Helichrysum italicum is one of the members of the Helichrysum italicum complex (Asteraceae family, Gnaphalieae tribe, Stoechadina (DC.) Gren. & Godr. section), which is widely distributed in the Mediterranean region. The species H. italicum is further divided into four subspecies italicum, siculum, microphyllum, tyrrenicum based on morphological features, geographical distribution and identified genetic variation (Herrando-Moraira et al. 2016). Overlapping of subsp. and their morphological plasticity often prevents a reliable classification of subspecies, supporting the necessity for new high-informative DNA markers. We report here the complete chloroplast genome sequence of Helichrysum italicum subsp. italicum from the North Adriatic region. The total genome size was 152,431 bp in length, containing 85 protein-coding genes, 36 transfer RNA genes, 8 ribosomal RNA genes, and 2 partial genes (ycf1 and rps19). Based on the available chloroplast genomes from Gnaphalieae tribe, the closest relationship was identified with Anaphalis sinica.

The aromatic plant immortelle contains valuable bioactive molecules and a unique fragrance. These key factors contribute to its attractiveness and implementation in agricultural ecosystems as well as applications in the pharmaceutical and cosmetic industries. In this study, we have characterized the complete chloroplast genome sequence of Helichrysum italicum subsp. italicum from the North Adriatic region. The total genome size was 152,431 bp in length, containing 85 protein-coding genes, 36 transfer RNA genes, 8 ribosomal RNA genes, and 2 partial genes (ycf1 and rps19). Based on the available chloroplast genomes from Gnaphalieae tribe, the closest relationship was identified with Anaphalis sinica.
Two plant species from the Gnaphalieae tribe, *Anaphalis sinica*, and *Leontopodium leiolepis*, formed a common group (Figure 1), whereas the closest relationship was with *Anaphalis sinica*. A close relationship of *Anaphalis* with *Helichrysum* genus was previously identified by Nie et al. (2013).

**Disclosure statement**

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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**References**

Amiryousefi A, Hyvönen J, Poczai P. 2018. IRscope: an online program to visualize the junction sites of chloroplast genomes. Bioinformatics. 34: 3030–3031.

Dong-Hyuk L, Won-Bum C, Byoung-Hee C, Jung-Hyun L. 2017. Characterization of two complete chloroplast genomes in the tribe Gnaphalieae (Asteraceae); Gene loss or pseudogenization of trnT-GGU and implications for phylogenetic relationships. Hortic Sci Technol. 35: 769–783.

FigTree - Molecular Evolution, Phylogenetics and Epidemiology. 2018. [accessed 2018 Nov 26]. http://tree.bio.ed.ac.uk/software/figtree/.

Herrando-Moraira S, Blanco-Moreno JM, Sáez L, Galbany-Casals M. 2016. Re-evaluation of the *Helichrysum italicum* complex (Compositae: Gnaphalieae): a new species from Majorca (Balearic Islands). Collect Bot. 35:e009.

Japelaghi R, Haddad R, Garoosi G-A. 2011. Rapid and efficient isolation of high quality nucleic acids from plant tissues rich in polyphenols and polysaccharides. Mol Biotechnol. 49:129–137.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30:772–780.

McKain MR, Wilson M. 2018. Fast-plast: rapid de novo assembly and finishing for whole chloroplast genomes. mrmckain/Fast-Plast: Fast-Plast v.1.2.8. Zenodo.

Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE); Nov 14; New Orleans, Louisiana: Institute of Electrical and Electronics Engineers (IEEE); p. 1–8.

Nie Z-L, Funk V, Sun H, Deng T, Meng Y, Wen J. 2013. Molecular phylogeny of *Anaphalis* (Asteraceae, Gnaphalieae) with biogeographic implications in the Northern Hemisphere. J Plant Res. 126:17–32.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30:1312–1313.

Tillich M, Lehwalk P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45:W6–W11.