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# P54

## Functional characterisation of cuticle-related grapevine genes

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The epidermal layer of aerial plant tissues is covered by a hydrophobic structure known as the cuticle. This cuticular layer plays a major role in protecting the plant against abiotic and biotic stress factors, namely water loss and pathogen infection, as well as contributing towards postharvest fruit quality traits such as colour, texture, firmness, and shelf-life. Despite its economic significance, there are still considerable knowledge gaps concerning cuticle biosynthesis and its regulation in grapevine. The aim of this study is to identify and functionally characterise cuticle-related grapevine genes. To this end, putative cuticle regulators were selected from RNAseq data generated from an *in vitro* VviERF045 overexpressing grapevine line displaying impaired cuticle development. The selected genes were cloned and then overexpressed in grapevine (VviERF045) and tomato (VviSOC1a, VviAG1, VviMYB141 and VviSHN3), as well as knocked out in grapevine (VviMYB141). Preliminary analysis of the T0 tomato populations showed potential involvement of these genes in cuticle accumulation, trichome development, conical cell formation, floral organ identity and fruit ripening. In addition, evaluation of the acclimated overexpressing and knockout grapevine lines exhibited observable alterations to the stomatal and trichome densities of leaves. Promoter transactivation assessment, using a dual luciferase assay, confirmed the association of all selected genes within the greater regulatory pathway of VviERF045.

**Keywords:** VviERF045, cuticle, trichome, floral identity, ripening, conical cell, transcriptional regulation