Poster Communication Abstract – 2.07

EPIGENETIC MECHANISMS CONTROLLING PEACH BUD DORMANCY AND ITS RELEASE

CANTON M., FORESTAN C., FARINATI S., BONGHI C., VAROTTO S.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (Italy)

Prunus persica, DNA methylation, chilling requirement, RNA-seq

To cope with critical environmental conditions during winter, perennial deciduous fruit trees have evolved adaptive mechanisms such as bud dormancy (a cease of bud growth). Bud dormancy is overcome by a period of chilling temperatures (Chilling requirement, CR). Recently, global warming makes always more often the environment unable to satisfy the CR of fruit trees. Consequently, fruit trees show irregular phenologies with detrimental effect on their productivity. A deletion in the tandemly arrayed family of six DORMANCY-ASSOCIATED MADS-box1-6 (DAM 1-6) genes has been proposed to be the cause of the non-dormant phenotype of the evergrowing (evg) mutant of peach (Prunus persica). Subsequently, it has been demonstrated that the expression of DAMs is epigenetically controlled, mainly through chromatin modifications, additionally DAMs gene expression has been shown to be regulated by environmental conditions. However, the knowledge on the genetic factors involved in the regulation of bud dormancy events is still scarce and fragmentary. The main goal of this work is to improve our knowledge on the genetic and epigenetic mechanisms involved in the control of bud dormancy and its release. To reach this goal we study a genotype originated by self-pollination from Fantasia (FAN), named slow ripening (SR), which phenotype seems to be due to an alteration of epigenetic mechanism regulating buds and fruit development. Preliminary results indicate that, at the same CR, DAM genes are differentially expressed, particularly DAM4 and DAM6, in SR and Fantasia. This result pointed out that SR and FAN are useful genotypes for studying epigenetic mechanisms regulating bud and fruit development. Here we present data integration of genome-wide analyses (RNA-Seq, DNA methylation and chromatin modifications) performed in vegetative and reproductive buds during dormancy and its release, for depicting a more complete picture of bud development epigenetic control.