

Exploring the inner secrets of grapevine: a journey through plant-microbe interactions

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Abstract

Throughout centuries of anthropocentric breeding, plants have been selectively bred to enhance their quality traits and yield, often overlooking the importance of neglected attributes, like those involved in the interactions with beneficial microorganisms. This phenomenon led to an alteration in the distribution of photosynthetic products, shifting from defence mechanisms to growth, commonly described as 'domestication syndrome'. Addressing the losses stemming from this condition is imperative just as unravelling the concealed communication between grapevines and beneficial microorganisms. To this aim, a Synthetic Community (SynCom) has been formulated, using grapevine endophytes and arbuscular mycorrhizal fungi, and applied to potted cuttings of diverse rootstock genotypes. Plant development and physiological parameters were carefully monitored throughout an entire growing season. Root samples were collected for: i) DNA extraction and metabarcoding analysis to identify the root-associated microbiota and ii) RNA extraction for transcriptomic analysis. Concurrently, leaf and root samples were collected for targeted metabolomics, focusing on compounds involved in microbial recruitment, including, among others, coumarins, strigolactones, salicylic acid, and jasmonic acid.

Employing an innovative multi-omics approach, phenotypic, physiological, biochemical, and molecular data will be integrated to improve our understanding of the complex interaction within grapevine and its associated microbiota. This could result in new breeding programs which will also consider these traits as selection criteria, thereby preserving the ability of grapevine to recruit beneficial microorganisms. Furthermore, these results will provide useful information for the development of a more effective SynCom to augment holobiont resilience and thus to promote more sustainable agricultural practices.

Keywords: Rootstock, Domestication syndrome, Endophytes, Microbial recruiting, Multi-omics.