Exploring clonal variation in 'Riesling'

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Abstract

Clonal selection has a long history in grapevine breeding and was initially started as a means to improve reduced yields due to virus infections. The concept of single vine selection, introduced by Froelich in 1886, and its huge success laid the foundation for clonal selection activities in many public and commercial programs. It has been shown for several traditional varieties that substantial trait variation exists. For example, there is a broad range of different shoot growth types, cluster architectures, Botrytis tolerances, titratable acidity, anthocyanins, tannins and flavour between clones of several varieties. The variability between commercially available clones of most varieties gives growers an opportunity to individually select most optimal planting material.

Increasingly variable environmental conditions as a consequence of climate change make it difficult to determine which trait configuration(s) to prioritise in breeding. In fact, climate change and changing markets necessitate the systematic conservation and characterisation of clonal variation within traditional varieties as a basis sustainable and competitive viticulture in the future.

Therefore, the Department of Grapevine Breeding at Geisenheim University has established a large collection of almost 1,200 clones of the variety Riesling over the last decades. Clones were selected from single vines grown in old vineyards in Germany and neighbouring countries and planted at the Department trial site with three vines per clone. Over more than ten years, key traits including yield, soluble solids, acid composition and concentration have been measured to assess the level of clonal variation and identify clones with interesting characteristics.

Mixed model-based variance decomposition reveals substantial between-clone variation for important traits. While it is established that mutations and epigenetics are the most likely underlying drivers the relative importance of genetic vs. epigenetic variation in Riesling remains unclear. To shed light on this and uncover (epi-)genomic factors underyling clonal variation in Riesling we are applying new genomics and epigenetics approaches. This will help to improve our understanding of the genetic architecture of important traits.

Keywords: Clonal selection, Riesling, clonal variation, mutations, epigenetics