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خلاصه مقاله:

Black cumin (Nigella sativa L.) is one of the most important plants in terms of medicine and economics in the world. Breeding of black cumin genotypes by using biotechnology and phytochemistry has always been an important area of different studies. In this study, ۲۴ ISSR molecular markers were used to evaluate the genetic diversity and population structure of Iranian black cumin genotypes. The primers produced a total number of ۲۲۳ bands, of which ۱۵۵ were polymorphic bands (indicating ۶۹% polymorphism). By analyzing the similarity matrix based on the simple matching similarity coefficient, the similarity ranged from ۰.۴۶ to ۰.۸۴. The genotypes were classified into three main groups in the phylogenetic dendrogram, which was based on the similarity matrix and UPGMA algorithm. The average of Polymorphism Information Content, Marker Index, Resolving power, and Observed number of alleles, Effective number of alleles, Nei's gene diversity, and Shannon's information index were ۰.۲۶, ۱.۵۶, ۳.۰۷, ۱۵.۷۹, ۱۳.۷۲, ۰.۲۶, and ۰.۳۸, respectively. In analyzing the population structure, when the K value was adjusted to range from ۲ to ۱۰, two subpopulations were revealed. However, there was a degree of inconsistency when comparing the results of the phylogenetic dendrogram with those of the population structure. The results of this study can expand future inquiries into the assessments of germplasms and provide opportunities for breeding black cumin genotypes.

کلمات کلیدی:

Breeding, germplasm, Polymorphism Information Content, similarity matrix, Subpopulation

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