

# New tool to unlock genetics of grape-growing

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University of Adelaide researchers have developed a new web-based tool to help unlock the complex genetics and biological processes behind grapevine development.

Published in the journal *BMC Genomics*, the researchers describe their online database that can be used to examine how almost 30,000 genes work together in groups and networks to produce the vine and its grapes.

"The complexity of plants is easily overlooked when we're enjoying a glass of wine," says project leader Associate Professor Christopher Ford at the University's School of Agriculture, Food and Wine. "But every part of the vine and the grape, each final attribute of flavour, colour and aroma, their ability to resist pests and adapt to salinity, all of these represent the outcomes of the coordinated expression - switching on or off - of sometimes thousands of individual genes, each encoding some small component of the final product.

"If we know the identity of these genes, and the patterns in which they are turned on and off, we will be better able to understand how their expression leads to these complex outcomes."

The work, conducted by PhD student Darren Wong and post-doctoral researchers Crystal Sweetman and Damian Drew, outlines a 'guilt by association' principle where genes turned on at the same time and in the same tissues are likely to be working together.

"For example, if we know there is a gene that is responsible for making an enzyme which is critical at a particular stage of grape production, then this tool will enable us to see which other genes are switched on in the grape at the same time," says Associate Professor Ford.

"By clustering genes based on patterns of this 'co-expression' it's possible to identify not just the genes we expected to be involved but others whose roles in a particular function we didn't suspect.

"In this way we can build up networks of identified [genes](#) that we can say are working together under certain conditions, and see which ones may be important, for instance, in helping the plant cope with drought or salinity."

The database (called VTCdb), is freely available as a resource for researchers and grapevine breeders.

"It will provide researchers and breeders with a comprehensive tool to help them make important decisions in their prioritisation of gene candidates for ongoing study of the biological processes related to all aspects of vine and grape development, metabolism and stress responses," says Associate Professor Ford.

"Ultimately, it will benefit the industry by helping produce new traits in

grapevines for improved flavour and quality and climate and environmental adaptation."

Provided by University of Adelaide

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