

## ‘Riesling Rot’ and other grapevine berry color mutants from the German-speaking area

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The first mention of ‘Riesling’ goes back to a bill of the Earls of Katzenelnbogen in Rüsselsheim from the year 1435. However, a unified spelling of the name ‘Riesling’ did not exist at that time. The variety was mentioned in the course of the 15th century as among others with the name Rueßelinge, Ruesseling, Rüzlinge or Ruszling. The origin of the name is to this day highly controversial. According to the latest findings by the researcher Prof. Dr. Jürgen Udolph, the name derives from the so called ‘Rußflecken’ (soot stains, lenticels), which become visible at a later ripening stage. As an offspring of ‘Heunisch Weiss’ and a presumed seedling of ‘Traminer’ and *Vitis sylvestris*, it can be assumed that ‘Riesling Weiss’ originated in the Rhine Valley between Karlsruhe and Worms. With an acreage of 23.440 hectares (22.9% of the total German winegrowing area) in the year 2014, ‘Riesling Weiss’ is the most widely planted grapevine variety in Germany.

About the origin of the colored variation ‘Riesling Rot’ it is not much known. However, it can be suggested that the cultivar was already present in the mixed plantings of the late Middle Ages with a low acreage. After the phylloxera crisis, the variety disappeared nearly completely, but survived in collections and was interspersed in a few old vineyards. After the process of clonal selec-

tion starting in 1991, ‘Riesling Rot’ is classified for the wine growing region Hessen since 2002. Compared to other color mutants, the variety shows a relatively high back mutation rate to white and due to its world famous relative ‘Riesling Weiss’, the public interest on the color origin of this cultivar is very high.

The anthocyanin biosynthesis in blue/black varieties is controlled by two adjacent MYB-related transcription factor genes, *VvmybA1* and *VvmybA2*, whereas two 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 white allele. Due to recombination events of the white allele, red-skinned cultivars like ‘Riesling Rot’ should possess at least one functional *myb*-gene variant leading to a weaker anthocyanin formation compared to typical red wine cultivars with blue/black berries.

This work focuses on the molecular analysis of the color recovery in ‘Riesling Rot’ and other color mutants of famous varieties from the German-speaking area like ‘Silvaner Blau’ or ‘Elbling Rot’.