

Automated evaluation and comparison of grapevine genotypes by means of grape cluster architecture

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Botrytis cinerea (*B. cinerea*) is a necrotrophic pathogen that causes the widely known grey mold disease. With the ability to infest more than 200 crop species and furthermore a high adaptability to fungicides, *B. cinerea* belongs to the high risk fungi in agriculture.

In viticulture *B. cinerea* is responsible for severe damage during warm and wet periods close to harvest. Neither *Vitis vinifera* nor other species do show resistance reactions against Botrytis. Therefore, resistance breeding in general is difficult. Thus, in viticulture the focus is on physical barriers, as they seem to play a promising part in Botrytis resilience.

Loose cluster architecture of grapes implements less favorable conditions for *B. cinerea*. Therefore, cluster architecture is defined by different traits e.g. the length of the rachis, length of the pedicels, and the number of berries etc. These traits become important goals for grapevine

breeding. However, determining these traits is complicated by slow and manual phenotyping, which requires invasive and time consuming methods in the lab. The total aim of this project is mapping of QTL, the development of marker and identification of candidate genes for a loose grape architecture.

In a segregating population of 150 F1-plants the data of cluster and berry traits are taken manually. At the same time, with the optical sensor *Artec Spider*, 3D point clouds of these grape clusters will be generated. These two data sets will be used for the development and evaluation of a novel automated high throughput phenotyping pipeline for grape clusters.

Furthermore, the dataset will be extended by 1000 F1-plants, with the new phenotyping pipeline. These phenotypic traits are then used for extensive QTL-analysis and fine mapping of loose grape bunch traits.