Proposition d'un sujet de stage au M2 ADAM (2017-2018)

Titre	Identification of class D MADS-box transcription factor targets genes during fruit development
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Résumé	MADS-box genes encode transcriptional regulators involved in different development processes in all Eukaryotes. In plants, the MADS-box genes are well known in reproduction biology: its key role in flower development is illustrated by the ABC model where the identity of the different floral whorls (sepal, petal, stamen and carpel) is determined by specific combinations of MADS-box transcription factors. The class D MADS box genes were initially studied for its involvement in the ovule and seed determination in Petunia and Arabidopsis. Recent works in the lab, using different transgenic tomato lines altering class D MADS-box genes expression (see picture), have evidenced its importance in controlling the development of several tissues in the young tomato berry: gel, placenta, and columella (1st article in press in J Exp Bot, 2nd in preparation). The modification of these tissues greatly affects several fruit quality traits - firmness, sugar content, ripening. Therefore, the identification of class D MADS-box transcription factors targets and the elucidation of the activation mechanism operated during early fruit development could open new perspectives for fruit quality improvement. During the internship, the student will take advantage of tomato lines over-expressing our MADS-box candidate genes associated with a GFP tag. The first step will consist in optimizing a chromatin immunoproecipitation protocol on young fruits and sepals. Latter, the target genes of MADS-box transcription will be validated by promoter-binding or co expression assays. The identification of potential targets will be completed by transcriptional studies in RNAi or over-expressing tomato lines exhibiting MADS-box gene down- or up-regulation.
Photo	 *Associated picture: Tomato development affected by class D MADS-box genes*