

Dormancy-associated microRNAs in sweet cherry (*Prunus avium* L.): a first draft.

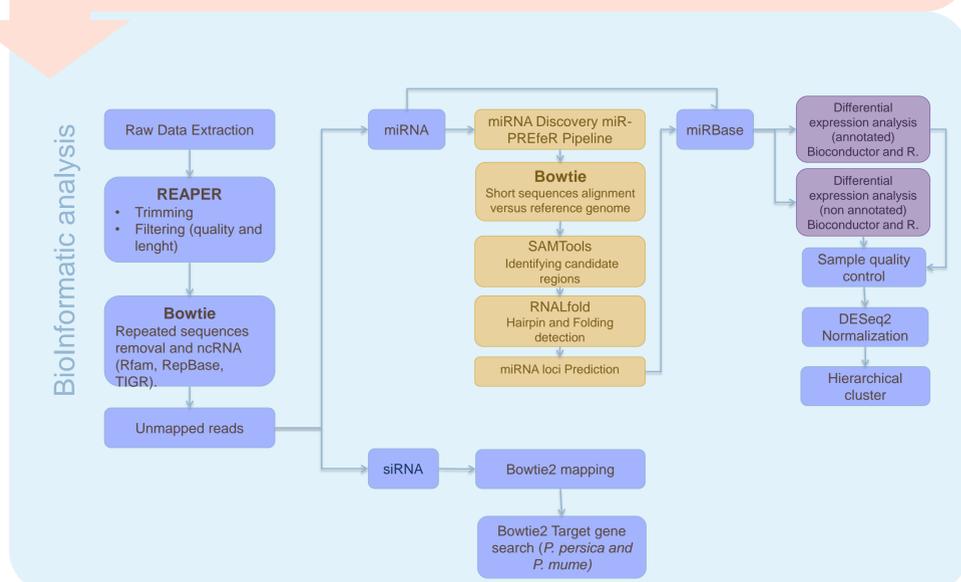
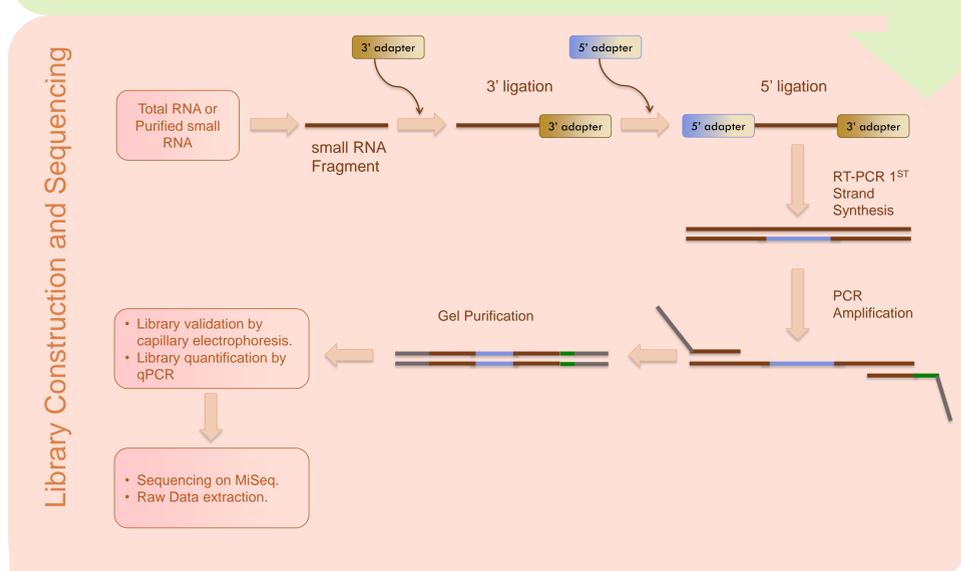
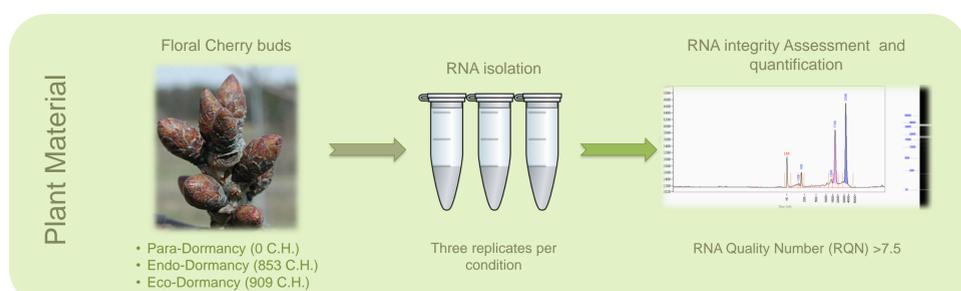
Evelyn Sánchez¹, Karin Rothkegel², Christian Montes¹, Paola Andrade¹, Pablo Cid¹, Andrea M. Almeida³ and Humberto Prieto^{1*}

¹Instituto de Investigaciones Agropecuarias, La Platina Station, Santiago, Chile. ²Centro de Biotecnología Vegetal, Universidad Andrés Bello, Santiago, Chile. ³FONDAP Center for Genome Regulation, Santiago, Chile. *Corresponding author: hprieto@inia.cl.

