

Identification and Differentiation of *Fagonia Arabica* and *Fagonia Indica* by Using DNA Barcode Region Matk

Authors : Noshaba Dilbar, Aisha Tahir, Amer Jamil

Abstract : During the last decade, DNA barcoding proved to be an authentic tool for discovery and identification of plants. In the present study, DNA barcoding of two species, *Fagonia arabica* and *Fagonia indica* was done for differentiation by using matK region. matK gene is considered as a universal barcode because of its easy alignment and high discrimination ability. In this study, matK yielded 100% sequencing results. The sequences from both plants were aligned at clustal W and observed that there is no nucleotide variation and polymorphism among both sequences. This was further analysed by BLAST which showed the similar sequences from different plants belonging to same family but didn't find sequence of both species. Considering this, the resulted sequence was submitted by the name of *Fagonia arabica* with accession number KM276890. In the end, we analysed the results from BOLD which gave us the final conclusion that both plants are same as their matK sequences are 100% identical. In literature, both *Fagonia indica* and *Fagonia arabica* names are used for this plant but there is no clear differentiation has been observed in these plants. Results evaluate that *Fagonia indica* and *Fagonia arabica* are the alternative names of same plant.

Keywords : DNA barcoding, *Fagonia arabica*, *Fagonia indica*, matK

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