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Phylogenetic analysis of *Anchusa* (Boraginaceae-Boraginoideae) Based on ITS Sequences from Iran

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Abstract

A molecular phylogenetic analysis of *Anchusa* was accomplished to compare former assumptions based on non-molecular evidence about the location of species within *Anchusa* genus. Phylogenetic relationships in this genus is required to be elucidated in order to recognize its taxonomic frontiers with regard to the dialectic detach genera *Hormuzakia*, *Gastrocotyle*, *Phyllocara*, *Anchusella* and *Cynoglottis*. DNA sequences from the nuclear ITS region were exerted from 22 samples of the *Anchusa*. The ITS sequences of six species from *Lithospermum* L. were used as out-groups. Sequences were aligned using Bioedit Ver. 7.0.9. The aligned data matrix was reconstructed by maximum parsimony (MP) and neighbor joining (NJ) employing MEGA Ver.7.0.26. We suggest a new classification into four sub-genus based on the phylogenetic data in our study. Also, *Anchusa* was supported as non-monophyletic group.

Keywords: *Anchusa*, ITS sequence, phylogeny, non-monophyly, taxonomy