Development of an image-based phenotyping system for fast investigation of grapevine root architecture

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In recent years, objective, sensor-assisted and automated phenotyping techniques have been developed in order to evaluate above-ground plant traits, e.g. grape bunch architecture or growth characteristics. The investigation of root architecture related traits, like the total root length or amount of secondary roots, is important with regard to adventitious root formation, drought stress tolerance and other abiotic and biotic stress factors in viticulture. One major aim within the project 'MureViU' is the establishment of an image-based phenotyping system for fast acquisition of grapevine root architecture related traits from several hundreds of plants.

In order to elucidate the growing root system, rhizotrons were developed following the example of the automated rhizotron phenotyping platform established at Forschungszentrum Jülich GmbH.

Dormant wood cuttings were planted in rhizotrons filled with dark potting soil and set in a slanted position with the roots growing along a transparent site. Usage of rhizotrons allows the non-invasive observation of the root system with high throughput and over time. By means of this method, several root characteristics, e.g. root length, root branches and growth rate can be measured.

Therefore, following preliminary experiments have started this year: First, a cost-effective rhizotron prototype setup was developed and several genotypes including rootstock varieties were screened. Second, the same set of genotypes was phenotyped with the established system in Jülich. And third, determination of root biomass (total dry weight per plant) as ground truth.

Furthermore, and in the course of establishing the new rhizotron system, phenotypic data from a mapping population of V3125 (*Vitis vinifera* 'Schiava grossa' × 'Riesling') and rootstock cultivar Börner (*V. riparia* × *V. cinerea*) will be collected. After repetition of this experiment in the following years, the data will be finally used for QTL analysis in order to identify gene loci associated with root system characteristics within this mapping population.