Berry color mutants of traditional grapevine cultivars

Franco Röckel[1], Ludger Hausmann[1], Erika Maul[1], Reinhard Töpfer[1]
[1] Julius Kühn-Institut, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen
Email of corresponding author: franco.roeckel@jki.bund.de

The color of the berries is one of the most important fruit traits in grape and can vary from green/yellow to blue/black. Responsible for the coloration is mainly the anthocyanin composition and concentration in the berry skin, whereas the berry flesh mostly remains colorless. It has been shown that anthocyanin biosynthesis is controlled by two adjacent MYB-related transcription factor genes, *VvmybA1* and *VvmybA2*, located on chromosome 2. Loss-of-function mutations in both genes, an insertion of a Ty3-gypsy-type retrotransposon (*Gret1*) in the promoter region of *VvmybA1* and two amino acid-changing mutations in the coding sequence of *VvmybA2*, were identified leading in combination to a non-functional allele. Independent genetic studies revealed that white-skinned cultivars are homozygous for the non-functional allele, whereas colored-skinned cultivars possess at least one functional allele.

Because berry color mutations are a relatively frequent event, a lot of different color mutants have been selected since the rise of viticulture. Color recoveries, from white to red berries, are the most observed mutations, all of which may have a different molecular reason. Large scale parentage analysis identified the white-skinned cultivar 'Heunisch Weiss', with at least 120 offsprings in the European wine growing countries, as the most prolific grape since its rise in the first millennium A.D. in Western Europe. For example, it could be confirmed that 'Heunisch Weiss' is a parent of the famous cultivars 'Riesling', 'Chardonnay', 'Elbling', 'Gamay' and 'Blaufränkisch'.

This study focuses on the analysis of the molecular basis of color recovery in the bud sports 'Heunisch Dreifarbig', 'Heunisch Rotgestreift', 'Riesling Rot' and 'Elbling Rot' and its underlying mechanisms.