Characterization of the *Rpv12* locus in a haplotype-separated grapevine genome sequence

Müllner, Sophia¹ (Co); Frommer, Bianca² (Co); Holtgräwe, Daniela²; Viehöver, Prisca²; Hüttel, Bruno³; Töpfer, Reinhard¹, Weisshaar, Bernd²; Zyprian, Eva^{1*}

¹Julius Kühn-Institute, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany ²Bielefeld University, Chair of Genetics and Genomics of Plants, Faculty of Biology & Center for Biotechnology (CeBiTec), Bielefeld, Germany

³Max Planck-Genome-Centre Cologne, Max Planck Institute for Plant Breeding Research, Cologne, Germany

Abstract

Grapevine downy mildew, caused by Plasmopara viticola, imposes a major challenge on viticulture since the 19th century. Attempts to counteract the disease by crossing the noble European Vitis vinifera with resistant American Vitis wild species in the early 20th century remained discouraging due to transmission of undesirable characteristics. The recent development of genetic marker analyses allowed to identify resistance mediating genomic regions from extra-European Vitis species and to follow them in cascaded back crosses to V. vinifera. More than 31 genetic loci are currently known to contribute to resistance to P. viticola. One of these is Rpv12 (resistance to P. viticola 12), initially identified in the Asian species V. amurensis. This locus was identified in 2013 (Venuti et al.) and it was compared to the American locus Rpv3 in transcriptomic and metabolomic studies (Chitarrini et al., 2020). However, these investigations were not yet able to identify candidate resistance genes. Thus, to delimit the locus and to reveal its possible resistance genes, the Rpv12 carrying genotype Gf.99-03 (Geilweilerhof 2014-099-0003, VIVC: 27131) was sequenced in combination with its parental genotypes 65-153-18 (VIVC: 41129) and Gf.43-21 (Geilweilerhof 2904-043-0021, VIVC: 27130). Long read data were computed into a high quality haplotype separated genome assembly of Gf.99-03. Gene annotation of the newly assembled genome sequence was supported by RNA-Seq analyses from various tissues such as leaves, stems, tendrils and roots. Also, comprehensive differential gene expression analysis of experimentally inoculated leaf discs at different time points after inoculation with P. viticola was performed. Approximately 600 differentially expressed genes were identified.

The *Rpv12* locus is delimited by the simple sequence repeat (SSR)-markers UDV-014 and UDV-370. Differentially expressed genes in the resistance carrying haplotype of Gf.99-03 were identified and checked for uniqueness. In addition, the locus was searched for typical resistance gene analogs like *NLRs* (nucleotide binding site leucine rich repeats). A cluster of putative resistance mediating genes including *CNLs* was identified in this region.

Keywords: downy mildew, fully-phased genome assembly, infection experiment, leaf disc assay, *Plasmopara viticola*, resistance, *Rpv12*, TrioBinning, *Vitis spec*.

^{*}eva.zyprian@julius-kuehn.de