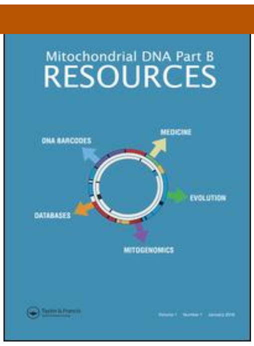

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Next generation sequencing reveals the complete plastome sequence of newly discovered cliff-dwelling *Sonchus boulosii* (Asteraceae: Cichorieae) in Morocco

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ABSTRACT

The complete chloroplast genome sequences of newly discovered cliff-dwelling species of *Sonchus*, *S. boulosii*, were reported in this study. The *S. boulosii* plastome was 152,016 bp long, with the large single copy (LSC) region of 83,988 bp, the small single copy (SSC) region of 18,566 bp, and two inverted repeat (IR) regions of 24,731 bp. The plastome contained 130 genes, including 88 protein-coding, six ribosomal RNA, and 36 transfer RNA genes. The overall GC content was 31.2%. Phylogenetic analysis of 12 representative plastomes within the order Cichorieae suggests that *S. boulosii* is closely related to *S. oleraceus*.

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Chloroplast genome; *Sonchus boulosii*; Morocco; Asteraceae; Cichorieae

The genus *Sonchus* L. belongs to the subtribe Hyoseridinae (formerly Sonchinae) of Cichorieae and, based on a new and broad concept of the genus, it includes approximately 90 species in eight distinct clades (Kim et al. 2007; Kilian et al. 2009). *Sonchus s.l.* includes not only some of the most spectacular examples of adaptive radiation on oceanic islands in the Atlantic (the woody *Sonchus* alliance in the Macaronesian Islands) and the Pacific (*Dendroseris* in the Juan Fernández Islands) but also some widely distributed weedy species (e.g. *S. asper*, *S. oleraceus*, *S. arvensis*, etc.) (Kim et al. 1996). Recently, a distinct new lineage of *Sonchus* was discovered in Morocco and, based on morphological and molecular divergence from other sections, it was subsequently recognized as a new section *Pulvinati* (Mejías et al. 2018). *Sonchus boulosii*, as a sole representative of new section *Pulvinati*, has been found only in four populations from three distinct biogeographic regions of Morocco (i.e., the Eastern Morocco mountains, the Middle Atlas, and the High Atlas). It is a very rare cliff-dwelling species and hypothesized to be quite old relic member within *Sonchus*, with sharing some primitive characteristics with section *Pustulati*. Although phylogenetic relationships among major lineages within *Sonchus s.l.* and closely related genera (*Reichardia* and *Launaea*) have been investigated rather thoroughly, additional resolutions and robust supports within and among lineages are warranted (Kim et al. 1996, 2007; Mejías et al. 2018). Furthermore, very little is known for chloroplast genome evolution within the genus *Sonchus* and the subtribe Hyoseridinae (Hereward et al. 2018). As an initial step to investigate the chloroplast genome evolution within this group, we reported the complete chloroplast genome of *S. boulosii* and assessed phylogenetic position within Cichorieae.

Total DNA (Voucher specimen: 32°35′11.5″N 4°08′55.7″W, ECWP s.n.) was isolated using the DNeasy plant Mini Kit (Quiagen, Carlsbad, CA) and sequenced by the Illumina HiSeq 4000 (Illumina Inc., San Diego, CA). A total of 51,623,340 paired-end reads were obtained and assembled *de novo* with Velvet v. 1.2.10 using multiple *k*-mers (Zerbino and Birney 2008). RNAs (rRNA) were identified using RNAmmer 1.2 Server (Lagesen et al. 2007) and the transfer RNAs (tRNA) were predicted using ARAGORN v 1.2.36 (Laslett and Canback 2004).

The total plastome length of *S. boulosii* (GenBank accession number: MK016665) was 152,016 bp, with large single copy (LSC; 83,988 bp), small single copy (SSC; 18,566 bp), and two inverted repeats (IRa and IRb; 24,731 bp each). The overall GC content was 37.6% (LSC, 35.8%; SSC, 31.2%; IRs, 43.1%) and the plastome contained 130 genes, including 88 protein-coding, six rRNA, and 36 tRNA genes. Two major inversions reported in Asteraceae were also found in S. *boulosii* (Timme et al. 2007). To confirm the phylogenetic position of *S. boulosii*, 12 representative species of Cichorieae were aligned using MAFFT v.7 (Katoh and Standley 2013) and maximum likelihood (ML) analysis was conducted using IQ-TREE v.1.4.2 (Nguyen et al. 2015). The ML tree (Figure 1) showed that *S. boulosii* is sister to *S. oleraceus*.

