



First genetic linkage map of chilling injury susceptibility in peach (*Prunus persica* (L.) Batsch) fruit with SSR and SNP markers

Arun Prabhu Dhanapal¹, 2*, Pedro J Martínez-García¹, Thomas M Gradziel¹ and Carlos H Crisosto¹

Plant Sciences Department, University of California Davis, One Shields Ave, Davis CA 95616, USA.

Abstract

Peach and nectarine (*Prunus persica* L.) are highly perishable; they ripen and deteriorate quickly at ambient temperature. Storage at low temperature (0–5°C) is a common strategy used to slow the ripening processes and extending shelf life. However, if susceptible varieties are held too long at a low temperature, they will not ripen properly and will develop chilling injury (CI) symptoms like mealiness, flesh browning, and flesh bleeding. Understanding the genetic control of these traits to produce CI resistant cultivars will greatly benefit producers, shippers and consumers. Mapping approach for a set of 40 candidate genes (CGs) obtained after a transcriptomic analysis of peach between high tolerant and sensitivity to CI were used, to identify CI controlling genes in Pop-DG progeny population and CI-susceptible (hermoza) and chilling injury-resistant (oded) peaches. A set of 142 CGs from detailed transcriptomic analysis of two different peach cultivars studied previously and additional 10 CGs nominated from published works and review articles of physiology and transcriptomic study of peach fruit subjected to

CI were localized in this study. In present study 12 CGs have been mapped on Pop-DG population with 8 SSR and 26 SNP markers.

Keywords: Chilling injury (CI), mapping, candidate genes (CGs), SNP and SSR

Biography: Arun Prabhu Dhanapal is a Research Scientist in the Division of Plant Sciences. His main research interests are in the area of quantitative genetics, genomics and molecular breeding. He has worked on several crop and fruit species (sugarcane, millets, wheat, soybean, peach, and kiwi). His present research is focussed on the analysis of water deficit and heat stress on soybean with emphasis on quantitative traits and using biotechnological and genomic tools. He has extensive expertise in high throughput genotyping using SSR and SNP markers; genetic diversity; population genetics; candidate gene mapping; gene identification and characterization; GWAS and QTL mapping.