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Study of Transcriptional Regulatory Network controlling Strawberry Fruit Ripening and Quality

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Ripening is a critical step for the development of flavor quality in fruits. This character has significantly declined in many fleshy fruits over recent decades. This is particularly significant in strawberry (*Fragaria × ananassa*), where current cultivars are derived from a narrow germplasm collection. Improving fruit quality requires two important breakthroughs: 1) a precise understanding of the fruit ripening process that will allow the targeting of relevant genes, and 2) the identification of novel alleles responsible for fruit quality traits.

In our project, we aim at the identification and characterization of key transcription factors involved in fruit ripening regulation and their target genes, in order to infer the Gene Regulatory Network controlling this process. Also, we are using a collection of around two hundred wild strawberry (*Fragaria vesca*) accessions to identify *loci* involved in important traits such as aroma, size or resistance to pathogens. Finally, we are implementing the use of the genome-editing tool CRISPR/Cas9 in the cultivated strawberry, which we expect it might open opportunities for engineering this species to improve traits of economic importance.

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