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**ASSESSMENT OF GENETIC VARIATION OF GENUS SALVIA L. BY
ISSR MARKERS**

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Salvia L. is an important and the largest genus of the Lamiaceae family which includes 900 species spread throughout the world. The genus consists of 58 species in Iran, which seventeen of them are endemic. The plants are considered as rich sources of di- and tri terpenoids, phenolic acids, and flavonoids and have been used therapeutically for treatment of diseases such as acquired immunodeficiency syndrome (AIDS), diabetic nephropathy, liver and Alzheimer. Despite *Salvia* is a valuable medicinal plant, there is no comprehensive data on genetics structure of its populations. Molecular markers provide a powerful tool for good description of germplasm and their organization [1]. In this study, a number of ISSR markers were applied to assess the level and pattern of genetic diversity in some of wild growing *salvia* species of Iran. After preliminary tests, five primers were chosen for further analysis. Amplicons size was estimated in a range of 400-5000 bp and bands were scored as 1/0 represents presence/absence of polymorphic bands. Based on our results, the ISSR primers generated polymorphic bands and detected polymorphism level represents high genetic distance at intra- and inter-species level. Results confirmed that ISSRs are efficient markers for genetic relatedness assessment in genus *Salvia* and are powerful enough to accurate assessment of genetic variation in *Salvia* species.

References

[1] Sepehry Javan, Z.; Rahmani, F.; Heidari, R. *Australian Journal of Crop Sciences*. **2012**, 6(6), 1068-1073.