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IDENTIFICATION OF BREEDING SIGNATURES IN GRAPEVINE HYBRIDS, DONORS OF RESISTANCE TO DOWNY AND POWDERY MILDEW

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Grapevine (*Vitis vinifera* L.) is one of the most valuable crops in the world. The most studied and interesting traits are strictly related to quality and disease resistance. Viticulture has often been plagued by encounters with new parasites that still represent a major constraint. This is a particularly important issue because, even though some inter-specific varieties (hybrids) between *V. vinifera* and *Vitis* spp. are widely present, the majority of cultivated grapevines are pure *V. vinifera* varieties, which are highly susceptible to pathogen attack. Fungal diseases, such as downy (DM) and powdery (PM) mildew, represent some of the most severe plagues and growers are obliged to use pesticides to prevent serious yield loss. Fungicides represent in fact the majority of plant protection products employed and viticulture one of the most intensively cultivated crops in terms of chemical usage. As a consequence, the research applied to breeding for resistance and the deployment of new resistant grapevine varieties are strongly encouraged as a step towards sustainable agriculture. Nowadays, grapevine genetics and genomics information, together with the associated technologies, are rapidly developing, leading to numerous discoveries with potential application such as the genome sequencing. Despite these advances, traditional breeding approaches are still dominant, while Marker-Assisted Breeding (MAB) implementation has been minimal both at the national and international level.

In this study we focus on the genetic characterization of numerous *Vitis* hybrids, donors of resistance to DM and/or PM, in order to identify selection signatures. In particular, 86 hybrids of European origin and of 100 American hybrids, along with 30 related *V. vinifera* varieties, have been genotyped at 70 SSR loci. These markers have been chosen based on their physical distance in order to have 10 SSRs well-scattered along each of the 7 chromosomes that carry Resistance Gene Analog (RGA) clusters according to the literature. Based on the SSR profiles, the historical pedigree information has been checked and, following the true-to-typeness validation for most of the studied hybrids, the Identity By Descent (IBD) analysis has been performed, tracing the allelic flow through the successive generations.

Here we report preliminary results about the identification of *non-vinifera* genomic intervals retained into the *vinifera* background and the anchoring of the discovered breeding signatures to the grapevine genome. Subsequently, the genotyping analysis will be extended to the other 12 chromosomes (120 SSRs) and possibly to new crucial genotypes. The final result of this study will be the release of molecular markers valuable for grapevine MAB, upon their validation in *ad hoc* segregating populations.