

عنوان مقاله:

Molecular phylogeny of the genus *Sanguisorba* from Iran : Evidence based on cpDNA and nrDNA sequencing analysis

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خلاصه مقاله:

In this research, the molecular phylogeny of the genus *Sanguisorba* including two species (*S. officinalis* and *S. minor*), and the three subspecies (*S. minor* subsp. *muricata*, *S. minor* subsp. *lasiocarpa*, and *S. minor* subsp. *minor*) were studied from Iran using nrDNA ITS and cpDNA rpl32-trnL(UAG). For this purpose, ۲۶ taxa, comprising four Iranian samples plus ۲۲ previously sequenced data received from GenBank were analyzed. The phylogenetic relationships were reconstructed within *Sanguisorba* using maximum parsimony and Bayesian analyses. The results of nuclear sequence analysis showed separation of two subfamilies (*Agrimoniinae* and *Sanguisorbinae*), monophyly of *Sanguisorba*, complete separation of *S. officinalis* (in *Sanguisorba* clade) from *S. minor* and the three subspecies (in *Poterium* clade). Although, the intraspecific relationship remained unresolved, but it was found that, the use of micro- and macromorphological criteria could be used as an important tool in different taxonomic ranks, especially in intraspecific identification. In addition, average sequence divergence, genetic differentiation, morphological, and micromorphological evidence are discussed.

کلمات کلیدی:

Bayesian, delimitation, Maximum parsimony, sequences divergence, Taxonomy

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