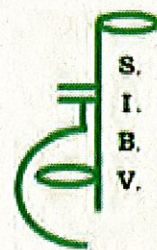




**FEEDING THE PLANET: PLANT SCIENCE AND BREEDING
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POSTER LIST

TRANSCRIPTIONAL PROFILING AND METABOLIC QTL ANALYSIS PROVIDE NEW INSIGHTS INTO THE FINE REGULATION OF ANTHOCYANIN AND FLAVONOL CONTENT IN RIPE BERRIES

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Vitis vinifera, flavonoids, metabolic profiling, microarray, quantitative trait locus

Anthocyanins and flavonols play a fundamental role in the colour, sensory attributes and health value of grapes and wine. In the last decade, great progress has been made in clarifying the main determinants of their accumulation in grape berry skin. However, several aspects are still not completely understood, like the molecular details of the fine variation in content and composition among cultivars, which ultimately contributes to wine typicity, and the interdependency in the synthesis of the two compound classes.

To shed light on these issues, a segregating progeny derived from the cross of two divergent *Vitis vinifera* cultivars, 'Syrah' and 'Pinot Noir', was analysed during four growing seasons for their anthocyanin and flavonol profile at mature berry stage, and an integrative approach combining metabolic, genetic, and transcriptional sources of information was adopted.

New candidates for the genetic control of anthocyanin and flavonol biosynthesis were identified by exploring the gene predictions in 24 mQTL (metabolic quantitative trait locus) regions and their expression profile during ripening in individuals with contrasting anthocyanin/flavonol accumulation. New information on some aspects scarcely investigated so far for anthocyanins, like sequestration into the vacuole and degradation, or completely neglected such as acylation was acquired. A large effect QTL, co-localizing with the major locus that controls the anthocyanin content, was discovered for flavonols, which represents a completely novel evidence of a common genetic control of the two flavonoid classes. Additionally, flavonol-specific mQTL regions were found to contain genes for transcription factors, methyltransferases, glucosyltransferases, and proteins involved in light signalling, which seem not to be associated to anthocyanin metabolism.

These genes represent a valuable resource in grapevine molecular-based breeding to select new high quality cultivars and to tailor wine properties according to consumer demand.