

Exploring the genetic control of graft incompatibility in apricot (*Prunus armeniaca* L.)

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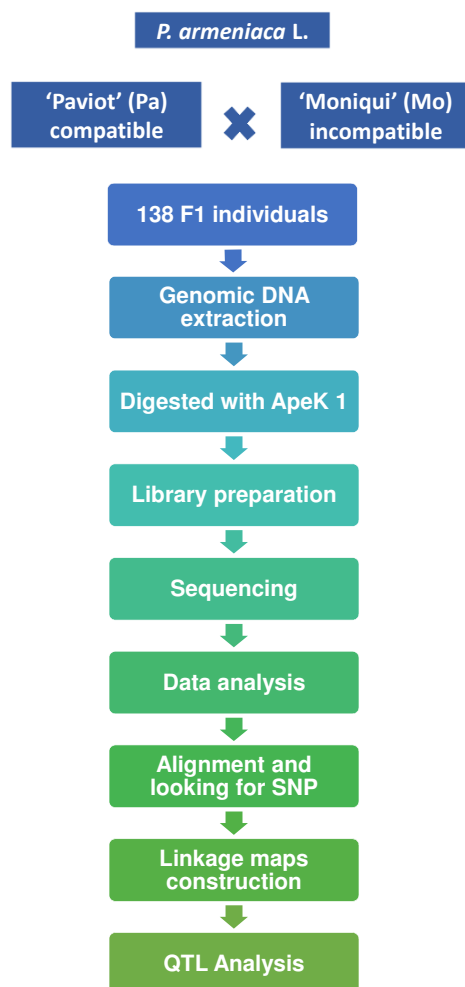


Introduction

Graft incompatibility between most popular *Prunus* rootstocks and apricot cultivars is one of the major problems for rootstock usage and improvement. Failure in producing long-leaving healthy grafts greatly affects the range of available *Prunus* rootstocks for apricot cultivation. In spite of recent advances related to the molecular mechanisms of a graft-union formation between rootstock and scion, information on genetic control of this trait in woody plants is essentially missing due to a lack of hybrid crosses, segregating for the trait. In this study, we genotyped an apricot F1 population 'Moniqui (Mo)' × 'Paviot (Pa)' segregating for ability to form successful grafts with universal *Prunus* rootstock 'Marianna 2664' and constructed high-density parental genetic maps for QTL analysis.



Material and Methods



Results and Discussion

To localize genomic regions associated with graft compatibility, we genotyped 138 individual from the 'Mo × Pa' cross by next-generation sequencing (NGS) technology and constructed medium density genetic maps for both parents. The female 'Mo' and male 'Pa' maps were composed of 557 and 501 SNPs organized in eight linkage groups and covered 780.2 and 690.4 cM of genetic distance, respectively. Parental maps were aligned to the *P. persica* v2.0 genome and revealed a high collinearity with the *Prunus* reference map. Two-year phenotypic data, anatomical patterns associated with graft incompatibility, were collected for 92 individuals from the 'Mo × Pa' cross in 2014 and 2015 (Irisarri et al., 2019) and used for detecting marker-trait associations in this study. We identified two genomic regions on LG5 (44.9 - 60.8 cM) and LG8 (33.2 - 39.2 cM) associated with graft (in)-compatibility characters such as necrotic line (NL), wood discontinuity (WD) and overall graft incompatibility (GI) scores and inherited from male parent 'Paviot'. However, we failed to detect QTL signals, i.e. marker-trait associations, for BD in both 2014 and 2015 datasets. Two QTLs, the qWD8-2014 and qNL8-2015 explaining 16.1 and 14.7% of phenotypic variance colocalized on LG8 and shared the same genetic interval with the qWD8-2015 and qGI8-2015 (Figure 1). To our best knowledge, this is the first report on quantitative trait loci (QTLs) for graft (in)-compatibility in woody plants. Results of this work will provide a valuable genomic resource for apricot breeding programs and facilitate future efforts focused on candidate genes discovery for graft (in)-compatibility in apricot and other *Prunus* species.

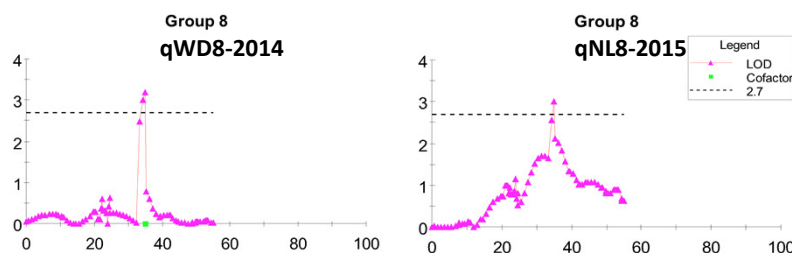


Figure 1. LOD score for quantitative trait loci (QTLs) associated with wood discontinuity (WD) in 2014 (qWD8-2014) and necrotic line (NL) in 2015, on the male 'Paviot'

REFERENCES

Irisarri P, Zhebentyayeva T, Errea P, Pina A (2019) Inheritance of self- and graft-incompatibility traits in an F1 apricot progeny. PLoS ONE 14(5): e0216371.

ACKNOWLEDGEMENTS

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