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Metabolic Profiling of UV-irradiated *Melissa officinalis* by GC/MS for Screening of Secondary Metabolite Overproducers

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Objectives

Plants have various metabolites which are the end products of cellular regulatory processes, which are estimated to be over 100,000. Their levels can represent the ultimate response of biological systems to genetic or environmental changes. Therefore, metabolomic data provide valuable information such as physiological state and reflect specific biochemical processes in plants. *Melissa officinalis* is a perennial herb occurring throughout the East Asia, and has recently attracted increased attention due to its health-benefiting effect mainly due to its secondary metabolites.

Materials and Methods

In this study, to investigate the metabolite profiles in treated groups of which metabolic pathways have been disrupted by UV, their metabolites were analyzed by GC/MS. To obtain metabolites from the plant samples, whole leaves of each cultivar were extracted by buffer containing MeOH:Chloroform:H_2O=2.5:1:1, and for GC/MS analysis, the extract was derivatized by the processes of methoximation and silylation.

Results

By using GC-MS, we identified more than 100 distinct compounds from *Melisa officinalis* leaf extracts. Analyzed metabolomic data by GC-MS showed over seventy metabolites were different in the control and treated groups. Change of metabolite levels of the control and various treated groups of *Melisa officianalis* were statistically analyzed by a multivariate analysis, principal component analysis (PCA). Through the PCA, phenotypic levels of several metabolites were found to be significantly affected by the UV irradiation on *Melisa officianalis*. The lemon balm samples treated with UV irradiation for different durations were clearly discriminated in score plots using a combination of PC1 and PC2 and discriminating metabolites are significantly distinguished in the loading plots of PC1 and PC2 in fig. 1. (a). As increasing the treatment UV irradiation time, the values of PCs for each group with a different recovery time showed a clear trajectory by moving clockwise in the score plot of the combination of PC1 and PC2. Glutamic acid (RT 10.05), citric acid (RT 11.59) and octadecanoic acid (RT 14.17) were found to be the major compounds discriminating among the samples treated UV irradiation for different times in fig. 1.

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(b). These data could be further used in the screening of cultivars overproducing high-value secondary metabolites.

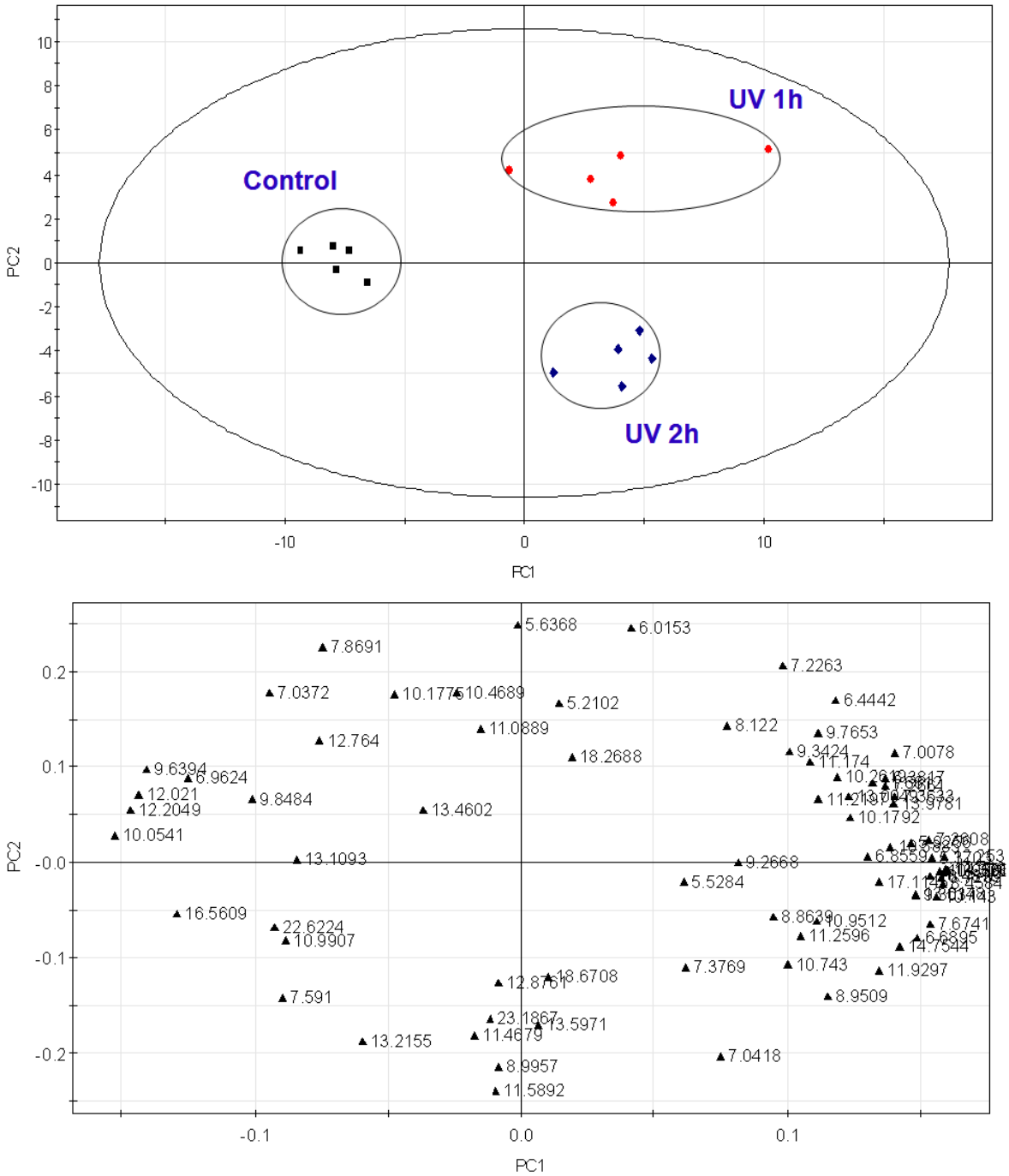

Fig. 1. (a) Score plot of PCA of various lemon balm extracts by the combination of PC1 and PC2, representing 50% and 18%. The ellipse represents the Hotelling T2 with a 95% confidence. (b) Loading plot of PCA for PC1 and PC2. PC1 has an explained variation of 0.58. Black square, control; red circle, lemon balm treated with UV irradiation for 1 h; blue diamond, lemon balm treated with UV irradiation for 2 h