


The complete chloroplast genome sequence of *Viscum coloratum* (Viscaceae), a semiparasitic medicinal plant

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ABSTRACT

Viscum coloratum (Viscaceae) is a kind of semiparasitic shrub used as medicinal plant. The complete chloroplast (cp) genome of *V. coloratum* was sequenced and characterized in this study. Length of total cp genome is 128,744 bp, which is constructed by four typical regions including a large single-copy region (LSC, 73,684 bp), a small single-copy region (SSC, 8630 bp) and a pair of inverted-repeat regions (IRs, 23,215 bp). 100 unique genes are predicted including 68 protein-coding genes, 28 tRNA genes and four rRNA genes. Phylogenetic analysis were performed based on 30 shared genes of 12 species in Santalales using maximum likelihood method. The results showed a close relationship between *V. coloratum* and *V. album*. The complete cp genome of *V. coloratum* would provide valuable genetic resources for further study on phylogeny, population genetics and identification in *Viscum*.

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Viscum coloratum; mistletoe; chloroplast genome; phylogenetic analysis

The plants of *Viscum* L. (Viscaceae), also called mistletoes, are usually perennial evergreen semiparasitic dwarf shrub. Mistletoe is a popular herbal medicine worldwide, especially in China. *Viscum coloratum* (Kom.) Nakai, which distributes from East to Northeast Asia and mainly parasitizes on the plants of Ulmaceae, Salicaceae, Betulaceae, Rosaceae and etc. (Qiu and Gilbert 2003), has been recorded in China Pharmacopoeia as a traditional Chinese medicine (National Pharmacopoeia Committee 2015). Nowadays, mistletoe has been paid more attention around the world because of its anticancer activity (Saha et al. 2016). Most study of mistletoes focused on chemistry and pharmacology (Tröger et al. 2013; Ma et al. 2015; Saha et al. 2016). In this study, complete chloroplast (cp) genome of *V. coloratum* was determined by using Illumina paired-end sequencing data. The annotated cp genome of *V. coloratum* was deposited at GenBank with accession number KY679303.

Viscum coloratum in this study was collected from Changbai Mountain (Jilin, China; 128.13°E, 42.11°N). The voucher specimen (HJS20161125) was deposited in the herbarium of Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences, Peking Union Medical College (IMD). Total genomic DNA was extracted from fresh leaves by using the Plant Genomic DNA Kit (Tiangen Biotech, Beijing, China) following the manufacturer's instructions and subsequently sequenced by Illumina HiSeq platform with a PE150 genomic library. Cp genomic reads were filtered by

BLAST++ and were used to assemble and extend to a complete cp genome by SOAPdenovo2 and SSPACE-STANDARD-3.0 (Boetzer et al. 2011; Luo et al. 2012). Cp genome annotation was performed by CPGAVAS (Liu et al. 2012). A circle gene map of cp genome was drawn by using the OrganellarGenomeDRAW tool (OGDRAW) as described in Liu et al. (2017). In order to clarify the position of *V. coloratum* in Santalales, 30 shared cp genes of 12 complete cp genomes were extracted, and phylogenetic analysis was constructed using maximum likelihood (ML) methods with *Arabidopsis arenicola* and *Arthraxon prionodes* as outgroups. ML analysis was performed using RAXML-HPCv8.1.11 on the CIPRES Science Gateway (<http://www.phylo.org/>) (Miller et al. 2010). jModelTest 2.1.4 was used to determine the best-fitting model (Posada 2008).

