

Evaluation of an automated 3D based phenotyping pipeline for grapevine bunches to determine bunch architecture traits

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In viticulture *Botrytis cinerea* (*B. cinerea*) is responsible for bunch rot infestations and can cause severe damage during warm and wet periods close to harvest. As *Vitis vinifera* does not show an active defense response, classical resistance breeding is difficult and therefore grapevine breeding put focus on physical barriers e.g. berry characteristics like tight berry skin and bunch architecture.

Loose bunch architecture is associated with an increased resilience against *B. cinerea* which results in unfavorable conditions for its growth.

For breeding purposes and research high numbers of plants have to be evaluated during the season e.g. for the development of genetic markers for marker-assisted selection. Bunch architecture is a complex trait (bunch volume in relation to berry number, total berry volume). Phenotyping of all these architecture related parameters is very time consuming and labor intensive. The aim of the present study was the development and validation of an automated phenotyping pipeline in order to characterize the mentioned traits for bunch

architecture with high-precision and high-throughput.

Therefore, the optical 3D sensor Artec® Spider was used to generate dense 3D point clouds. For an efficient analysis of the 3D sensor data, the software '3D-Bunch-Tool' with a user friendly graphical interface was developed to analyze acquired 3D data automatically. Finally, a list of all selected traits (Number of Berries, Berry Diameter, Berry Volume, Total Berry Volume, Convex Hull Volume, Bunch Width and Bunch Length) is exported.

The pipeline was applied to phenotype 75 bunches of four different varieties and a set of 150 F1 plants of a segregating population. For validation, the results were compared with ground truth data. High correlations and a considerably faster data acquisition compared to the reference data could be achieved.

Artec® Spider was further applied in the field for direct and non invasive phenotyping of grape bunch morphology parameters.