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Taxonomic Discrimination of Higher Plants by Pyrolysis Mass Spectrometry

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Objectives

In this study, we analyzed leaf tissues of six species and one variety of higher plants and eight cultivars of *Catharanthus roseus* by PyMS to assess whether PyMS can be used for taxonomic classification of higher plants and for distinction of genotypes of the same species, respectively.

Materials and Methods

1. Materials: Leaf tissues of six species and one subspecies of plants (*Hepatica asiatica* Nakai, *H. insularis Nakai, Sedum sarmentosum* Bunge, *S. karmtschaticum* Fisch., *S. takesimense* Nakai, *Rosa multiflora* Thunb. and *R. multiflora* var. *platyphylla* Thory) and eight cultivars (Cooler Grape, Cooler Peppermint, Little Bright Eye, Apricot Delight, Equator Grape, Equator Rose, Equator White Eye, and Equator White) of *Catharanthus roseus* (L.) G. Don grown in a growth chamber were used for PyMS analysis

2. Methods: The pyrolysis mass spectrometer RAPyD-400 (mass range 12-400 Da; ion counting to 25 MHz) was used. Curie-point pyrolysis was conducted at 530C for 3s.

Results and Discussion

Pyrolysis mass spectrometry (PyMS) is a rapid, simple, high-resolution analytical method based on thermal degradation of complex material in a vacuum and has been widely applied to the discrimination of closely related microbial strains. Water extracts of leaf tissues of six species and one variety of higher plants and eight *C. roseus* cultivars were subjected to PyMS for spectral fingerprinting. A dendrogram based on principal component analysis (PCA) of spectral fingerprinting of seven species and two subspecies was in agreement with the known taxonomy of the plants. PCA enabled to cluster higher plant species into different cultivar series. These results suggest that higher plants can be classified on the basis of pyrolysate profiling even at the cultivar level.

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