

# MOLECULAR ANALYSIS OF BUD DORMANCY REGULATION BY TEMPERATURE IN SWEET CHERRY

Mathieu Fouché<sup>a</sup>, Bénédicte Wenden<sup>a</sup>, Hélène Bonnet<sup>a</sup>, Xavier Lafon<sup>a</sup>

<sup>a</sup> INRAE, UMR 1332 Biologie du Fruit et Pathologie, Adaptation du cerisier au changement climatique, Villenave d'Ornon, France

**Program theme:** Genetics and Epigenetics.

**Oral**

**Abstract**

Over the past decades, climate change has already led to a higher frequency of mild winters. In particular, the rising temperatures impact winter dormancy, a resting period which is a key step of the tree life cycle, preventing growth under unfavorable conditions.. Sweet cherry trees, in particular, are very sensitive to temperatures; therefore their production is greatly threatened by climate change. We investigated the effect of milder temperatures on sweet cherry flower buds during dormancy onset and maintenance, using both phenological observations and molecular analyses. Potted trees of the sweet cherry cultivar 'Regina' were submitted to several levels of cold deprivation from bud set to flowering. In order to highlight candidate genes that are regulated by temperatures during dormancy progression, we performed a global transcriptomic analysis using RNA-Seq on bud tissues. Our results showed that cold deprivation induced a marked delay in senescence and in flowering date. Molecular analyses revealed that these conditions strongly affected gene expression patterns compared to natural winter temperatures. We defined six main gene groups based on their global expression patterns and their response to temperature changes, allowing the identification of genes and signaling pathways specifically activated and/or repressed by cold temperatures.