Abstract

DNA barcoding uses a series of DNA sequences from standard genome fragments to identify species on a large scale. The *Malvaceae* have several species. In this study, nine genotypes of *Malva Sylvestris* species were sequenced by ribosomal and chloroplastic genes. In this research, ITS and rbcl genes were used for sequencing this species genotype. At first, seeds of 9 genotypes of medicinal herbs were collected and their DNA extracted using the Deloporta method. The sequencing of sequenced ribosomal genes and sequenced chloroplasts can be studied in other phylogenetic and evolutionary studies for comparison between species and provide more accurate results on a large scale. The quality of the sequences was evaluated using Chromas software and then clustered with MegAlign software by ClustalW method, and a dendrogram of phylogenic relationships and sequence similarity matrix were mapped. The results of this study showed that the numerical value (d_N / d_S) in the cultivars and genotypes with the ITS and rbcl markers was 0/554 and 03/03 respectively, which indicates that in these areas pure selection of genes The investigation has taken place and has not caused any key changes. The results also showed that ITS and rbcl genes are suitable for evaluation between species and these areas can be used as bar codes for identifying *Malva* species.

Key words: Germplasm*, Malva sylvestris*, Marker, DNA, Barcoding

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