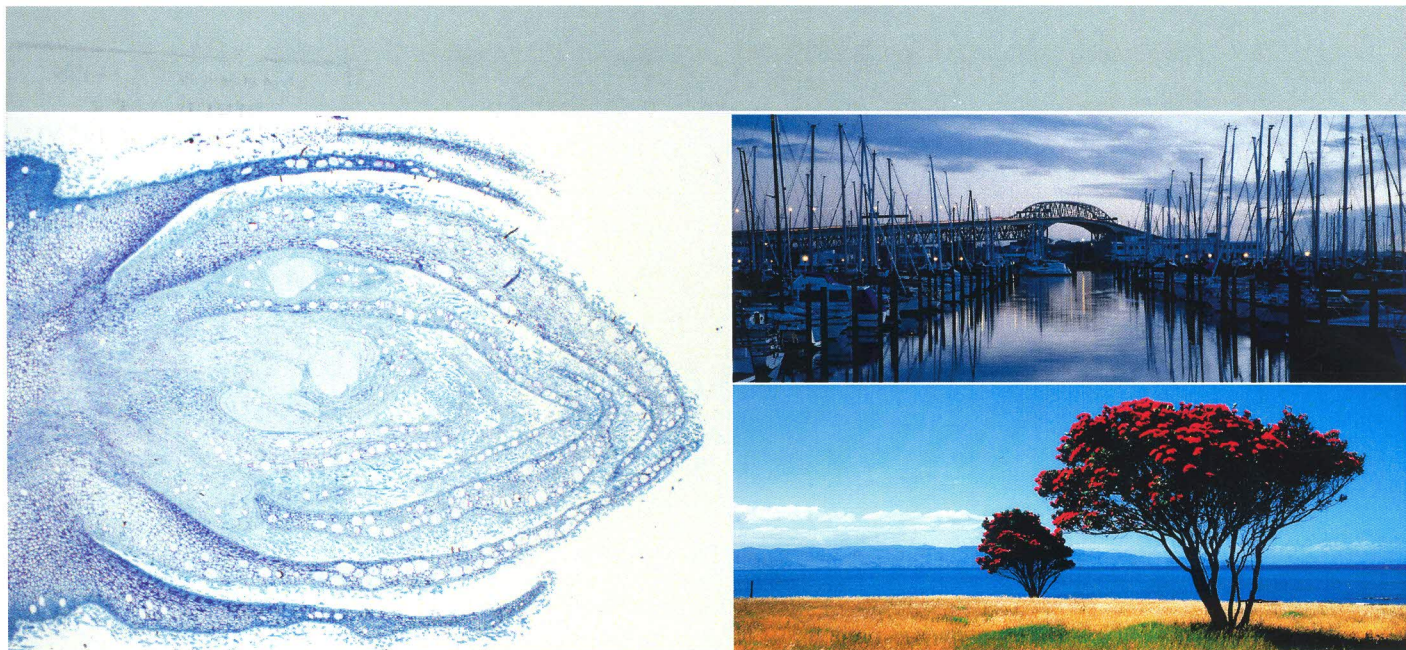




PLANT DORMANCY SYMPOSIUM 2013

4-7 November 2013

Auckland
New Zealand



THE 5TH INTERNATIONAL PLANT DORMANCY SYMPOSIUM

ABSTRACT AND PROGRAMME BOOK



The 5th International Plant Dormancy Symposium

The New Zealand Institute for Plant & Food Research Limited and the International Society for Seed Science are proud to present the
5th International Plant Dormancy Symposium.

Venue

Hilton Auckland Hotel
Aquamarine Room 3
Princes Wharf
147 Quay Street
Auckland City
New Zealand

Conference Dinner Venue

Royal New Zealand Yacht Club
101 Curran Street
Westhaven 1011
Auckland
New Zealand

Integrating genetics, genomics and modeling of bud dormancy to improve apple adaptation to climatic changes

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Brazilian apple production regions are generally characterized by insufficient chilling as well as by temperature fluctuations during winter with negative impacts on apple yield. These mild winter conditions tend to be intensified considering the global warming predictions. Therefore, knowledge of the genetic and physiological mechanisms that control bud dormancy is valuable for breeding and management efforts. By integrating linkage mapping strategies, genomic approaches and phenological modeling, a collection of useful data was generated to better characterize this complex agronomic trait. High density linkage maps were constructed based upon two segregating populations for chilling requirement associated traits from the cross between 'Fred Hough' X 'M13/91' and 'Fred Hough' X 'Castel Gala'. Major quantitative trait loci (QTL) associated with initial vegetative bud burst and time of flowering were identified in linkage group 9, explaining 30 and 70% of the total variation, respectively. Transcriptomic characterization of genes related to bud dormancy were performed on microarrays representing all apple predicted genes and by suppression subtractive hybridization. Among the differentially expressed candidates, genes with potential roles in the circadian clock, hormonal signaling, growth regulation, flower development and cold responses were identified. Genotypes contrasting in phenological bud burst data under different thermal regimes and biochemical data enabled the development of a theoretical model to characterize dormancy. Essentially, the hypothetical model considers endodormancy induction and fulfillment, and ecodormancy as distinct phases which are modeled by different variables. Bud burst evaluation employed the Gompertz growth function to estimate precociousness, uniformity and maximum bud burst. Linkage mapping and transcriptomic data were integrated with the apple reference genome employing bioinformatic tools to generate high resolution chromosomal ideograms and a web-based application to explore the results. These resources allowed better cross-examination of data and selection of candidate genes putatively associated with the bud dormancy processes. The results confirm that a major QTL in linkage group 9 has important genetic determinants for the control of dormancy-related traits and provide additional support to narrow the search for genes related to the control of dormancy progression in apples. Moreover, the theoretical model of bud dormancy can serve as the basis for future construction of a mathematical model to accurately simulate dormancy levels in apples adapted to mild winter regions such as the South of Brazil.