Flavour

COMMENTARY Open Access

Systems biology of vintage and terroir: adding some flavor to the wine grape transcriptome

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Abstract

High-throughput genomic tools provide an unprecedented opportunity to study the impact of environmental variables on complex phenotypes at the genome scale. We welcome the establishment of an experimental framework that uses omics approaches to determine the effect of the climate and viticultural practices on the grape berry physiology. However, in this commentary, we argue that genomics and genetics studies of wine grapes need to be integrated with descriptive sensory analysis of their resulting wines.

Commentary

Del Santo et al. [1] have published a study in Genome Biology, which provides a first serious attempt to establish a rigorous and quantitative experimental approach to answer important questions on the relationship between environmental factors, agronomical practices, and grape berry metabolism. The same approaches can and should be applied to multiple varieties with one of the pertinent questions being 'Are the plastic and constitutive genes conserved across varieties?' Additionally it is important to keep in mind that wine is a very complex matrix and it is entirely possible that relatively large effect in the berries translate to negligibly small effects in the resultant wine and in some cases, even if larger effects are found, consumers (the ultimate reason for producing the wine) may not notice these effects. Therefore it would be fascinating to start looking at well establish concepts of wine making, such as the vintage effect, in terms of genes and metabolites. Will we be able to predict a good, an excellent, or a bad year by measuring the activities of specific genes during berry development? A deeper understanding of the grapevine transcriptional and metabolic plasticityin relation to environmental, geographical or agronomical variables will require not only more data (more genotypes, more environments, more years), experimental designs controlling for specific effects and co-variables, and genetic perturbations, but also that we extend and integrate genomics level data with quantitative sensory profiles of the wines produced from the very same berries used for the genomics studies.

Many of the flavors associated with wine are grape-derived, such as 2-methoxy-3-isobutyl pyrazine which adds a green pepper flavor to especially Cabernet sauvignon and Sauvignon blanc wines [2], while others are glycosidically bound in the grape berry but are released during the fermentation process, for example 3-mercaptohexyl-acetate which adds a passion fruit-like odorto Sauvignon blanc wines [3]. Other flavor compounds such as esters are produced by the yeast during fermentation [4] and some are produced by the malolactic bacteria after fermentation (an example would be the buttery flavor of diacetyl [4]). Additionally, aging in oak barrels adds yet more flavor compounds such as vanillin and eugenol [5]. The resultant complex flavor matrix can be evaluated quantitatively through sensory descriptive analysis (DA). In DA a group of about 12 panelists are trained to describe differences among wines using consensus derived attributes that are anchored by specific reference standards [6]. The wines are evaluated by each panelist in triplicate and the data are analyzed using multivariate techniques that are very similar to those used by systems biologists [7]. The quantitative nature of sensory DA data would make it relatively simple to integrate the sensory data with transcriptomic and metabolomic data [8]. Santos et al. (2013, [1]) found that the warmer year (2007) resulted in very specific gene regulation changes that were also relatable to the metabolomic profiles of the 2007 grape berries. Sadras et al. (2013 [9]) in a replicated artificially heated vineyard

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study found that elevated grapevine temperatures led to changes in phenolic content. Similarly, Heymann et al. (2013 [10]) found that a warmer year (interestingly also 2007 but in California) led to very different sensory profiles for the resultant wines than wines made in 2006 and 2008.

It would be fascinating to extend the grape berry phenotype to the "real" wine grape phenotype, the wine. Ideally, one would need to do a fully replicated vineyard experiment to determine the variability in the transcriptome and the grape berry metabolomics within a vineyard and across vineyards with differing climate and viticultural practices. The berries should be harvested at the same maturity levels and then fermented into wine using highly controlled replicate fermentations at moderate scale to determine fermentation variability. The resultant wines should then be chemically analyzed for volatile and non-volatile compounds as well as sensorially using a well trained descriptive analysis panel. If any large changes are found due to vineyard effects then a consumer panel should evaluate the wines hedonically.

The work by Del Santo et al. provides an effective experimental frameworkthat should be extended in future works to the chemical and sensory evaluations of wines. Wine grapes used for the genomics analysis can be fermented into wine under controlled conditions and the chemical and sensory changes in the wines can be then integrated with transcriptomic and metabolomicprofilesto determine the impact of environmental and agronomical factors on the ultimate wine grape phenotypes, the wines.

Abbreviations
DA: Descriptive analysis.

Competing interests
The authors declare that they have no competing interests.

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