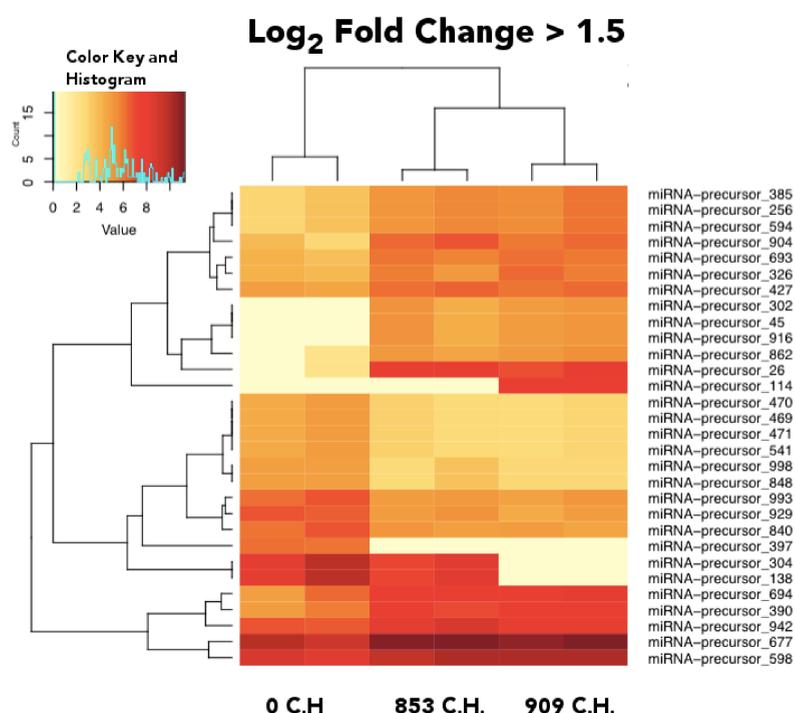
Abstract

During the winter, sweet cherry (*Prunus avium* L.) has a restricted growth period of both floral and vegetative buds in which they enter a dormant state. Dormancy is defined as the inability to resume meristem growth under favorable conditions. To be able to exit from this state, an extended cold period, termed the chilling requirement, is needed. Recent information about this species allows for the molecular understanding of dormancy and involves several pathways, including epigenetic modification and gene expression. In this latter group of events, microRNAs (miRNAs) play relevant roles. During dormancy, flowering transition is controlled by two main miRNA families (miR156 and miR172), which have been identified in the juvenile-to-adult and vegetative-to-reproductive transitions, respectively. The miR159, miR319, miR390, and miR399 families have also been described as playing key roles in flowering. In the present study, which is understood as part of a general dormancy study of this species, we present preliminary results about candidate miRNA species during sweet cherry dormancy. Massive small RNA sequencing experiments were conducted with small RNA samples from field trees. Previously identified 21- and 22-nt small RNAs were filtered. The candidate molecules were then aligned to microRNA and reference *Prunus* spp. genomic databases in order to generate a primary set of candidate miRNAs involved in the chilling and dormancy processes; these are currently undergoing experimental verification.

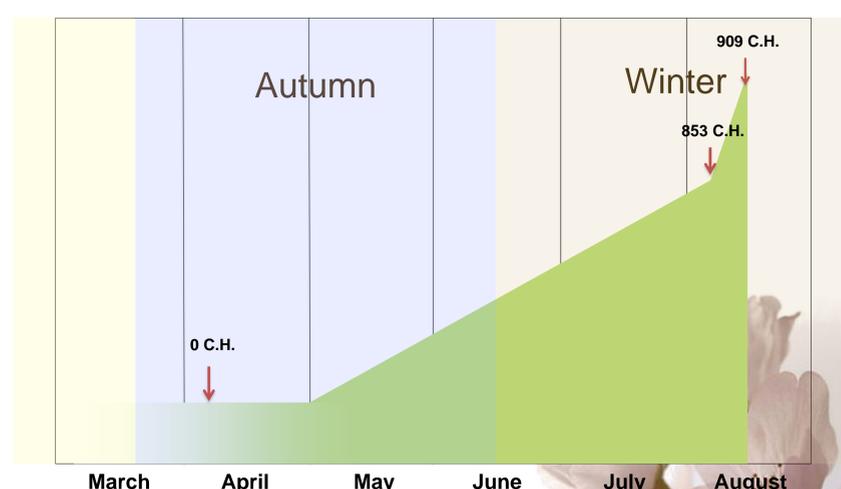
Materials and Methods



Results



Hierarchical cluster analysis of smallRNAs accumulation, in *Prunus avium* buds with different chilling hours. This analysis was made with nine sequencing libraries, in three different stages of cold accumulation. The short sequences obtained were treated in accordance with the bioinformatic pipeline described above, identifying new miRNA precursors.



RNA-precursor-862 (Pav-miR156-like) accumulation Scheme. This diagram shows a representation of temporal accumulation of Pav-miR156-like between autumn and winter (South Hemisphere).