



ICGBG

XII International Conference on
GRAPEVINE BREEDING and GENETICS

July 15-20, 2018
Bordeaux FRANCE

ABSTRACT BOOK
GBG 2018 – Bordeaux, France
15 – 20 July



A *Vitis* hybrid 'library': comparing diverse R-loci combinations and mildew resistance levels in field

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Nowadays, it is almost universally recognized that the viticulture of the future will require the management of grapevine pests and diseases with fewer chemical inputs. The development and the deployment of novel varieties - which are now extremely resistant to mildews as well as hold the potential to display a durable resistance during the coming years - are considered one of the most promising strategy towards an eco-friendly viticulture.

In the frame of the Euregio project VITISANA, a collection of approximately 100 grapevine accessions - including (mid-)resistant genotypes derived from cross pollination between *Vitis* hybrid and vinifera varieties or backcrosses - was studied. Their leaf and cluster level of downy (DM) and powdery (PM) mildew resistance was evaluated in an untreated field (Marlengo, I) at veraison and harvesting time in both 2016 and 2017. In addition to attempting a true-to-type analysis, an exhaustive genetic characterization was carried out at the 12 exploitable loci associated to mildew resistance (R-loci) available in the literature to date. Besides genotypes carrying a single R-locus associated to DM or PM resistance, our findings highlighted the pyramiding of R-loci against DM in 15% and against PM in 35% of the total accessions. In particular, 56 genotypes resulted pyramided for R-loci to both mildews. Finally, combining the R-loci-based characterization of the studied traditionally bred resistant varieties with their pathogen response in untreated field, we will understand the impact of diverse R-loci assets on overcoming disease attacks under the same environmental conditions.

Keywords: downy mildew, powdery mildew, natural infection, pyramiding, resistance-associated markers