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AN ANALYSIS OF GENETIC DIVERSITY IN LEMON BALM (*MELISSA OFFICINALIS* L.) ACCESSIONS USING AFLP MARKERS

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Melissa officinalis, a member of the Lamiaceae family, is one of the most important medicinal herbs that are applied in different fields of industry worldwide. *M. officinalis* contain essential oil and phenolic acids that have pharmaceutical properties including sedative, carminative, anti-microbial, anti-oxidant, neuroprotective effects and anti-cancer. In this study, genetic diversity and structure of 21 *M. officinalis* accessions were examined using amplified fragment length polymorphism (AFLP) markers. For this purpose, 15 primer combinations generated a large number of scorable fragments per primer pair (1592 scorable bands), of which 1402 bands were polymorphic. The primer combination P₆₆/M₄₈ showed the highest markers polymorphism values (PIC=0.28, DI =0.34, and I=0.51), while the lowest values (PIC=0.17, DI=0.20, and I=0.32) is obtained from the P₁₄/M₄₉ combination. The marker index (MI) values with an average of 18.46 showed high values for both primer combinations E/M and P/M. All of the accessions, based on Neighbor-Net clustering method and structure analysis, are assigned to five clusters; with the maximum genetic dissimilarity of 0.51 belonging to accessions from Gilan (Roodbar and Damash). In addition, the principal coordinate analysis (PCoA) data confirmed the results of the clustering. In this study, the genetic distance was not often related to geographical distance. More likely the relationship among them is due to seed dispersal through human interactions. Our findings indicate that AFLP technique is a powerful tool for assessing DNA polymorphism of lemon balm accessions. Also, high genetic diversity of *M. officinalis* accessions provides important baseline data and a better understanding of conservation, management, and collection strategies in germplasm of this species.

Keywords: Genetic diversity, Molecular marker, Medicinal plants, Fingerprinting, AFLP.