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The genetic variation of *Anchusa L.* genus (Boraginaceae) as medicinal plants from Iran based on trnL-F sequences data

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Abstract

Delimitation and intrageneric classification of the *Anchusa* genus is indistinct. phylogenetic relationships of this genus are poorly known because of their poverty of molecular data. Total genomic DNA was isolated from dried leaves using the standard CTAB extraction protocol. The trnL-F region of each sample were amplified by PCR employing trnLUAAF (TabC) and trnFUAAR (TabF) primers. The trnL-F sequences of species of *Lithospermum L.* genus were availed as out-groups. Sequences were aligned with Bioedit Vers. 7.0.9. and adjusted manually. The aligned data matrix was reconstructed by maximum parsimony (MP) and neighbor joining (NJ) using MEGA Ver.7.0.26. The results of phylogenetic trees underscored the non-monophyly of *Anchusa*. Also, we suggest a new classification for this genus.

Keywords: *Anchusa*, Genetic variation, trnL-F sequence, non-monophyly, Iran