



Fruit Self-Thinning: A Trait to Consider for Genetic Improvement of Apple Tree

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Titre	Fruit Self-Thinning: A Trait to Consider for Genetic Improvement of Apple Tree
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Auteur	Celton, Jean-Marc [1], Kelner, Jean-Jacques [2], Martinez, Sébastien [3], Bechti, Abdel [4], Touhami, Amina Khelifi [5], James, Marie José [6], Durel, Charles-Eric [7], Laurens, François [8], Costes, Evelyne [9]
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Résumé en anglais	<p>In apple (<i>Malus × domestica</i> Borkh), as in many fruiting crops, fruit maintenance vs abscission is a major criteria for production profitability. Growers routinely make use of chemical thinning agents to control total fruit load. However, serious threats for the environment lead to the demand for new apple cultivars with self-thinning properties. In this project, we studied the genetic determinism of this trait using a F1 progeny derived from the cross between the hybrid INRA X3263, assumed to possess the self-thinning trait, and the cultivar 'Belrène'. Both counting and percentage variables were considered to capture the fruiting behaviour on different shoot types and over three consecutive years. Besides low to moderate but significant genetic effects, mixed models showed considerable effects of the year and the shoot type, as well as an interaction effect. Year effect resulted mainly from biennial fruiting. Eight Quantitative Trait Locus (QTL) were detected on several linkage groups (LG), either independent or specific of the year of observation or the shoot type. The QTL with highest LOD value was located on the top third of LG10. The screening of three QTL zones for candidate genes revealed a list of transcription factors and genes involved in fruit nutrition, xylem differentiation, plant responses to starvation and organ abscission that open new avenues for further molecular investigations. The detailed phenotyping performed revealed the dependency between the self-thinning trait and the fruiting status of the trees. Despite a moderate genetic control of the self-thinning trait, QTL and candidate genes were identified which will need further analyses involving other progenies and molecular investigations.</p>
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