PROPOSAL ABSTRACT:

Title	**Epigenetic control of maturity date in *Prunus persica* by integrating transcriptomic and epigenomic approaches**
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The Chilean fruit export industry, which includes various fruit species such as peaches and nectarines, is the largest in the Southern Hemisphere—consumers of fresh fruit demand high-quality products, which are achieved through several quality traits. In Prunus persica, the maturity date (MD) is a crucial fruit trait for maintaining fresh fruit and extending shelf-life. This trait is also important from a genetic perspective due to its pleiotropic effects on other quality traits such as sugar content, acidity level, and juiciness. While some candidate genes have been identified for MD, such as those related to ethylene and jasmonate biosynthesis, and cell wall modification, their roles in the molecular regulation of MD in stone fruits are still unknown. Moreover, complex genetic control is at play, and the candidate genes identified have largely been dependent on the plant material used. To better understand the molecular regulation of MD, we propose to integrate transcriptome and methylome data. Epigenetic influences such as DNA methylation and non-coding RNAs regulate firmness and skin colour during fruit development. The proposed model suggests that the interaction between phytohormones, transcription factors, and epigenome reprogramming allows for the transition into the ripening state.

We hypothesise that **differences in MD among Prunus persica varieties are regulated by changes in the levels of DNA methylation and non-coding RNAs, which determine the differential expression of genes related to jasmonate biosynthesis and cell wall modifications during fruit development**. We will focus our search on previously identified regions and genes and expect to detect new (epi)genetic factors associated with MD, integrating genetic, physiological, transcriptomic, and epigenetic data. Our primary goal is to identify the epigenetic control elements in expressing cell wall modifications and jasmonate biosynthesis genes associated with MD during fruit development in P. persica. To accomplish this, we will phenotype fruit development and harvest time in contrasting individuals for MD from a collection of P. persica varieties. We will determine associations between differentially expressed non-coding RNAs, cell wall modifications, and JA biosynthesis genes during fruit development using RNA-seq. Additionally, we will estimate the association between DNA methylation levels, location, and transcript levels from previously identified genes during fruit development using whole-genome bisulfite sequencing. Finally, we will validate the levels of DNA methylation, coding, and non-coding RNA as candidate biomarkers associated with MD in P. persica by RT-qPCR analysis and amplicon custom bisulfite sequencing**. Therefore, our study will yield the following outcomes**: 1. A comprehensive database of phenotypic data from peach and nectarine varieties collection, including fruit quality traits such as MD, SSC and firmness, among others, over three seasons. Additionally, we will analyze changes in JAs levels and cell wall composition during fruit development. 2. Identification of non-coding RNAs associated with MD-related genes, mainly JA biosynthesis and cell wall modification-related genes. 3. Detection of Differentially Methylated Regions (DMRs) associated with MD. 4. Validation of non-coding RNAs and DMRs related to MD. By studying the different layers of information, such as gene expression and epigenetic regulation, we aim to understand better the (epi)genetic control mechanisms behind MD. This knowledge will be the foundation for developing potential biomarkers and their subsequent application in peach breeding programs.