

	CRIPTION FACTOR PLAYS A KEY ROLE IN THE REGULATION OF FRUIT RIPENING IN THE CULTIVATED STRAWBERRY FRAGARIA × ANANASSA  P0254  Carmen Martín Pizarro <sup>1</sup> , Victoriano Meco <sup>1</sup> , María Urrutia <sup>1</sup> , José G. Vallarino <sup>1</sup> , Jeremy Pillet <sup>1</sup> , Ana Casañal <sup>1</sup> , Sonia Osorio <sup>1</sup> , Miguel Ángel Botella <sup>1</sup> , Victoriano Valpuesta <sup>1</sup> , David Posé <sup>1</sup> ,  1Laboratorio de Bioquímica y Biotecnología Vegetal, Instituto de Hortofruticultura Subtropical y Mediterránea (IHSM), Universidad de Málaga-Consejo Superior de Investigaciones Científicas. Departamento de Biología Molecular y Bioquímica, Facultad de Ciencias, Universidad de Málaga, Spain  3 Genomics of fruit, nut or flower quality	
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## **ABSTRACT:**

Strawberry is becoming a model for studying the molecular mechanism of ripening in non-climacteric fruits. However, a limited number of transcriptional regulators of this process have been identified so far. In this study, we have identified and characterized a gene encoding for a NAC transcription factor (TF), named as FaRIF (Ripening Inducing Factor). FaRIF expression presents a fruit-specific pattern, which is upregulated during ripening. In order to functionally characterize this TF, we have generated silencing and overexpressing stable transgenic lines. While the RNAi lines showed an apparent delay of fruit ripening, the overexpressing lines displayed an acceleration of this process. Transcriptomic analysis of the silenced lines showed a significantly altered expression of genes involved in development, hormone metabolism, flavonoid pathway, and cell-wall disassembly, being many of these confirmed by phenotypical and metabolomics analysis. Our results support a main role of FaRIF in the control of relevant ripening-associated processes in strawberry fruit.