

Ripening secrets of the vine revealed

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Whether you prefer a Cabernet Sauvignon or a Pinot Noir grape variety, two new research articles published in the online open access journal, *BMC Genomics*, offer a host of new genetic information on fruit ripening for this economically important fruit crop.

The grapevine's gene expression analysis reveals two distinct molecular and functional phases that correspond with the green and red grape stages. And researchers have reported the first biochemical evidence that reactive oxygen species accumulate during the colour transition.

Stefania Pilati and fellow researchers from the IASMA Research Center, San Michele all'Adige, Italy, investigated ripening Pinot Noir grapes (*Vitis vinifera* L.) to identify fruit ripening genes and investigate seasonal influences. They found a core set of more than 1,400 ripening-specific genes that fluctuated similarly across three growing seasons and a smaller gene group strongly influenced by climatic conditions.

During the green berry (pre-véraison) phase, numerous genes involved in hormonal signalling and transcriptional regulation were modulated, suggesting large-scale cellular metabolism reprogramming. Auxin, ethylene and light played pivotal roles. During the following ripening (post-véraison) phase, genes for cell-wall organization and biogenesis, carbohydrate and secondary metabolisms, and stress response came into play, whereas photosynthesis was strongly repressed.

These transcriptional events tally with the processes of berry softening and accumulation of sugar, colour and aroma compounds, which

ultimately determine berry and wine quality. At véraison, the intervening point when grapes slow down their growth and change colour, this study highlighted an oxidative burst involving hydrogen peroxide (H₂O₂), and an extensive modulation of the enzymatic anti-oxidative network.

Meanwhile, Laurent G. Deluc and colleagues from the University of Nevada, Reno and the Boston University School of Medicine, USA, took a closer look at the *V. vinifera* Cabernet Sauvignon variety, surveying seven different stages of grape berry development. The team mapped pronounced differences throughout development in messenger-RNA (mRNA) expression for genes that play key functional roles in a host of processes. These included organic and amino acid metabolism, photosynthesis, circadian cycles and pathogen resistance.

In particular, the researchers recorded changes associated with transcription factor expression patterns, abscisic acid (ABA) biosynthesis, and calcium signalling genes that identified candidate factors likely to participate in véraison, or aroma compound production, and in pathway regulation and sequestration of flavonoid compounds. Some mRNAs were observed to decrease or increase specifically throughout ripening and sugar metabolism gene expression pattern analysis revealed an alternative and previously uncharacterised pathway for glucose and triose phosphate production invoked from véraison to mature berries.

Despite the grapevine's importance, genetic cues underlying the biochemical and physical changes during berry and flavour development have lain undiscovered - until now. "The large number of regulatory genes we have identified represents a powerful new resource for dissecting the mechanisms of fruit ripening control in non-climacteric plants", Pilati and co-workers say. Meanwhile, the second team say they have identified "a set of previously unknown genes potentially involved in critical steps associated with fruit development that can now be

subjected to functional testing".

Source: BioMed Central

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