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Anthracoze, caused by *Colletotrichum acutatum*, is responsible for significant yield losses in commercial strawberry production worldwide. For this reason, it is of interest to uncover the molecular basis underlying this strawberry/pathogen interaction. Previously, *FaWRKY1* was identified as an important element mediating defence responses. This gene encodes an AtWRKY75-like transcription factor (type IIc), which is upregulated in strawberry following *C. acutatum* infection. In this study, *Agrobacterium*-mediated transient transformation was used to both silence and overexpress the *FaWRKY1* gene in fruit, with the aim to clarify its function in the strawberry defense mechanism. Analyses of *FaWRKY1*-RNAi strawberry fruits showed resistance to *C. acutatum* infection, 5 d after inoculation with this pathogen. Overexpression of this gene in strawberry fruit showed increased susceptibility to *C. acutatum*. Molecular analysis is being carried out with these fruit samples to elucidate candidate genes transcriptionally regulated by *FaWRKY1*. Furthermore, *in vitro* DNA-binding assays have revealed a tentative consensus sequence [G/T][T/C]TGAC[T/C], containing the core sequence TGAC (W box), as the likely target sequence for *FaWRKY1* binding. These analyses will strengthen genome-wide promoter target site prediction for *FaWRKY1*.

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Evidence that the putative movement protein (MP2) of Broad bean wilt virus 1 is a pathogenicity determinant. C. CARPINO^{1,2}, I. FERRIOL¹, L. ELVIRA-GONZÁLEZ¹, L. RUBIO^{1,3}, E. PERI², S. DAVINO^{2,4}, L. GALIPIENSO^{1,3,4}. ¹Instituto Valenciano de Investigaciones Agrarias (IVIA), Ctra. CV-315, 46113 Moncada, Valencia, Spain. ²Department of Agricultural and Forestry Science, University of Palermo, Piazza Marina 61, 90133 Palermo, Italy. ³Euro-Mediterranean Institute of Science and Technology (IEMEST), Vía Michele Miraglia 20, 90139 Palermo, Italy. ⁴Departamento de Biotecnología, Escuela Técnica Superior de Ingeniería Agronómica y del Medio Natural, Universidad Politéc-

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Broad bean wilt virus 1 (BBWV-1, genus *Fabavirus*, family *Secoviridae*) infects crops of economic importance, such as broad bean, pepper, tomato, spinach, and ornamental plants. The virus genome is constituted by two molecules of positive single stranded RNA, each encoding a polyprotein which is further processed by proteolytic cleavage. RNA1 encodes the proteins involved in viral replication and expression, while RNA2 encodes the movement protein (MP) and two coat proteins (LCP and SCP). RNA2 contains an alternative second start codon rendering a smaller putative movement protein, called MP2. To date, the BBWV-1 proteins related to pathogenicity are unknown. The roles of MP2 in symptom determination, post-transcriptional gene silencing (PTGS) and elicitation of hypersensitive response (HR) were examined. Expression of MP2 in *Nicotiana benthamiana* through *Potato virus X* (PVX) caused necrotic lesions, indicating that MP2 is a symptom determinant. Analysis of O₂⁻ accumulation and necrosis staining revealed that this protein elicited the cellular HR. Transient expression of MP2 in *N. benthamiana* 16C, that constitutively expresses Green Fluorescent Protein (GFP), and a complementation assay with a vector based on *Turnip crinkle virus* sequence (TCV-sGFP) showed that this protein acts as a suppressor of PTGS.

Chlorophyll degradation pathway is linked to stomatal and photosynthetic dysfunctions observed in oats resistant to powdery mildew. G. MONTILLA-BASCÓN¹, M. ROCA², L.A.J. MUR³, PRATS E¹. ¹Department of Plant breeding, Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Alameda del Obispo s/n, P.O. Box 4084, 14004 Córdoba, Spain. ²Food Phytochemistry Department, Instituto de la Grasa, Consejo Superior de Investigaciones Científicas (CSIC), University Campus Pablo de Olavide, Building 46, Sevilla 41013, Spain. ³Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK.

Cost of resistance is usually associated with the energy and nutritional penalties linked to induction of defenses. Currently, a mechanistic understanding of the sources of these costs is lacking, other than vague