Functional characterisation of genetic elements regulating bunch morphology in grapevine

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Vitis vinifera L., is considered one of the world's most important cultivated fruit crops. In agriculture, bunch morphology is a grapevine-specific trait, which directly impacts fruit quality and health.

Bunch size, shape, and compactness are major aspects of bunch morphology, with the degree of compactness emerging as an important trait for grapevine genetic enhancement and vineyard management. The importance of this trait stems from its impact on disease susceptibility, berry ripening, and other grape quality properties. However, current knowledge of the genes controlling it remains limited.

This study aims to identify and characterise genetic elements regulating grapevine bunch formation, while also providing valuable understanding of molecular and cellular regulation of this important process. This will be done by carrying out three planned objectives, summarised as: identification of candidate genes, overexpression of candidates in model plants, and genetically engineering grapevine for selected genes.

Ten candidate genes were identified based on their presence in loci associated with bunch architecture traits, expression patterns during flower development, and sequence homology with genes regulating plant architecture in other species. These genes were cloned into plant expression vectors that were used to transform tomato and *Arabidopsis thaliana* plants. The research anticipates observing phenotypic evidence in the transformed model plants, which may suggest a potential role in grapevine bunch architecture regulation. The identification and characterisation of genes controlling bunch morphology offer promising avenues for advancing grapevine breeding and cultivation practices, benefiting the viticulture industry and consumers alike, by improving growth, health, and fruit production.

Keywords: bunch morphology, overexpression, grapevine, compactness, transformation