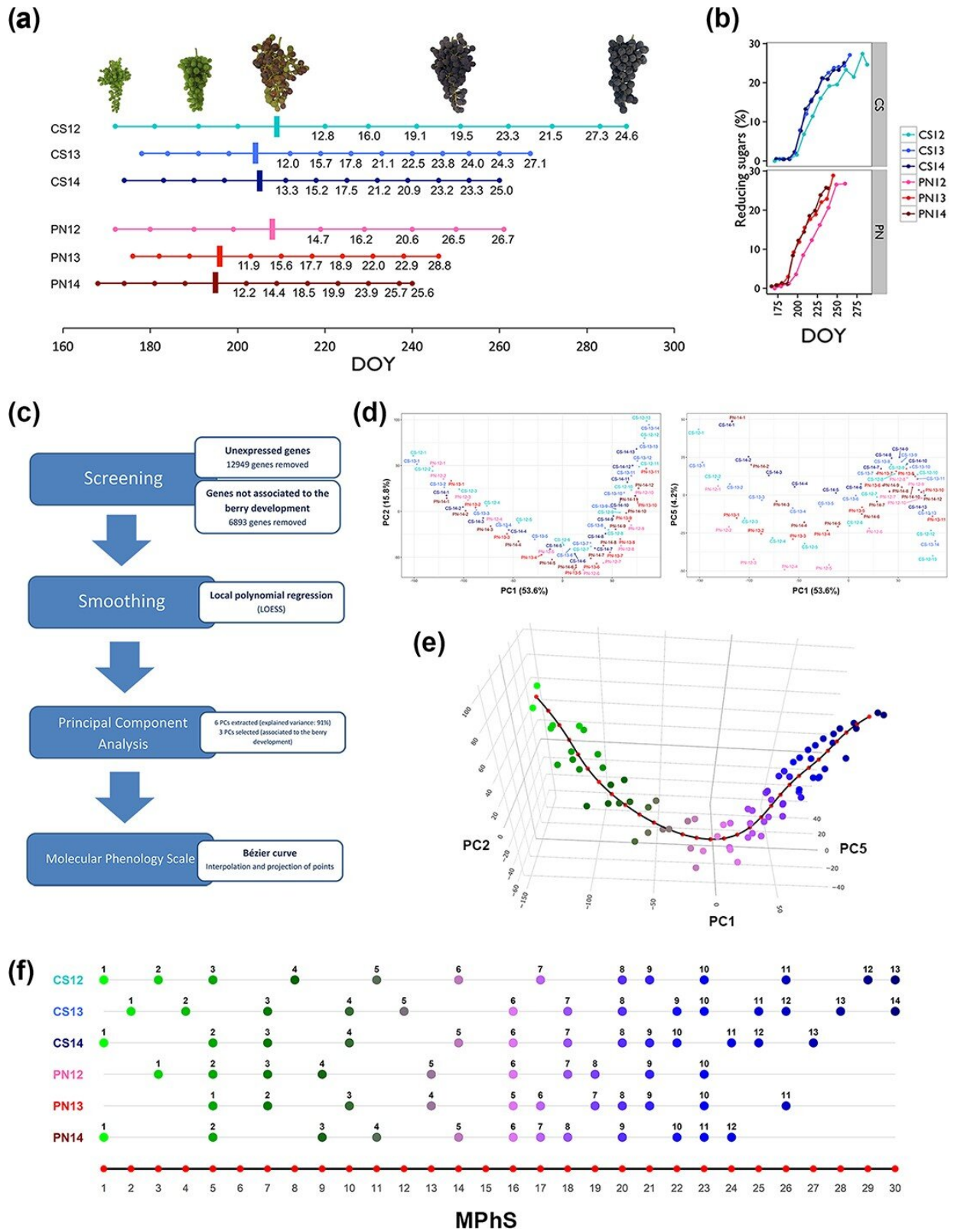# Deciphering grape development: A molecular phenology scale for grapevine berry maturation

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Molecular phenology map creation. Credit: Horticulture Research

Fruit development encompasses a series of physical, biochemical, and physiological shifts influenced by both genetic programming and environmental factors. The growth patterns of fruits like grapes are generally consistent within the same species, but can vary due to genetics and environmental conditions.

Grape growth is typically tracked using phenological scales, such as the Eichhorn and Lorenz (E-L) and BBCH systems, that categorize various developmental stages from setting to maturity based on observable traits or measurable parameters. Despite these scales, determining exact developmental stages can be tough due to influences like climate and genotype.

Recent advancements in next-generation sequencing offer possibilities to enhance these classification systems using gene expression data. The existing challenge lies in successfully integrating this molecular information into current classification systems.

In March 2023, *Horticulture Research* published a research paper titled "A molecular phenology scale of grape berry development ."

To understand the molecular development of grapevine berries, researchers utilized an RNA-sequencing dataset of 219 samples from Fasoli and the research team. These samples spanned the complete development cycle of Cabernet Sauvignon (CS) and Pinot noir (PN) grapevine berries, collected at intervals of 7–10 days over three years.

Analysis revealed that the onset of ripening, influenced by annual variations, occurred earlier in 2013 and 2014 compared to 2012. This was especially pronounced in the PN variety, which generally ripens sooner than CS. By implementing statistical and data mining techniques,

the dataset was refined from its initial 29,971 genes to a core set of 10,129 genes that consistently demonstrated gene expression during berry development.

This core set was evaluated against other datasets for validation. From this, researchers constructed a Molecular Phenology Scale (MPhS) by employing Principal Component Analysis on the standardized, smoothed gene expression data. This scale presented a three-dimensional scatter of points, where each point correlated to a specific experimental condition. These points were then mapped onto a Bézier curve, with 30 marks evenly distributed.

When samples from the three-year CS and PN series were projected onto the MPhS, the majority aligned chronologically, validating the core gene set's effectiveness in tracking berry development.

Researchers further explored the functions of genes associated with the 20-to-30 MPhS stage progression to delve deeper into the underlying biology of the late MPhS ripening stages. Several transcription factors and genes involved in DNA/RNA metabolism and transport were found in the top 20 positively correlated genes, while genes responsive to hormone stimulation, signal transduction, and transcription factors were found in the top 20 negatively correlated genes.

When evaluating the relationship between MPhS and time, researchers discovered that transcriptome progression in 2012 was slower than in other years for both grape varieties.

Furthermore, an analysis of the relationship between temperature and phenology suggested that fruit development's intrinsic variations were not directly influenced by seasonal temperature changes. The effectiveness of the MPhS was further validated by projecting other grapevine berry transcriptomes onto it. This proved the scale's ability to

recalibrate studies that were previously organized based on time, offering a more accurate representation of berry phenological stages.

To enhance the MPhS's usability, the study concluded by identifying a reduced core set of genes that could efficiently map berry transcriptomic samples onto the MPhS.

This approach holds potential for future applications in aligning time-series fruit samples, offering a refined system to study fruit maturation, and addressing challenges like climate change's impact on grape development.

More information: Giovanni Battista Tornielli et al, A molecular phenology scale of grape berry development, *Horticulture Research* (2023). DOI: 10.1093/hr/uhad048

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