Identification of *loci* controlling phenology, fruit quality and post-harvest quantitative parameters in Japanese plum (*Prunus salicina* Lindl.)

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Abstract

Japanese plums are popular fruits since they are exceptionally nutritious with high fiber and antioxidant content. This work has aimed to analyze the most critical phenology, fruit quality and postharvest parameters from a genomic point of view to identify molecular markers closely linked to the most significant Quantitative trait loci (QTLs). A genetic linkage map of an F1 population of 151 individuals from the cross '98–99' × 'Angeleno' was constructed using previously reported Single Nucleotide polymorphism (SNP) data and 25 additional Simple Sequence Repeat (SSR) markers. Twenty-three phenotypic traits evaluated during three harvest seasons were assayed to estimate best linear unbiased predictors by using two genomic association QTL analysis approaches: General Linear Model-based single marker-trait associations (GLM) and Multiple QTL Model analyses (MQM). In addition, loss of weight and chlorophyll degradation between days 1 and 7 as well as fruit softening for days 1, 4, and 7 were monitored during two consecutive seasons. The most significant identified QTLs were linked to fruit development period and fruit weight in Linkage Groups (LG) 4 and 2, respectively. Regarding postharvest parameters, the identified QTLs related to chlorophyll degradation and loss of weight showed lower significance than phenology or fruit quality traits. In contrast, minor QTLs for fruit firmness evolution using destructive and non-destructive methods were confirmed in LG 4 and 5.