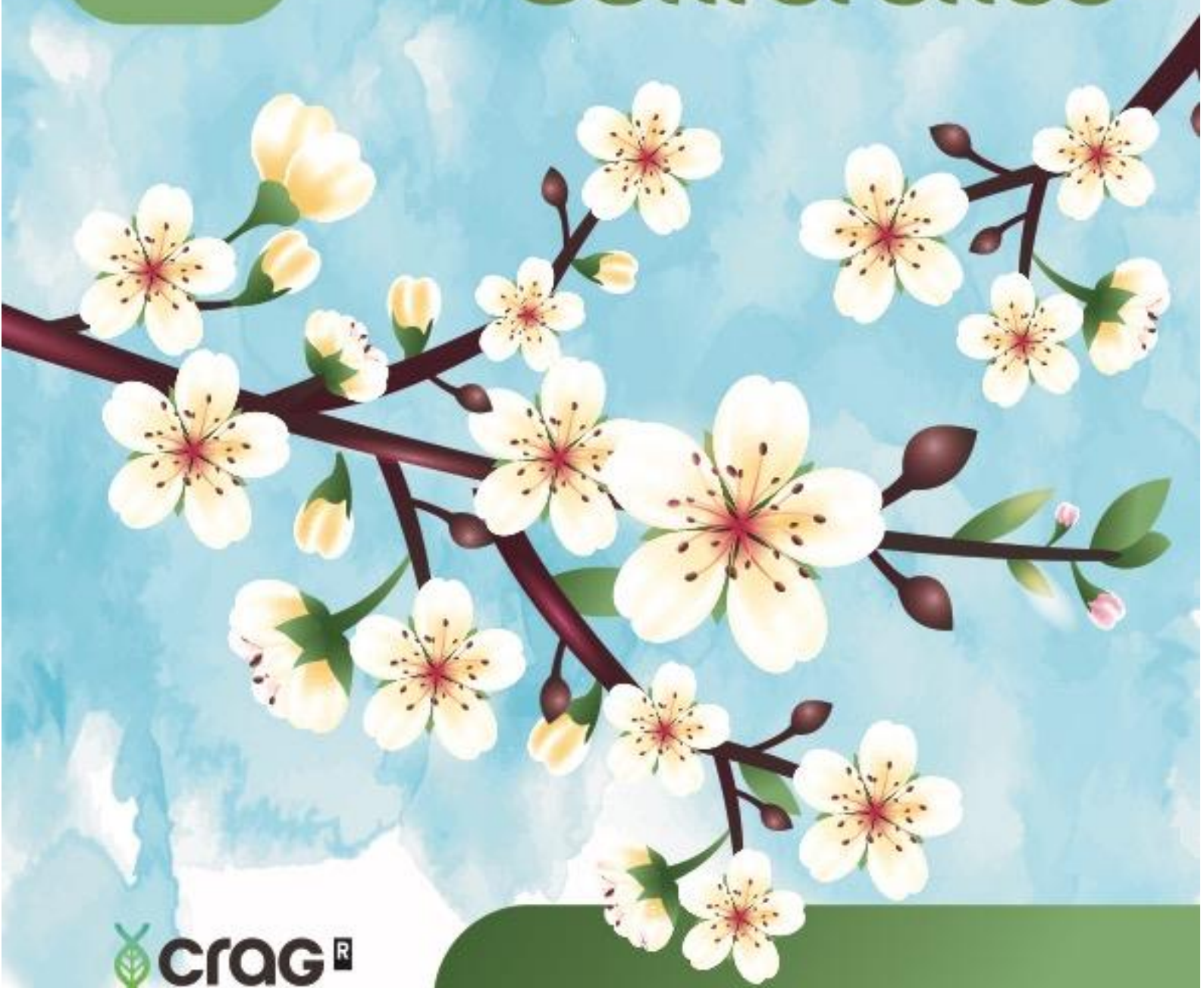


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VALIDATION OF SNP MOLECULAR MARKERS LINKED TO THE MAJOR ROSY APPLE APHID RESISTANCE GENE DP-FL ON A LARGE DIVERSITY PANEL

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Abstract

Apple is one of the most important fruit crops in Europe but still requires between 20 to 35 phytosanitary treatments to control pests and diseases. Among these, rosy apple aphid (*Dysaphis plantaginea*) becomes increasingly problematic and is positively impacted by global warming. To limit this pest, genetic control will be an efficient solution to complement other crop management practices. The major resistance gene *Dp-fl* was previously located on linkage group LG08 and could be a good candidate to promote genetic resistance. In this context, SNP molecular markers were developed in biparental progenies derived from the resistant cultivar 'Florina' crossed with susceptible parents but they appeared too progeny-specific. In order to integrate the *Dp-fl* resistance gene in our Marker Assisted Breeding program, broadly efficient molecular markers were needed to screen progenitors and seedlings in any new breeding populations. The present work describes the methodology used to develop three additional SNP molecular markers validated on a large diversity panel. To do so, the GDDH13 V1.1 genome associated with specific sequencing data was used to select the most accurate SNP candidates. Molecular markers were tested first on a biparental progeny, and then on ~200 individuals from the INRAE/NOVADI breeding program. Validated SNP markers allowed to better characterize the rosy apple aphid resistance in progenitors and are now routinely used for