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**IDENTIFICATION OF DIRECT TARGET GENES AND FUNCTIONAL  
CONSERVATION OF FaRIF, A KEY REGULATOR OF FRUIT  
RIPENING IN STRAWBERRY**

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We have identified FaRIF, a NAC transcription factor (TF) that plays a central role controlling strawberry fruit ripening. Thus, our data showed that FaRIF is involved in multiple ripening-related processes, such as ABA biosynthesis and signalling, cell wall degradation and modification, phenylpropanoid pathway, etc. (Martín-Pizarro *et al.*, 2021). In order to further characterized the mechanism by which FaRIF regulates strawberry fruit ripening, we aimed at identifying direct target genes. For that purpose, we have optimized the Chromatin Immunoprecipitation (ChIP) methodology in strawberry plants using *35S:FaRIF-GFP* lines. Our data has allowed us to identify loci directly bound by FaRIF which are in the promoter regions of ripening-related genes. Furthermore, the binding has been confirmed by transactivation assays using Luciferase.

*FaRIF* belongs to a clade of NAC TFs with a role in fruit ripening and senescence in different species, as well as in different fruit and ripening types, suggesting conservation in their ultimate role for seed dispersal. Our results have shown partial complementation of the mutant in *Arabidopsis* for the closest homolog genes to FaRIF, i.e., the redundant genes *NARS1* and *NARS2*, supporting the conservation of the role for this NAC TFs clade.

*References*

Martín-Pizarro. (2021). *The Plant Cell*. 33:1574-1593

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