SEMINAR

Generation of haplotype separated grapevine genome sequences to support analyses of pathogen resistance loci

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European grapevine (*Vitis vinifera*) is highly susceptible to various pests and pathogens. Current grapevine breeding aims at developing new cultivars with increased resilience to pathogens to reduce the mandatory applications of protective chemicals. The source of genetic disease resistances or tolerances are wild grapevines from America and/or Asia. Genetic mapping and quantitative trait analyses allow the localisation of resistance loci in the genome. However, the detailed genetic structure and the gene composition of such loci can only be resolved at the DNA sequence level. I will report about the generation of high-quality, haplotype separated genome sequence assemblies of two genotypes. These genotypes are the interspecific grapevine rootstock cultivar 'Börner' (*V. riparia* GM183 x *V. cinerea Arnold*), and the grapevine breeding line Gf.99-03 (*V. vinifera* with an introgression from *V. amurensis*). Using trio binning, truly phased haplotype assemblies of both grapevine genotypes were generated. One resistance locus will be presented in detail.

05 September 2023
h. 14:00 - 15:00

ROOM 6302
PRC BUILDING - FEM
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(1) Phased grapevine genome sequence assembly of an Rpv12 carrier for exploration of Rpv12 associated positional and functional Plasmopara viticola resistance genes
Frommer B, Muellner S, Holtgräwe D, Viehöver P, Huettel B, Toepfer R, Weisshaar B, Zyprian EM (2023)
Frontiers in Plant Science 14:1180982 https://doi.org/10.3389/fpls.2023.1180982

(2) A fully phased interspecific grapevine rootstock genome sequence representing *V. riparia* and *V. cinerea* and allele-aware annotation of the phylloxera resistance locus *Rdv1*
Frommer B, Hausmann L, Holtgräwe D, Viehöver P, Hüttel B, Reinhard R, Töpfer R, Weisshaar B
Preprint at bioRxiv https://doi.org/10.1101/2022.07.07.499180