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GENETIC STRUCTURE OF *HYPERICUM PERFORATUM* POPULATIONS
IN IRAN'S NATURAL HABITATS

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The theoretical purpose of the present work was to study genetic relationship and genetic structure of Iranian populations of *Hypericum perforatum*. Genetic structure of 19 population of *H. perforatum* collected from different region of Iran were identified by inter simple sequence repeat (ISSR) markers. 15 ISSR primers were used and detected a total of 323 scorable fragment. Molecular variation within and among the populations were estimated 71% and 29% of total variance, respectively. According to the Nei's (1973) gene diversity and Shannon's Information index, the most genetic diversity observed in Karaj ($h=0.1955$ and $I= 0.2927$) and Sari ($h= 0.1424$ and $I= 0.2131$) populations respectively. Results showed suitable gene flow ($Nm= 1.14$) and low F_{st} (0.17) among and within populations. Total heterozygosity (H_t) was 0.24 and most of it belonged to Heterozygosity within populations ($H_s= 0.2$). Differentiation among-population ($G_{ST}=0.3$) and Heterozygosity among populations ($D_{ST}= 0.04$) was low. The result showed populations of *Hypericum perforatum* in natural habitat of Iran are in proper relationship and over times differentiation hasn't occurred among them.

References

[1] Nie, M. Proceedings of the national academy of sciences of USA. Analysis of gene diversity in subdivided populations. 1973. 70: 3321-3323.