Mapping the Dagger Nematode, *Xiphinema index,* Resistance Gene

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Vitis vinifera is susceptible to a wide range of pests and diseases including grapevine fanleaf virus (GFLV) and its dagger nematode vector, *Xiphinema index*. This virus/nematode complex causes fanleaf degeneration, which is considered to be one of the most severe viral diseases of grape. The virus spreads through propagation with virus-infected stock and by the feeding of *X. index*, which moves GFLV by feeding on root tips. Chemical control of *X. index* in the vineyards has been inefficient and no longer been recommended because of the high cost, its ineffectiveness and the nematicides' detrimental effects on the environment (Raski and Goheen 1988). Therefore, resistance to *X. index* has been an important objective in grape rootstock breeding programs. We have previously demonstrated that resistance to *X. index* derived from *V. arizonica* is controlled by a major QTL, *XiR1*, on chromosome 19 (Xu et al. 2008). Genetic studies that lead to the isolation and characterization of genes conferring resistance to *X. index* are expected to have immediate impact on our understanding of the resistance mechanisms and help control the viral vector *X. index*. In this report, we are presenting the development of high resolution genetic and physical maps in the *XiR1* region.

Materials and Methods

Three mapping populations of 1,375 F_1 genotypes were used to construct the high-resolution genetic map of the *XiR1* QTL region. The first was the 9621 population derived from D8909-15 × F8909-17, in which the *XiR1* QTL was initially identified. We have expanded the 9621 population to 943 F_1 individuals. The second was population AT0023 consisting of 178 F_1 individuals from a cross D8909-15 × *V. vinifera* B90-116. The third was population 05384 consisting of 253 F_1 individuals obtained from a cross D8909-15 × *V. vinifera* Airen. The common female parent D8909-15 is the source of resistant to *X. index*, whereas all three male parents F8909-17, *V. vinifera* B90-116 and *V. vinifera* Airen are susceptible. D8909-15 was a selection derived from a cross *V. rupestris* A. de Serres × *V. arizonica* b42-26. The maternal grandparent *V. rupestris* A. de Serres is also susceptible to *X. index* while the paternal grandparent *V. arizonica* b42-26 is highly resistant to *X. index*.

Results and Discussion

The *XiR1* major QTL was previously mapped near marker VMC5a10 on chromosome 19, and the putative region of *XiR1* was located within a 5.6 cM interval between two markers VNG3a10 and M4F3F (Xu et al. 2008). To physically locate *XiR1*, VMC5a10 – the co-segregating simple sequence repeat (SSR) marker, was used to screen two bacterial artificial chromosome (BAC) libraries: one constructed from a resistant source D8909-15 and the other from the susceptible cultivar Cabernet Sauvignon (developed by E&J Gallo Co.). A total of 21 BAC clones were identified and 9 markers tightly linked to *XiR1* were developed from the BAC ends (Figure 1A). To fine-scale map the *XiR1* region, the two flanking markers VMC3a10 and M4F3F were used to identify informative recombinant genotypes from the three mapping populations 9621, AT0023 and 05384. Genotypic data showed that the two markers segregated normally with an expected 1:1 ratio (χ^2=1.34, P=0.10-0.25 for VMC3a10, and χ^2=0.16, P=0.50-0.75 for M4F3F) in the three combined populations. Of 1,375 individuals analyzed, 99 were identified as recombinants within the interval. The 99 recombinants were further evaluated for *X. index* resistance and revealed 61 resistant and 38 susceptible. When the location of the newly developed markers and nematode assay results were combined, 10 key recombinants were identified in the *XiR1* region. The *XiR1* locus was delimited in an interval of 0.51 cM (7 recombinants) between the two closest flanking markers 1N2R3b and M4F3R (Figure 1B). In addition, sequence analysis of a BAC clone from the resistant source is in progress and will be presented.

References

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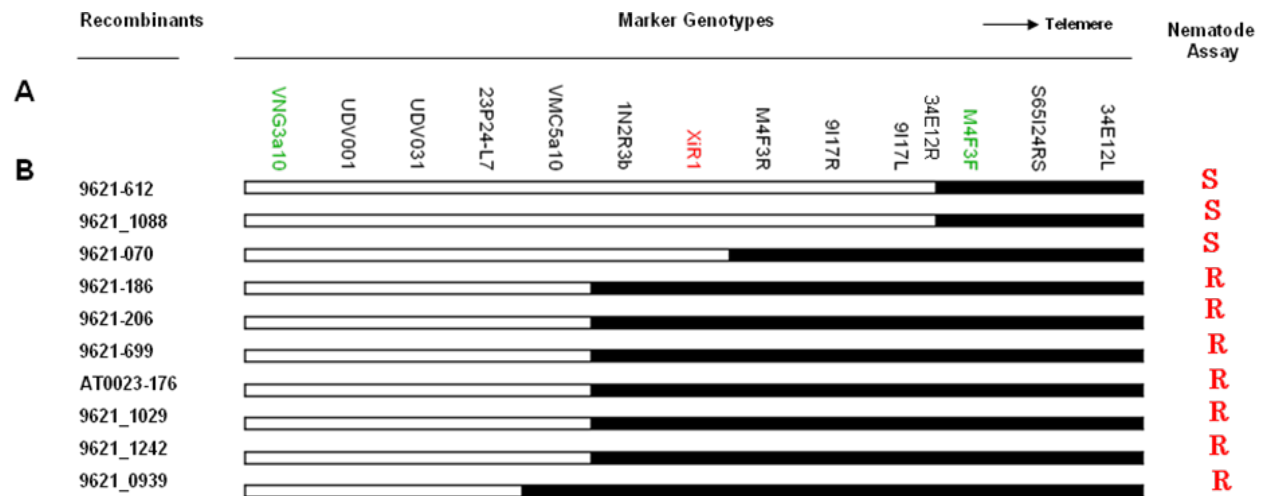
Figure 1: Physical maps of the *XiR1* region and Schematic representation of genotypes for 10 key recombinant plants.

(A). High-resolution genetic map of *XiR1* locus on chromosome 19. (B). The solid bars stand for the D8909-15 chromosomal segments originated from *V. arizonica* b42-26 resistant to *X. index* ("R" genome origin) and the open bars are for those from *V. rupestris* A. de Serres ("S" genome origin). The crossover break-points were shown by the junctions between the solid and open bars.



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