The complete cp genome of *V. coloratum* was 128,744 bp in length with the typical circular quadripartite structure of angiosperm cp genomes. A large and a small single-copy (LSC and SSC) regions, which were 73,684 bp and 8630 bp in length respectively, were separated by a pair of inverted-repeat regions (IRs) of 23,215 bp. A total of 100 unique genes, including 68 protein-coding genes, 28 tRNA genes and four rRNA genes, 21 of which were duplicated in IR regions. Four genes, including *ccsA*, *matK*, *rpoC2* and *ycf15*, were pseudogenes because of the present of internal stop codons. Four tRNA genes and seven protein-coding genes contained a single intron and two protein-coding genes contained two

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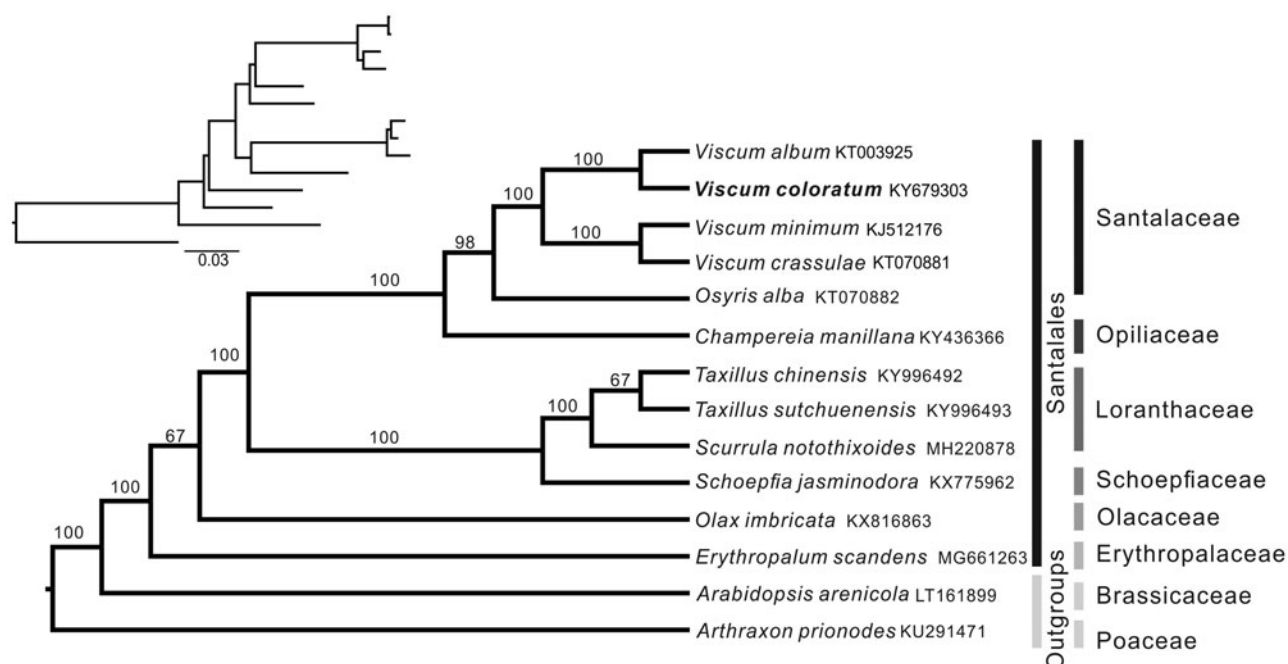


Figure 1. Phylogenetic tree of Santalales based on 30 concatenated chloroplast genes using maximum likelihood analyses. Relative branch lengths are indicated at the top-left corner. Numbers above the branches represent bootstrap values from ML analyses. Accession numbers are shown behind species names.

introns. The GC content of the whole cp genome was 36.3%, while GC content was not evenly distributed in the LSC (33.4%), SSC (24.3%) and IR (43.1%) regions. The uneven distribution of GC content may be an important factor leading to the difference of conservation between SC and IR regions (Yang et al. 2014).

ML analysis indicated that four species of *Viscum* formed a highly supported clade and clustered in Santalaceae, which was congruent with the results of APGIV (Angiosperm Phylogeny Group 2016). *Viscum coloratum* had the closest relationship with *V. album* which mainly distributes in Europe. The complete cp genome of *V. coloratum* would provide valuable genetic resources for further study on phylogeny and population genetics in *Viscum* and be used as a super-barcode for species identification which will greatly enhance the clinic safety of the medicinal herb (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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