

A GRAPEVINE GENETIC LINKAGE MAP TO FIND OUT QUANTITATIVE TRAIT LOCI RESPONSIBLE FOR LOWER SUSCEPTIBILITY TO FLAVESCENCE DORÉE

CASARIN S.* , TARANTO F.** , D'AGOSTINO N.*** , MIGLIARO D.* , MONTEMURRO C.**** , PANZERI M.* , GUADAGNINO S.* , FILIPPIN L.* , FORTE V.* , BERTAZZON N.* , ANGELINI E.* , CRESPIAN M.*

*) Research Centre for Viticulture and Enology, CREA (Italy)

**) Institute of Biosciences and Bioresources, CNR (Italy)

***) Department of Agricultural Sciences, University of Naples Federico II (Italy)

****) Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro; Institute for Sustainable Plant Protection–Support Unit Bari, CNR (Italy)

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Flavescence dorée (FD) is one of the most destructive grapevine yellows (GY) diseases, and a quarantine pest in Europe. It is caused by phytoplasmas, which are transmitted among plants by the leafhopper *Scaphoideus titanus* Ball. Although grapevine varieties completely resistant to FD have not been uncovered yet, some inter- and intra-specific differences in susceptibility have already been observed as poor presence of infected vines in vineyard, no severe symptoms and recovery ability of plants. The different behavior among grapevine varieties suggests the presence of putative several loci, not yet disclosed, associated with high or low susceptibility to FD. In this context, the development of a genetic map is the first crucial step to dissect the genetic basis that regulate FD incidence. The aim of our study is to build a high-density genetic linkage map using F1 progeny from a cross 'Chardonnay x Tocai friulano', characterized by high and low susceptibility to FD, respectively. Two hundred and thirty F1 individuals were first checked with ten SSR (Simple Sequence Repeats) markers to exclude self-fertilized individuals. A total of 184 individuals and their parents were then subjected to Genotyping by Sequencing (GBS). A panel of 122,049 Single Nucleotide Polymorphisms (SNPs) generated by GBS was filtered and used to construct a genetic linkage map using the JoinMap 4 software. The genetic map resulted in 2,923 markers, distributed among 19 linkage groups and covering 1336.05 cM, with an average distance of 2 cM between two markers. At the same time, the F1 population is undergoing phenotyping. The information derived from the genetic map will be combined with phenotypic data points to identify QTLs involved in high or low FD susceptibility.