



GENETIC LINKAGE MAPPING APPLIED TO THE GENERATION OF TOOLS FOR BREEDING PURPOSES AND GENETIC DISSECTION OF GRAPEVINE AGRONOMICAL TRAITS AT EMBRAPA UVA E VINHO

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A genetic linkage map of grapevine was constructed using a pseudo-test cross strategy based on a cross between ‘Crimson Seedless’ and the complex hybrid ‘Villard Blanc’, resistant to powdery and downy mildew. For both parents, 19 linkage groups were obtained, covering 1111 cM and 926 cM for ‘Villard Blanc’ and ‘Crimson Seedless’ respectively. The position of SSR loci in the obtained maps was consistent with the genomic sequence. Quantitative traits loci (QTLs) for seedlessness and resistance to powdery and downy mildew were investigated. While two major effect QTLs for downy mildew resistance and seedlessness were mapped on the same region of the linkage group (LG) 18, one main QTL for powdery mildew resistance was identified in LG 15. These QTLs explain 25-55,7% and 54-62,4% of total variance, respectively for downy mildew resistance and seedlessness and 12,7-34% to powdery mildew resistance. The MADS box gene *VvAG3*, located in seedlessness QTL detected on LG 18, was identified as a candidate gene to control seed development in grape. *VvAG3* gene expression characterization revealed strong evidence suggesting its involvement in grapevine seed morphogenesis. Co-localization were also found in the same region, between the position of the *Rpv3* (*Resistance to Plasmopara viticola 3*) locus, which is very rich in TIR-NBS-LRR resistant gene analogs (RGAs) and the main QTL identified for downy mildew resistance. By exploring genomic analysis tools, we selected a collection of RGAs for molecular characterization under downy mildew infection conditions. Our results confirmed that the same region of LG 18 contains important genetic determinants for seedlessness and downy mildew resistance in grapevine and provided basis for the development of SSR haplotypes to assist the selection of seedlessness and downy mildew simultaneously in a marker-assisted breeding approach.

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