

Objectives: Variation in the composition of volatile oil and genetic variation were studied in diverse wild populations of *Origanum syriacum* L. in Israel, in a search for breeding sources that would lead to high quality products from this spice plant.

Methods: Populations were surveyed along a N to S gradient. For analysis of the volatile oil, 5-15 plants in each population were sampled. The test plants were cloned, and a part of each plant was raised in a controlled environment. In each plant, the volatile oil components of leaf extracts were separated, using gas chromatography / mass spectrometry (GCMS). The percentages of these components were normalized by arcsine of square root transformation. Oil profiles were examined using canonical discrimination analysis and two-way clustering (Ward's algorithm).

In parallel, genetic variation within and between the test populations was estimated with the use of 4 different AFLP primer combinations. The AFLP gels were translated into binary arrays and clustered, using the hierarchical unsupervised growing neural network procedure (the sotarray algorithm see Herrero, J. et al. *Bioinformatics*. 17: 126-136).

Results of volatile oil analyses: The field samples of the wild populations surveyed can be divided into 5 geographically distinct groups and the uniform-environment samples into 2 groups, i.e. only part of the variation is genetically founded. Both analyses revealed similar patterns (Figs. 1, 2). Unrelated to the geographical area, the tested plants can be divided into a predominantly carvacrolic and a significantly different predominantly thymolic group, with a correlation eq. of -0.944 between the respective oil components.

Results of molecular survey: The ALFP markers, used so far for estimates of genetic diversity result in high variation in band patterns within each population, and no significant among-population variation can be discerned. An exception is seen in primer set E-ACT / M-CAA, which shows a distinct cluster in the Mt. Hermon population (Fig. 3).

Conclusions: The results from oil profiles point to some genetic variation between northern and southern populations, which is maintained under uniform growing conditions. Under selection in the natural habitat five geographical distinct groups were identified. At this stage, our studies of molecular variation are inconclusive.

Fig. 1 Two-Way Clustering Analysis of Essential-Oil Composition in *O. syriacum* Populations. Wild-Growing Plants

Two-Way Clustering Analysis of Essential-Oil Compositions in *O. syriacum* Populations. Plants Grown in Controlled Environment

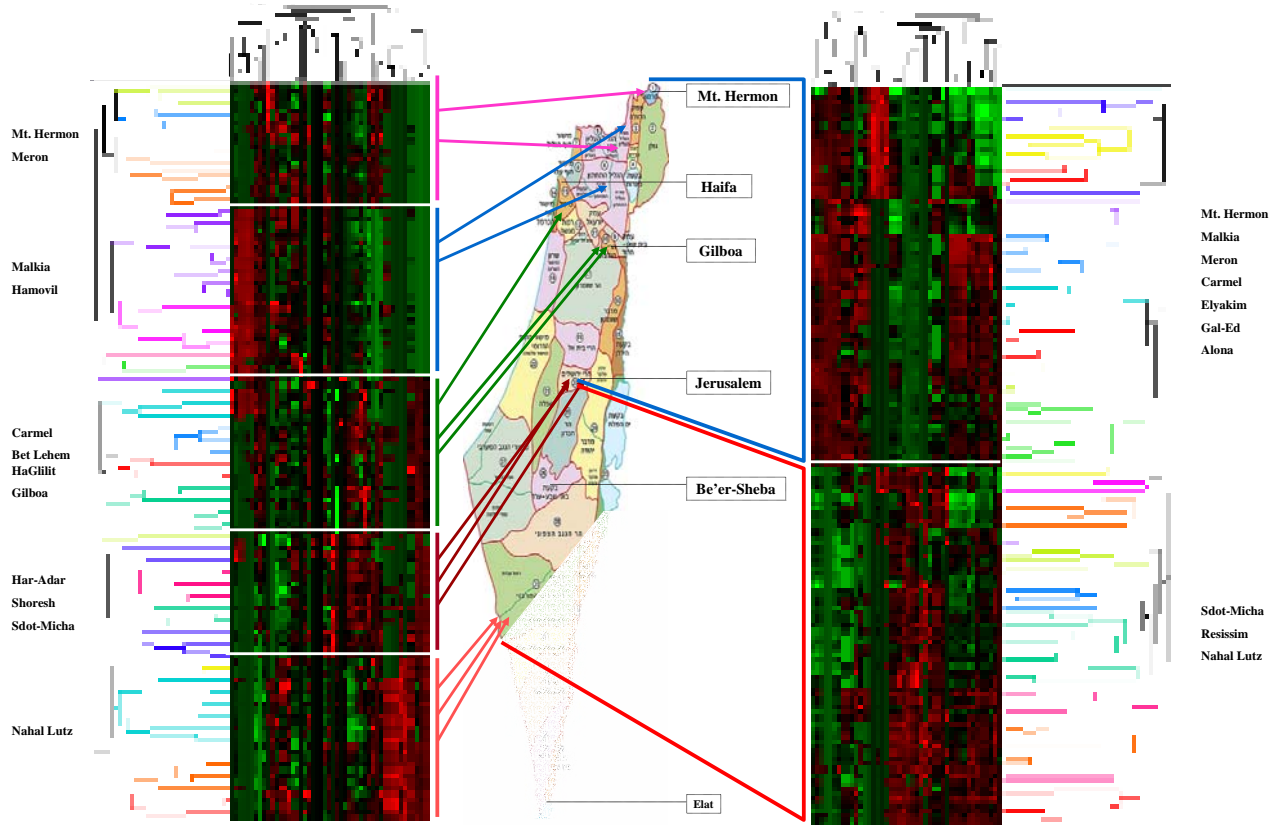
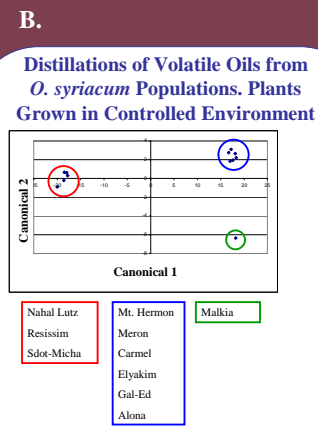
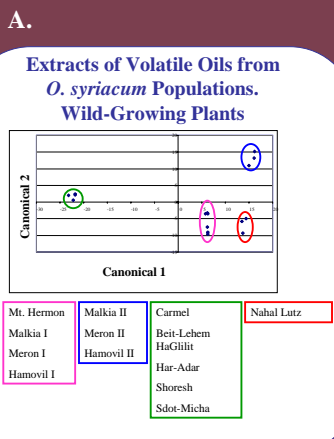


Fig. 2 Distribution of Canonical Discrimination Analysis



Canonical discrimination analysis was used for linear combinations that had the highest F-values. The distribution of the populations in the first and second canonicals is shown

Fig. 3 Clustering of Binary AFLP Arrays