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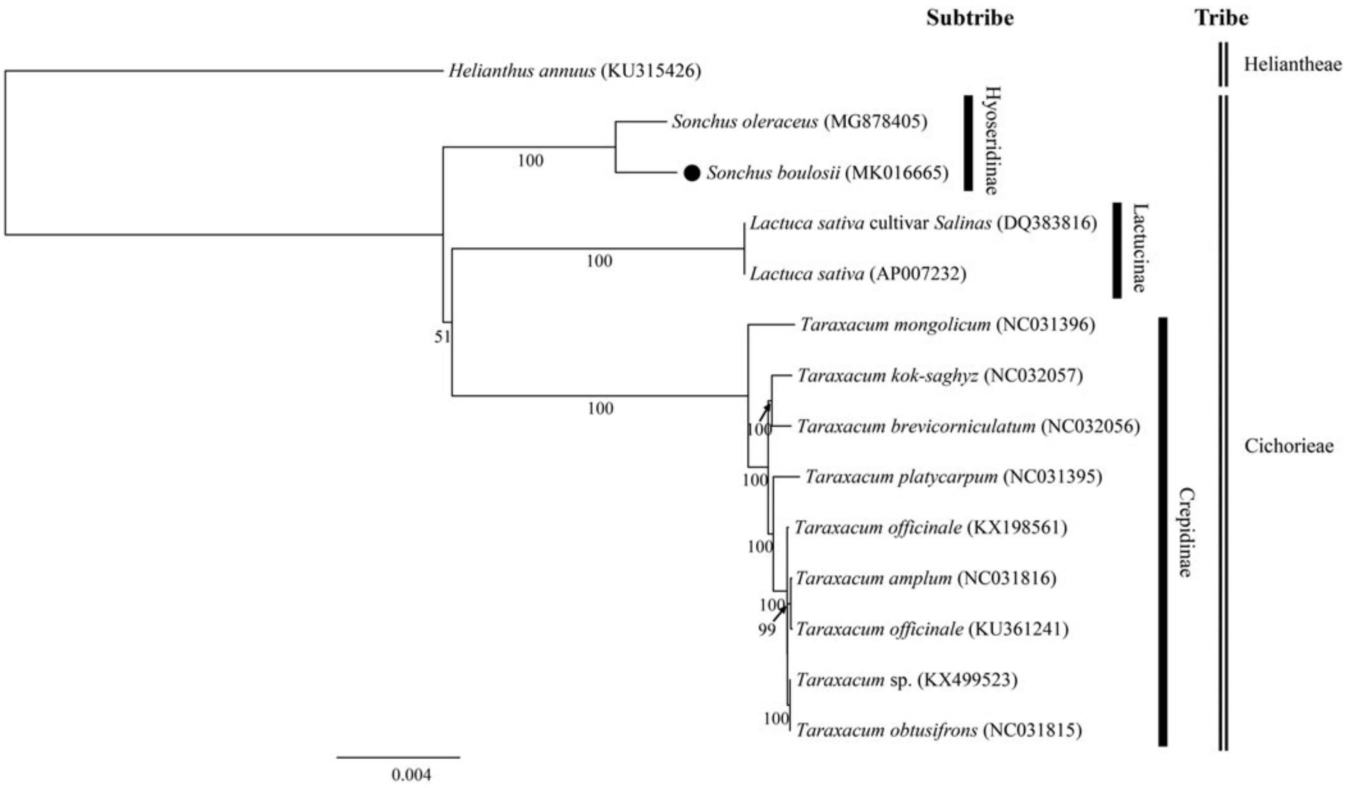

Figure 1. The maximum-likelihood (ML) tree based on the 12 representative chloroplast genomes of Cichorieae. The bootstrap value based on 1000 replicates is shown on each node.

Disclosure statement

The authors declare that there is no conflict of interest regarding the publication of this article. The authors alone are responsible for the content and writing of the paper.

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Disclosure Statement

No potential conflict of interest was reported by the author.

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