



Max Rubner Conference 2016
Food Metabolomics

October 10-12, 2016
Karlsruhe, Germany

Targeted metabolomics approach for the characterization of wild *Vitis* genotypes

Silvia Ruocco, Marco Stefanini, Daniele Perenzoni, Jan Stanstrup, Fulvio Mattivi, Urska Vrhovsek
Department of Food And Quality Nutrition, Fondazione Edmund Mach, San Michele all'Adige, Italy
Department of Agricultural, Food, Environmental and Animal Sciences, University of Udine, Udine, Italy

Wine is one of the most popular beverages in the world which is exclusively produced from *Vitis vinifera* varieties due to the superior quality of their grapes. However, today a large amount of pesticides are used in viticulture in order to protect grapevine from their pathogens with a strong impact on environment and human health. For this reason, research has focused on the development of new interspecific hybrids using wild American genotypes in order to introgress their resistant traits to pests and diseases in *V. vinifera* cultivars. Despite this, little is known regarding the metabolic profile of wild genotypes.

The aim of this work was to characterize the grape composition of two hybrids varieties (41B and K5BB) and five American genotypes (*V. andersonii*, *V. arizonica* Texas, *V. champinii*, *V. cinerea* and *V. californica*) in six different vintages. Also *V. vinifera* cultivars (Pinot Noir and Cabernet Sauvignon) were taken into consideration as references. A targeted metabolomics strategy was used for the investigation of simple phenolic compounds, anthocyanins, proanthocyanidins and lipids. Grape skins anthocyanins were analyzed using LC-DAD [1]. In three wild genotypes less than 5% of the total anthocyanins detected were diglucosides. In the four remaining genotypes, diglucosides accounted for more than 40% of the total. Maximum acceptable limit for diglucosides contained in wine is 15 mg/L [2].

LC-MS/MS methods were used for the study of phenolic compounds and lipids [3,4]. The results obtained showed that three wild genotypes contained higher average amount of total phenols and that the one out of seven non-*V. vinifera* genotypes contained a higher content of total lipids compared to *V. vinifera* cultivars. Analysis of proanthocyanidins by LC-MS showed that wild genotypes were mainly rich in oligomers and short-chain polymers [5]. Heat-map analysis was used to point out the differences in genotypes' content for the different metabolites studied.

This work demonstrates the existence of a significant genotypic diversity between the grape composition of *V. vinifera* and other species. The information gained could be very useful for the future grapevine breeding.

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[3] Vrhovsek U. et al. J. Agric. Food Chem 2012, 60, 8831-8840.

[4] Della Corte A. et al. Talanta 2015, 140, 52-61.

[5] Gris F. E. et al. Food Chem 2011, 126, 213-220.

Max Rubner-Institut
Federal Research Institute of Nutrition and Food

Address Haid-und-Neu-Straße 9, 76131 Karlsruhe

Phone +49 (0)721 6625 201

Fax +49 (0)721 6625 111

E-Mail mrc@mri.bund.de

Internet www.mri.bund.de