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Characterization of bunch compactness and identification of associated genes in a diverse collection of cultivars of *Vitis vinifera* L.

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Compactness is a complex trait of *V. vinifera* L. and is defined ultimately by the portion of free space within the bunch which is not occupied by the berries. A high degree of compactness results in poor ventilation and consequently a higher susceptibility to fungal diseases, diminishing the quality of the fruit. The easiness to conceptualize the trait and its importance arguably contrasts with the difficulty to measure and quantify it. However, recent technical advancements have allowed to study this attribute more accurately over the last decade. Our main objective was to explore the underlying genetics determining bunch compactness by applying updated phenotyping methods in a collection of *V. vinifera* L. cultivars with a wide genetic diversity.

A collection of 116 genotypes composed by 24 wine, 56 table and 26 mixed usage varieties was characterized over two seasons measuring several traits determining Compactness Indexes (CI), as proposed in literature. CI-18 performed the best on this collection and genotypes with extreme values with loose and dense bunches were further studied (n = 10 each group). RNA of these samples was collected at key developmental stages to study the expression of VvUCC1, VvGRF4 and other genes associated to this trait. We also evaluated the performance of automated phenotyping for this wide collection of varieties by applying precision phenotyping through 3D scan and point cloud library-based methods. Combining this data with 127,631 informative SNPs identified by genotyping-by-sequencing could lead to identify further loci associated with this attribute through GWAS.

Keywords: Bunch compactness, qPCR, GBS, automated phenotyping.