



EFFECT OF PLOIDY LEVEL ON THE NUCLEAR GENOME CONTENT AND
ESSENTIAL OIL COMPOSITION OF ANISE HYSOP
(*AGASTACHE FOENICULUM* [PURSH.] KUNTZE)

Seyyedeh Farahnaz Talebi^{1*}, Mohammad Jamal Saharkhiz^{1,2}, Maryam Jafarkhani Kermani³
Yavar Sharafi⁴, Fatemeh Raouf Fard¹

¹Department of Horticultural Science, Faculty of Agriculture, Shiraz University, Shiraz, Iran

²Medicinal Plants Processing Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

³Department of Tissue Culture and Gene Transformation, Agricultural Biotechnology Research
Institute of Iran

⁴Department of Horticultural Science, Shahed University, Tehran, Iran

Anise hyssop (*Agastache foeniculum*) is one of the important medicinal-ornamental plant species. In medicinal plants, polyploidy induction is usually associated with an increase in total nuclear genome content and a change in the quality and quantity of important medicinal compounds. In the present investigation, flow cytometry was used to compare the nuclear genome content of diploid and tetraploid plants of anise hyssop. The essential oils (EOs) of different ploidy levels, obtained by hydro-distillation method, were analyzed by GC and GC-MS instruments. The results showed the total nuclear genome of tetraploid and diploid plants was 2.15 ± 0.001 pg and 1.06 ± 0.02 pg, respectively. The change in ploidy level also significantly ($P < 0.05$) affected the EO content and most of its components. The percent of EO in diploid and tetraploid plants was 1.32 ± 0.1 and 2.78 ± 0.1 , respectively. The proportion of Methyl cavicol, which is the major EO component of anise hyssop, significantly ($P < 0.05$) increased in tetraploid plants (81.02 %) compared to the diploids (78.75 %). DNA content increases by chromosome doubling that occurs with polyploidy induction. Polyploidy can affect the physiological and biochemical behaviors such as net photosynthesis, transpiration, enzymes activity, photosynthetic electron transport and isozyme expression. All these changes might affect secondary metabolites biosynthesis and alter their accumulation in plants. Polyploidization significantly changed the concentrations of EO constituents. Polyploid induction may also change the secondary metabolites biosynthesis pathways and gene expression in the medicinal plants.

References

- [1] Moghbel, N.; Khalili Borujeni, M.; Bernard, F. *J Gene Engin and Biote.* **2015.** *13:* 1–6.
- [2] Ahmadi, T.; Jafarkhani Kermani, M.; Mashayekhi, K.; Hasanloo, T.; Shariatpanahi, M.E. *Int. Res. J. App. and Bas. Sci.* **2013.** *4:* 3840-3849.
- [3] Wohlmuth, H.; Smith, M.K.; Brooks, L.O.; Myers, S.P.; Leach, D.N. *J. Agric. Food Chem.* **2006.** *54:* 1414-1419.



GENETIC DIVERSITY OF *MELISSA OFFICINALIS* BASED ON SRAP MARKER

Saeede Noroozy¹, Yavar Sharafi^{2*}, Daryush Talei³, Amir Mohammad Naji⁴

¹Shahed University Graduate Student of Agricultural Biotechnology

²Department of Horticultural Sciences, Faculty of Agriculture, Shahed University, Tehran, Iran

³Medicinal Plants Research Center, Shahed University, Tehran, Iran

⁴Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahed University, Tehran, Iran

Melissa officinalis L. (Lemon Balm) belongs to lamiaceae family is a medicinal plant native to East Mediterranean regions. Essential oil of the plant has Antioxidant, Anticancer properties and expectorant capacity (1, 2). Sequence related amplified polymorphism (SRAP) markers are new to amplify the sequence open reading frame (ORF) by PCR (1, 2). This technique uses a combination of primers, for amplifying ORF regions. In this study, SRAP marker with using 10 combine markers was used to evaluate genetic diversity of 20 different *Melissa officinalis* accessions. The results showed a total of 144 bands that 131 bands were polymorphism. The greatest number of bands was related to me3-em3 marker. Cluster analysis using the un-weighted pair-group method with arithmetic averages (UPGMA) produced three groups between these accessions. The genetic similarity was between 0.54 to 0.90 ranges. The average information polymorphism for these markers was 0.90, which indicated high level of genetic diversity. All of the SRAP markers have showed high polymorphism between these accessions.

References

- [1] Haidari, P.Z.; Mehrabi, A. A.; Nasrolah Nezhad ghomi, A. A. *Biharean Biologist*, **2013**. 7(2): 94-98.
[2] Daniel, W. H. R; Andrea, D. W. *Application in Plant Science*, **2014**. 2(7): 140-1407.