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CHARACTERIZATION OF RIPE FRUIT EPIDERMIS-SPECIFIC TRANSCRIPTION FACTORS IN STRAWBERRY

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The epidermis is the external cell layer in direct contact with the environment, and it plays essential biological roles. Transcriptome analysis (RNA-seq) of *Fragaria vesca* fruit receptacles at four ripening stages (green, white, turning and red) and of different tissue types of receptacles (pith, vascular bundles, cortex and epidermis) at two ripening stages (green and red) allowed us to infer tissue- and stage-specific Gene Regulatory Networks (GRN). Due to the potential role of the epidermis in defense and in the differential anthocyanin accumulation pattern that shows at the ripe stage of *F. vesca* fruits (the skin is red, while the inner part is white), we have focused on the GRN of the ripe epidermis. In this study, we aim at the functional characterization of two transcription factors (TFs) that constituted the main hubs of this GRN: a MYB-like gene, and a member of the NAC family of TFs. A MapMan analysis of the genes constituting the GRN in ripe epidermis showed that wax and flavonoid biosynthesis were significantly overrepresented functions in this tissue at the ripe stage. Using the Luciferase/Renilla (Luc/Ren) system, the interaction of the MYB and NAC TFs with their wax-related putative targets was validated. To gain insight into the target genes of these two TFs, we mapped the genome-wide binding sites using DAP-seq analyses. Consistently, MYB bound to a set of genes involved in cuticle formation and flavonoid biosynthesis, while a number of genes involved in solute transport were enriched among the NAC targets. Currently, we are generating CRISPR/Cas9 mutant lines to functionally characterize these two TFs. Furthermore, we are performing protein interaction assays to decipher whether the MYB and NAC TFs interact with each other and with other TFs from the red epidermis GRN.

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