



219

GENETIC DIVERSITY OF NAEIN-E HAVANDI (*ANDROGRAPHIS PANICULATA* L.) ACCESSIONS USING PROTEIN ANALYSIS

Daryush Talei^{1,*}

¹*Department of Medicinal Plants Research Center, Shahed University, Tehran, Iran
E-mail: d.talei1348@gmail.com*

Naein-e Havandi (*Andrographis paniculata*) is a medicinal herb in the family Acanthaceae. The leaves of the plant contain abundant diterpenoids of medicinal properties [1]. Knowledge of seed protein diversity improves the efficiency of germplasm conservation and development. The present study aimed to investigate the genetic diversity of 12 accessions of *A. paniculata* using seed protein analysis. The results revealed the presence of 15 different types of proteins ranged from 13 to 105 kDa, yet, only two of them with low molecular weight were found polymorphic. The two polymorphic proteins consisted of a 30 kDa protein, which was absent only in accession 11228, and a 20.5 kDa protein band, which was present in accessions 11228, 11266, 11306 and 11348. The results indicated that most of the bands were similar in all accessions. The Unweighted Pair Group Method with Arithmetic Average (UPGMA) cluster analysis of the accessions based on the protein profiles using the Ward method generated three clusters. The first cluster contained eight accessions, indicating the close similarity among most accessions, the second cluster contained only one accession and the third cluster comprised of three accessions. Accession 11228, which was lacking the 30 kDa protein was located separately in the second cluster. Although, the cluster analysis showed that the accessions possessing the 20.5 kDa protein are much more related together than those accessions which were lacking this protein, and were located in the third cluster. Overall, the outcomes of the present study were indicated the presence of high genetic variability among the *A. paniculata* accessions. Our findings suggest that these protein bands can serve as useful markers to hybridization and breeding programs to generate useful recombinants in the segregating generations, the genetics and breeding programs for improvement of *A. paniculata*.

Reference

[1] Valdiani, A.; Mihdzar, A.K.; Tan, S.G.; Talei, D.; Puad, M.A.; Nikzad, S. *Mol Biol Rep.* **2012**, *39*, 5409-5424.