



CHANGINS

Hes·so

Macrowine 2016

June 27 - 30, 2016 - CHANGINS (NYON), Switzerland

Conference programme

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**METABOLOMIC PROFILE OF RED NON-V. VINIFERA GENOTYPES**


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*Vitis vinifera* L. is the most widely cultivated *Vitis* species which includes numerous cultivars. Owing to their superior quality of grapes, these cultivars were long considered the only suitable for the production of fine wines. However, the lack of resistance genes in *V. vinifera* against major grapevine pathogens, requires for its cultivation frequent spraying with large amount of fungicides. Thus, the search for alternative and more sustainable methods to control the grapevine pathogens have brought the breeders to focus their attention on other *Vitis* species. In fact, wild *Vitis* genotypes present multiple resistance traits against pathogens, such as powdery mildew, downy mildew and phylloxera. For this reason, these genotypes have been used in breeding programs in order to introgress resistant traits to pests and diseases in *V. vinifera* species. The aim of this work was to study the metabolite profiles (simple phenolic compounds, anthocyanins, lipids and proanthocyanidins) of two hybrid varieties (41B and K5BB) and seven American *Vitis* species (*V. andersonii*, *V. arizonica*, *V. champinii*, *V. cinerea*, *V. riparia*, *V. slavini* and *V. californica*) in six different vintages. The results were compared with two *V. vinifera* cultivars (Pinot Noir and Cabernet Sauvignon). Grape skin anthocyanins were analyzed by HPLC-DAD [1] and twenty different anthocyanins were detected and quantified. In four genotypes less than 5% of the total amount of anthocyanins detected were diglucosides (from 11.6 to 56.9 mg/kg). In the five remaining genotypes more than 50% of the total were found to be diglucosides (from 522.1 to 2657.6 mg/kg). Analysis of phenolic compounds by UHPLC-MS/MS [2] showed that three non-*V. vinifera* genotypes contained higher average amount of total phenolics compared to *V. vinifera* cultivars. A rapid LC-MS/MS method [3] was used to identify and quantify thirty-three lipids. The total lipids of eight out of nine non-*V. vinifera* genotypes was higher compared to *V. vinifera* cultivars. The differences between the genotypes' content of anthocyanins, phenolics and lipids were investigated by heatmap analysis. The data was scaled to unit variance, the correlation of variables was used as the distance measure and Ward's minimum variance method was used for hierarchical clustering. Up to our knowledge this is the most extended metabolomics profiling study on wild *Vitis* grape genotypes. Altogether, this study highlights the presence of a significant genotypic diversity between the composition of the fruits of *V. vinifera* and other species. The knowledge of their composition can greatly influence the further breeding programs, since being responsible for both the quality and the resistance traits of new grape interspecific varieties. [1] Mattivi F. et al. JAF 2006, 54, 7692-7702 [2] Vrhovsek U. et al. JAF 2012, 60, 8831-8840 [3] Della Corte A. et al. Talanta 2015, 140, 52-61

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