



## Genomic basis of the differences between cider and dessert apple varieties

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Auteur	Leforestier, Diane [1], Ravon, Elisa [2], Muranty, H�el�ene [3], Cornille, Amandine [4], Lemaire, Christophe [5], Giraud, Tatiana [6], Durel, Charles-Eric [7], Branca, Antoine [8]
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Mots-cl�s	Malus domestica ;BayeScan;outlier; FST ;linkage disequilibrium;genome-wide association [9]
R�sum� en anglais	<p>Unravelling the genomic processes at play during variety diversification is of fundamental interest for understanding evolution, but also of applied interest in crop science. It can indeed provide knowledge on the genetic bases of traits for crop improvement and germplasm diversity management. Apple is one of the most important fruit crops in temperate regions, having both great economic and cultural values. Sweet dessert apples are used for direct consumption while bitter cider apples are used to produce cider. Several important traits are known to differentiate the two variety types, in particular fruit size, biennial <i>versus</i> annual fruit bearing and bitterness, caused by a higher content in polyphenols. Here, we used an Illumina 8K SNP chip on two core collections, of 48 dessert and 48 cider apples, respectively, for identifying genomic regions responsible for the differences between cider and dessert apples. The genome-wide level of genetic differentiation between cider and dessert apples was low, although 17 candidate regions showed signatures of divergent selection, displaying either outlier <math>F_{ST}</math> values or significant association with phenotypic traits (bitter <i>versus</i> sweet fruits). These candidate regions encompassed 420 genes involved in a variety of functions and metabolic pathways, including several colocalizations with QTLs for polyphenol compounds.</p>
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### Liens

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