

Abstract

Barberry fruit is known as a medicinal plant in the world, and it is one of the most important horticultural crops in South Khorasan province. Genetic diversity has a basic role in the successful reforms of crop varieties with durable resistance to biotic and abiotic stresses. Molecular markers are reliable tools for evaluating genetic diversity because a direct reflection of the level of DNA. In this study, 20 ecotypes of *Berberis* were collected from different regions of South Khorasan Province to assess the genetic diversity using ISSR marker. Totally, 10 ISSR primers, with the amplification of suitable polymorphic bands were selected. A total of 98 bands were detected, between 300 to 1300 bp in size. Polymorphic ISSR-7 primer amplified the highest number of bands with 17 bands, while ISCS50 primer amplified only two polymorphic bands. The ISCS57 and ISCS50 markers have the highest and lowest polymorphic information content (PIC), respectively. The estimated Nei's and Shannon index for gene diversity were 0.24 and 0.35, respectively. Dendrogram was drawn based on ISSR data using NTSYS pc 2.18 software according to Jaccard similarity matrix and UPGMA algorithm. Based on cluster analyzing, five main groups were identified. The first group included 12 ecotypes of Birjand, Behdan, Ghehardeh, Razg and Noghab, the second group also includes two ecotypes of Birjand and was Behdan. In Group 3, three ecotypes Behdan and Nozad, in Group IV Behdan ecotype and Group V, two ecotypes were Afin and Dorokhsh. Analysis of molecular variances revealed that high level of total variation was due to within populations, rather. There for it will be better to do selection within populations in breeding programs.

Key words: *Berberis vulgaris*, Genetic diversity, ISSR marker

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