Open Conference on
Grapevine Physiology
and Biotechnology
LOGROÑO - LA RIOJA
7-11 July 2024

Exploring the regulatory role of the grapevine MIXTA homologue in cuticle formation and abiotic stress resilience

Carlotta Pirrello[1*], Jenna Bryanne Jolliffe[1,2], Lorenzo Vittani[1], Luis Orduña[3], Paolo Sonego[1], Michele Faralli[1,4,] José Tomás Matus[3], Stefania Pilati[1], Justin Graham Lashbrooke[2,5], Claudio Moser[1]

[1] *Research and Innovation Centre, Edmund Mach Foundation, San Michele all'Adige, 38098, Italy*
[2] *South African Grape and Wine Research Institute, Stellenbosch University, Stellenbosch, 7600, South Africa*
[3] *Institute for Integrative Systems Biology (I2SysBio), Universitat de Valencia-CSIC, Paterna, 46908, Valencia, Spain*
[4] *Center Agriculture Food Environment (C3A), University of Trento, via Mach 1, San Michele all'Adige, 38098, Italy*
[5] *Department of Genetics, Stellenbosch University, Stellenbosch, 7600, South Africa*

[*] *Corresponding author: carlotta.pirrello@fmach.it*

Abstract

The outer waxy layer of plant aerial structures, known as the cuticle, represents an important trait that can be targeted to increase plant tolerance against abiotic stresses exacerbated by environmental transition. The MIXTA transcription factor, member of the R2R3-MYB family, is known to affect conical shape of petal epidermal cells in *Anthirrinum*, cuticular thickness in tomato fruit and trichome formation and morphology in several crops. The aim of this study was to investigate the role of the grapevine *MIXTA* homologue by phenotypic and molecular characterization of overexpressing and knock-out grapevine lines. The leaf cuticle was observed by light microscopy, indicating that stomatal density and other anatomical features, such as trichomes and pavement cell number, were affected by modulation of *VviMIXTA.* GC-MS analysis found that epicuticular wax loads and composition were similarly impacted. Physiological parameters collected on a randomized set of plants in controlled conditions showed that stomatal conductance was also affected. Selected lines, identified via *VviMIXTA* gene expression analysis, underwent RNA-seq to evaluate the transcriptomic impact of modulating VviMIXTA expression. The results were cross-referenced with DAP-seq data to identify MIXTA high confidence target genes. Additionally, further integration of the experimental data with *in silico* resources available for grapevine (e.g., OneGenE and aggregated tissue-specific GCNs) is being conducted for reconstructing MIXTA´s gene regulatory network. Our work explores the potential regulatory role of VviMIXTA in epidermal cell fate and cuticular wax composition in the grapevine leaf, paving the way for molecular breeding to enhance plant resilience and improve berry quality traits.

Keywords: Vitis vinifera, cuticle, stomata, trichomes, multi-omics data