

P-37 (24)**GENETIC DIVERSITY ANALYSIS OF SOME NATIVE EREMURUS ACCESSION BASED ON GENOTYPING BY SEQUENCING**

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The genetic diversity of ornamental plants is valuable resources that should be preserved. To evaluate genetic diversity within and between existing populations at the DNA level, the use of molecular markers is needed. However, developing different markers such as SNPs for non-model plants can be challenging and cost prohibitive. There are limited numbers of ornamental plants that have publicly available complete genome sequences. Recent advances in high throughput next generation sequencing technology, have made it possible to analyze genome on a wide scale through genotyping by sequencing (GBS). This approach is based on reduction of genome complexity using restriction enzymes, and no prior genetic information is needed. Genetic diversity-focused GBS uses simultaneous genome sequencing and SNP calling to generate marker data for analyzing genetic diversity of non-model plants. *Eremurus*, also known as foxtail lily, is a genus of *Asphodelaceae* family. There are 45 species of *Eremurus* in Eurasia, with 7 species and 4 subspecies being native to Iran. Most of these perennial species are of great horticultural value. There is no information about inter- and intra-species diversity in *Eremurus* germplasm. Therefore, gd-GBS is being used to characterize an *Eremurus* germplasm collection. Sampling was performed during spring and summer of 2015 and 2016 from different habitats of Iran. Among the collected samples, 96 accessions from 30 populations were selected to analyze genetic diversity.

Keywords: Genotyping by sequencing, plant genetic diversity analysis, SNP calling, genome reduction con, *Eremurus*