

## METHODOLOGICAL ADVANCES IN RELATING DEEP ROOT ACTIVITY TO WHOLE VINE PHYSIOLOGY

### SCIENTIFIC ORAL PRESENTATION

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#### Abstract:

**Context and purpose of the study** – Full understanding of grapevine responses to variable soil resources requires assessing the grapevine root system. Grapevine root systems are expansive and examining deep roots (i.e., >40 cm) is particularly important in conditions where grapevines increase reliance on deep soil resources, such as drought or plant competition. Traditional methods of assessing roots rely on morphological traits associated specific functions (e.g., root color, diameter, length), while recent methodological advances allow for estimating root function more directly (e.g., omics). Yet, the potential of applying refined methods remains underexplored for roots at deep depths. Here, we present and discuss studies from our team from 2017-2020 that examined absorptive root responses up to 1-m. By comparing these techniques, we sought to identify which approaches have the most potential to link deep root functions with whole plant response to soil resource variability.

**Material and methods** – Studies were completed in a Pennsylvania research vineyard designed to examine long-term responses of Noiret grapevine (*Vitis* hybrid) to rootstock genotype (Riparia vs. 101-14 MGt) and an under-vine fescue cover crop in comparison to herbicide (2x2 factorial). Absorptive roots (1<sup>st</sup> and 2<sup>nd</sup> order) were accessed up to 1-m depth with soil cores and root boxes (i.e., rhizotrons). Root systems were evaluated for several metrics: root length, morphology (e.g., diameter), transcriptomic profiles (RNA-seq), and secondary metabolites (LCMS).

**Results** – Our results from herbicide-treated plots indicated that with increasing soil depth, absorptive root length density decreased and morphological traits shifted (e.g., increased diameter); this suggested decreases in total resource uptake with depth. In comparison, the transcriptomic and metabolomic profiles had more muted differences between depth increments, indicating that functions of individual absorptive roots may not shift substantially with depth. A universal methodological challenge was accessing deep roots, which led to low sample numbers and statistical power. Though, when transcriptomes of known function were targeted, they clearly demonstrated that grapevines deepen N-uptake activity when cover crop was present and distinctly for each rootstock. This demonstrated the potential for transcriptomics to identify root functions with greater functional nuance than other approaches. Yet, more accessible methods based on morphology were still able to coarsely indicate deep root activity and clarify aboveground responses to cover crop. Taken together, the results from these studies suggested that examinations of deep roots (>40 cm) were necessary to disentangle the differing responses of grapevines on the two rootstocks to a cover crop. Future work can increase the accessibility of whole-grapevine research by standardizing protocols, expanding bioinformatic infrastructure, and garnering resources for the intensive nature of deep root research.

**Keywords:** Whole-grapevine, Roots, Omics, Physiology, Methods, Soil