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The complete chloroplast genome of ornamental liana *Sarcodum scandens* (Fabaceae)

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ABSTRACT

Sarcodum scandens is a tropical ornamental liana, distributed in southeastern Asia. The complete chloroplast genome was sequenced using the Illumina HiSeq X-Ten platform. The genome lacks an inverted repeat (IR) region, containing 76 protein-coding genes, 30 tRNAs genes and 4 rRNAs. The overall GC content is 34.1%. A phylogenetic tree based on the whole chloroplast genomes of 14 species indicated that *S. scandens* belonged to a monophyletic tribe Wisterieae, which was sister to *Glycyrrhiza* and nested in IRLC group of the subfamily Papilionoideae (Leguminosae).

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The tropical liana *Sarcodum scandens* Lour. (Fabaceae, the legume family) was a species of ornamental plant in southeastern Asia with its showy, purplish-red flowers (Ding 1994; Adema 1999). The natural distribution of *Sarcodum scandens* covered the circum-South China Sea region (Geesink 1984; Clark 2008). Noticeably, this species was recorded in central and southern Hainan island of China (Clark 2008; Sun and Pedley 2010), but it has been barely witnessed according to our field investigation during the last decade. Few previous study focused on the genome of *S. scandens*, a good know-

ledge in genomic information of this species would contribute to the study of population genetics, diversity, gardening and the establishment of efficient protection strategy toward the decreasing natural resource.

The fresh leaves of *Sarcodum scandens* was collected in Quang Binh, Vietnam (17°29'46"E, 106°19'59"N), and the voucher specimen was deposited in the herbarium of South China Botanical Garden, Chinese Academy of Sciences (IBSC, collection #: *P.K.Loc 11552*). We extracted the total genomic DNA with CTAB approach (Doyle 1987), the genomic library

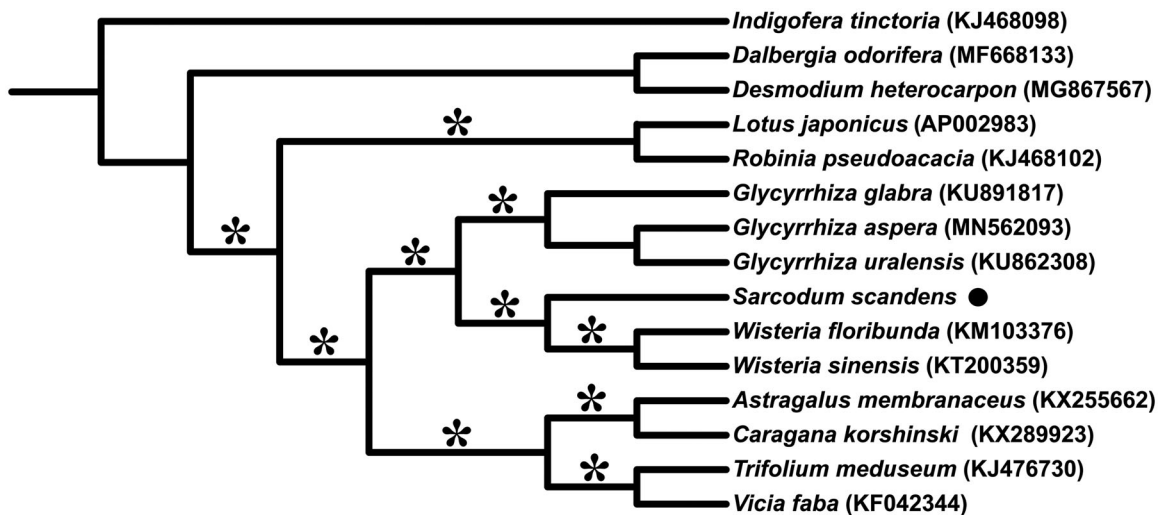


Figure 1. Maximum likelihood (ML) phylogenetic tree based on 14 chloroplast genomes of Fabaceae. The position of *Sarcodum scandens* is indicated with black dot. The bootstrap values of 100% are shown on branches with asterisks.

was prepared and sequenced using the Illumina HiSeq X-Ten platform (Illumina Inc., San Diego, CA, USA). The resultant sequences were filtered following Yao et al. (2016), the adaptor-free reads were then assembled with SPAdes 3.11 (Bankevich et al. 2012). We annotated the assembly of complete chloroplast (cp) genome using the Dual Organellar Genome Annotator (DOGMA) (Wyman et al. 2004) and deposited the genomes in GenBank (accession number: MT039380).

About 1.88 Gb raw reads of *S. scandens* were obtained, with coverage of $375\times$ and 132,503 bp in length. The cp genome lacked inverted repeat (IR) region. The genome contained 76 protein-coding genes (CDS), 30 transfer RNA genes (tRNA), 4 ribosomal RNA genes (rRNA), within which 16 genes (*atpF*, *clpP*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl2*, *rpl16*, *rpoC1*, *rps12*, *trnA-UGC*, *trnG-UCC*, *trnI-GAU*, *trnK-UUU*, *trnL-UAA* and *trnV-UAC*) had one intron; on the other hand, genes of *rps12* and *ycf3* had two introns, respectively. Overall GC content of the whole genome was 34.1%.

To infer the phylogenetic relationships among this species and its related taxa, whole cp genomes of 13 Papilionoideae species were downloaded from GenBank, which were aligned with that of *S. scandens* by applying MAFFT v.7 (Katoh and Standley 2013). Based on the alignment, a maximum-likelihood (ML) tree was constructed using IQ-TREE v.1.6 (Nguyen et al. 2015). The result (Figure 1) showed that the *S. scandens*, *Wisteria floribunda*, and *W. sinensis* constituted the well-supported tribe Wisterieae [as in Compton et al. (2019)], serving as sister of the licorice genus, *Glycyrrhiza*. This tribe was nested in the inverted repeat-lacking clade (IRLC), which in turn belonged to the clade of Hologalegina as suggested by previous study (Wojciechowski et al. 2004; Schrire 2005).

Disclosure statement

No potential conflict of interest was reported by the author(s).

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