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Grapes were domesticated from wild vines for their berries that were among the sweetest fruits consumed by early human gatherers. Originally, wild dioecious vines produced small clusters and small dark-colored berries. However, cultivation has led to a large panel of hermaphrodite varieties producing large clusters and fleshy berries with a wide panel of berry colors. The grape berry color is one of the easiest traits to observe and to study. Research on berry color has identified the association of a lack of anthocyanin pigment with the insertion of *Gret1*, a retrotransposon, in the promoter region of *VvmybA1*, a gene encoding a transcription factor that induces the anthocyanin pathway (Kobayashi *et al.* 2004). Surprisingly, molecular biology revealed that most of the modern varieties are linked by parent-offspring and sibling relationships (Myles *et al.* 2011). At the berry color locus, Kobayashi *et al.* (2004) showed that all colored varieties were heterozygous, associating a white allele mutated by the *Gret1* insertion and a functional colored allele. Conversely, all white varieties were found to be homozygous for the white allele.

The study of a large panel of Pinot clones with blue-black (Pinot noir), grey (Pinot gris) or green-yellow (Pinot blanc) berries gives us the opportunity to identify novel somatic mutations resulting in the conversion of the 'colored' allele into a 'white' allele. For several clones, color mutations do not affect the whole plant; rather, they affect only one cell layer, leading to clones that are periclinal chimeras. Occasionally, cellular rearrangements in the chimera led to homogenization of the genotype of the whole plant and to new berry color types. The berry color of the clones can be considered as a model to investigate molecular and cellular mechanisms leading to the drift of grapevine genotypes and to the genome evolution through vegetative propagation (Pelsy 2010).

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