 66:242–250.

Ku TC, Robertson KR. 2003. *Rosa*. In: Wu ZY, Raven PH, editors. Flora of China. Vol 9. Beijing and St. Louis: Science Press and Missouri Botanical Garden Press; p. 296–339.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33: 1870–1874.

Meng J, Marie FD, Zhang LB, Li DZ, Yi TS. 2011. Untangling the hybrid origin of the Chinese tea roses: evidence from DNA sequences of single-copy nuclear and chloroplast genes. Plant Syst Evol. 297:157–170.

The National Environment Protection Agency, Institute of Botany CAS. 1987. Directory of rare and endangered protected plants in China. Beijing: Science Press.

Wang GL. 2015. Old roses in China. Beijing: Science Press.

Wylie AP. 1954. The history of garden roses. J Roy Hortic Soc. 79: 555–571.