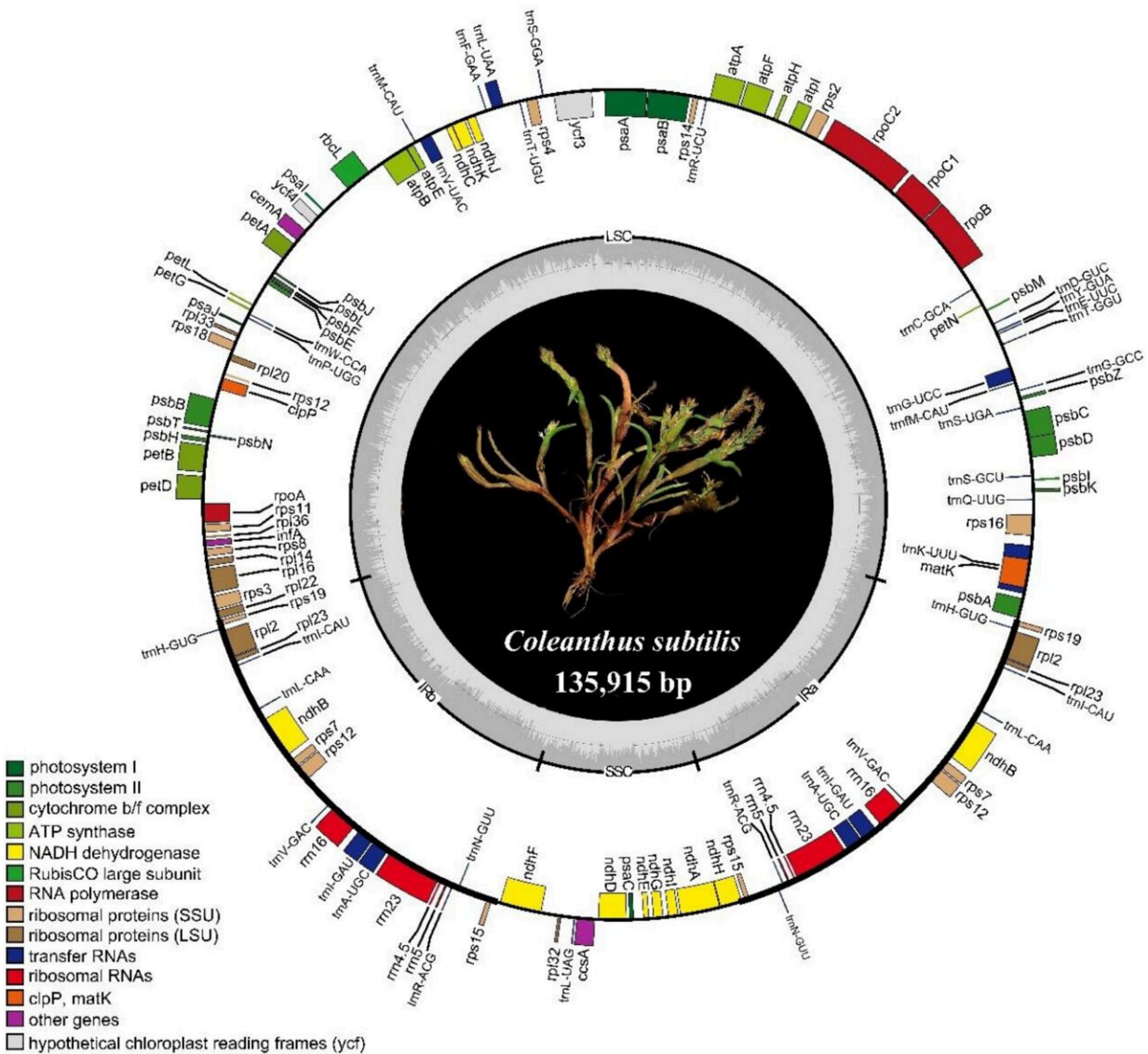


# Complete chloroplast genome of *Coleanthus subtilis*, a protected rare species

May 17 2022, by Zhang Nannan



Chloroplast genome map of *C. subtilis*. Credit: Ren Jing

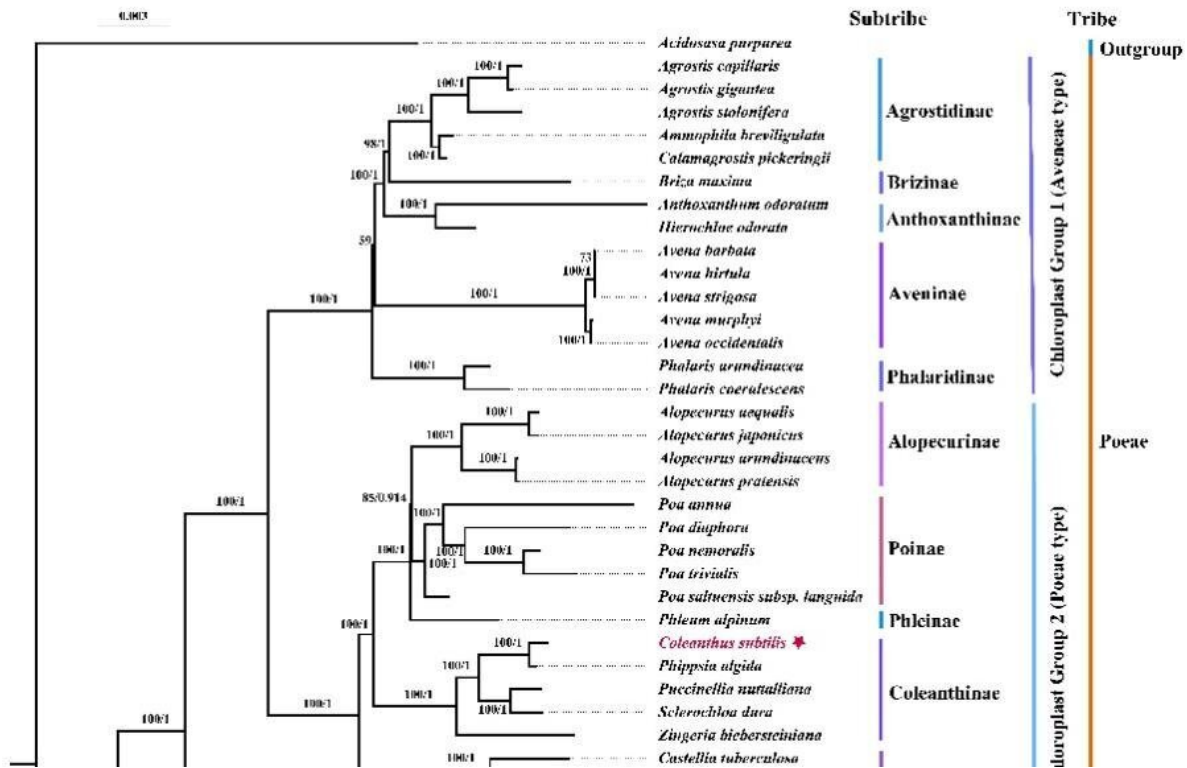
*Coleanthus subtilis* (Tratt.) Seidel (Poaceae) is a rare grass in the monotypic genus *Coleanthus* Seidl. It has been protected in many countries, such as the Czech Republic, North America and China, because of the extremely short life cycle, strict habitat and breeding conditions, and habitat destruction. In addition, *C. subtilis* has a remarkable ability to reappear in its previous habitats after long time intervals.

In March 2021, researchers collected specimens on the beaches of the Yangtze River, and subsequently, it was discovered by researchers from the Wuhan Botanical Garden (WBG) of the Chinese Academy of Sciences in the Songhua River basin in Harbin, which is nearly 100 years after its last appearance in China.

Interestingly, its distribution has never been recorded along the Yangtze River before, and the factors responsible for this particular distribution are unclear. The phylogenetic position of *C. subtilis* and the composition of the subtribe Coleanthinae are controversial, and the absence of information on the [chloroplast genome](#) greatly limits the comprehensive understanding of its phylogeny.

The researchers of WBG sequenced and assembled the [chloroplast genome](#) of *C. subtilis* for the first time, and did a comparative and [phylogenetic analysis](#) with other species in the family Poaceae.

