

**Title** Chilling injury susceptibility in an intra-specific peach [*Prunus persica* (L.) Batsch] progeny  
**Author** C.M. Cantín, C.H. Crisosto, E.A. Ogundiwin, T. Gradziel, J. Torrents, M.A. Moreno and Y. Gogorcena  
**Citation** Postharvest Biology and Technology, Volume 58, Issue 2, November 2010, Pages 79-87  
**Keywords** Mealiness; Graininess; Browning; Bleeding; Internal breakdown; SSR; CGs; QTLs

### **Abstract**

Chilling injury (CI) is the collective term for various disorders that occur during prolonged cold storage and/or after subsequent ripening of stone fruit. Major symptoms of CI include mealiness, graininess, flesh browning, loss of flavor (off flavor), and red pigmentation (bleeding). These symptoms were evaluated over 2 years in an intra-specific progeny population derived from the cross of cultivars ‘Venus’ (freestone, melting and yellow-flesh nectarine) and ‘BigTop’ (clingstone, melting and yellow-flesh nectarine) after storage of fruit at 5 °C (CI inducing conditions) for 2 and 4 weeks. All the evaluated traits in the progeny showed continuous variation which is typical of quantitative or polygenic inheritance. Longer cold storage periods increased the incidence and severity of CI symptoms, except for bleeding and leatheriness, which were not affected by time of storage. CI symptoms showed high and significant heritability or genotype effect in the studied population, with no significant effect of harvesting year. Browning, mealiness and graininess were significantly correlated and were the main CI symptoms observed in this population. Mealiness and graininess were negatively correlated with stone adhesion which reflects the higher susceptibility to CI disorders of freestone fruit. A genetic linkage map of linkage group 4 (LG4) was constructed with SSR and candidate genes (CGs). Significant quantitative trait loci (QTLs) for mealiness, graininess, leatheriness and bleeding were found in this linkage group, validating QTLs for CI symptoms previously reported in this linkage group from an unrelated progeny population. In addition, QTLs controlling other agronomic and fruit quality traits were also localized in this linkage group.