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Polyphenomics based on UPLC-QqQ-MS for deciphering the genetic bases of grapevine response to drought

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Phenolic compounds represent a large family of grape secondary metabolites, essential for the quality of grape and wine and playing a major role in plant defense against biotic and abiotic stress. Phenolic composition is genetically driven but also greatly affected by environmental factors and in particular by drought. A major challenge for selection of grapevine cultivars adapted to climate change and with high potential for winemaking is to dissect the complex plant metabolic response involved in adaptation mechanisms.

A targeted metabolomics approach based on UPLC-QqQ-MS analysis in the MRM mode (Lambert et al., 2015) has been developed for high throughput profiling of the phenolic composition of grape skins. This method enables rapid, selective, and sensitive quantification of 96 phenolic compounds (anthocyanins, phenolic acids, stilbenoids, flavones, flavanones, flavan-3-ol monomers and oligomers...), and of the constitutive units of proanthocyanidins (i.e. flavan-3-ol oligomers and polymers, also called condensed tannin), giving access to detailed polyphenol composition.

It has been applied on the skins of mature berries from a core-collection of 279 *V. vinifera* cultivars grown with or without watering to assess the genetic variation for polyphenol composition as a response to differential water availability, in the frame of the EU project Innovine. Chemometrics analysis of the phenolic composition data has shed light on the genetic diversity of vine metabolic response to drought.

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Reference:

Lambert M, Meudec E, Verbaere A, Mazerolles G, Wirth J, Masson G, Cheynier V, Sommerer N, 2015. A high-throughput UHPLC-QqQ-MS method for polyphenol profiling in rosé wines, *Molecules*, 7890-7914.