The chloroplast (cp) genome of *C. subtilis* exhibited a tetrad structure of 135915 bp in length, which is similar to the length and structural characteristics of cp genomes of other Poaceae species. The *accD* gene and the introns of both *clpP* and *rpoC1* genes have been lost within the cp genomes of *C. subtilis*, while *ycf1*, *ycf2*, *ycf15* and *ycf68* were pseudogenes, which is a relatively common phenomenon in Poaceae.



Phylogenetic trees were generated based on the 76 shared protein-coding sequences of 53 species using maximum likelihood and Bayesian methods. Credit: Ren Jing

Although the cp genome structure of *C. subtilis* was relatively conserved, 26 simple sequence repeats and 13 highly variable loci were detected, which could be developed as important genetic markers for the Poaceae.

Furthermore, the results of the phylogenetic analysis strongly supported that *Coleanthus* and *Phippsia* were sister taxa to each other and enlightened the relationships between *Coleanthus*, *Zingeria* and *Colpodium*.

This study presents the initial chloroplast genome report of *C. subtilis*, providing an essential data reference for further research on its origin and has implications for population genetics and conservation of this species.

The research was published in *Frontiers in Plant Science* with the title "Comparative and phylogenetic analysis based on the chloroplast [genome](#) of *Coleanthus subtilis* (Tratt.) Seidel, a protected rare species of monotypic genus."

**More information:** Jing Ren et al, Comparative and Phylogenetic Analysis Based on the Chloroplast Genome of *Coleanthus subtilis* (Tratt.) Seidel, a Protected Rare Species of Monotypic Genus, *Frontiers in Plant Science* (2022). [DOI: 10.3389/fpls.2022.828467](https://doi.org/10.3389/fpls.2022.828467)

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