Correlation of grape leaf metabolites with *Plasmopara viticola* resistance traits

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Plasmopara viticola is an obligate biotrophic oomycete which infects all cultivars of the European grapevine (*Vitis vinifera*). In contrast to *V. vinifera* the native American species such as *V. labrusca* or *V. riparia* are resistant to the pathogen. In the 19th century *P. viticola* was unintendedly imported from Northern America to Europe, where it encountered with the highly susceptible European grapevines. The oomycete infiltrates the host tissue through the stomata of leaves, flowers and small berries. Though infection can happen throughout the whole vegetation phase, it bears the highest potential of severe yield losses at time of flowering. Once stomata penetration occurs, the susceptible European vines fail to stop the proceeding infection. However, American vine species have gained the necessary traits to stop or at least slow down host internal growth of *P. viticola*. Though resistance mechanisms are not yet fully understood, it is assumed that secondary metabolites are involved as active components or signaling compounds. Thus, we screened leaf metabolites of eleven grapevine genotypes with different *P. viticola* resistance traits. Leaf homogenates were analyzed by GC-MS and LC-MS to cover the patterns of volatile as well as non-volatile metabolites. Non-targeted chemometrical data processing was used to obtain metabolite fingerprints of grapevine leaves at the plant developmental stage of flowering. Leaf metabolites of the eleven tested genotypes were analyzed in two subsequent years.

Principal component analyses (PCA) of the metabolite fingerprints arrange all susceptible *V. vinifera* cultivars close to each other. Interspecific genotypes and the resistant *V. labrusca* samples are positioned in close proximity, and the *V. riparia* samples segregate from both groups. These observations apply to the fingerprints of volatiles as well as of non-volatiles. PCA generates groups which divide the grapevine genotypes into their biological filiation which is at the same time a separation into susceptible and resistant genotypes. Resistance traits of the genotypes were correlated with their metabolite profiles. Spearman rank correlation isolated all together four different metabolites with high correlation coefficient moduli in both of the two subsequent years. These were methyl salicylate, (*E*)-beta-ocimene and two known-unknown compounds. Further identification with approved mass spectrometry tools are in progress. Whereas only methyl salicylate could be found in intense correlation with high resistance traits, the other three where strongly correlated with susceptibility.