SOIL–PLANT–MICROBE INTERACTIONS IN VINEYARDS: IMPLICATIONS FOR NUTRIENT CYCLING, GRAPEVINE NUTRITION AND SUSTAINABLE PRODUCTION

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Background.

Grapevine (Vitis vinifera L.) productivity, nutrient status and fruit quality depend not only on the physicochemical properties of the soil but on the diverse microbial communities that inhabit the rhizosphere and bulk soil, which mediate the transformation and supply of nitrogen, phosphorus and water to the vine [1]. Viticulture is a long-lived perennial cropping system in which reliance on synthetic fertilizers and fungicides has historically been high; however, rising input costs, climate change and the progressive restriction of copper-based and systemic fungicides are pushing the sector toward more biologically based management strategies that preserve and exploit the natural soil microbiome [2]. Beyond their agronomic role, rhizosphere and soil microorganisms have recently been linked to the sensory identity of wine through the concept of "microbial terroir" [3]. Evidence on these soil–plant–microbe interactions is nevertheless scattered across mycorrhizal physiology, soil microbial ecology, viticultural agronomy and oenology literatures, and is rarely synthesized within a single framework relevant to applied vineyard management.

Aim of the Study.

The aim of this thesis is to synthesize recent peer-reviewed evidence on the contribution of arbuscular mycorrhizal fungi (AMF), plant growth-promoting rhizobacteria (PGPR) and the broader vineyard soil microbiome to nutrient cycling and grapevine mineral nutrition, and to evaluate the implications of this evidence for sustainable, microbiome-informed vineyard management in warm-climate and semi-arid viticultural systems.

Materials and Methods.

Within a structured narrative literature review, 21 peer-reviewed sources — field and inoculation trials, metagenomic surveys, and review articles — were synthesized. The search was conducted in PubMed Central, MDPI, Frontiers, Springer Nature, Nature Portfolio and American Society for Microbiology (ASM) journal databases using combinations of the keywords vineyard soil microbiome, arbuscular mycorrhizal fungi, grapevine, plant growth-promoting rhizobacteria, rhizosphere, microbial terroir, cover crop, organic vs. conventional management, Trichoderma and grapevine trunk disease. Priority was given to studies reporting quantitative nutrient, colonization, yield, functional-gene or microbial diversity outcomes for Vitis vinifera, with particular attention to Mediterranean and other warm-climate or semi-arid viticultural systems comparable to major wine-growing regions worldwide.

Results and Discussion.

Field evidence on arbuscular mycorrhizal fungi is directionally consistent. AMF inoculation significantly increased leaf phosphorus concentration in Crimson Seedless grapevine relative to non-inoculated controls [4,5], while a five-region metagenomic survey in the Czech Republic showed that AMF colonization of the grapevine endorhizosphere (up to 98.7% of the LSU fungal community) tracked

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soil phosphorus, organic matter and pH, and collapsed almost entirely in the sub-region receiving the most frequent fungicide applications [6]. Comparable colonization-dependent benefits were reported in Italian integrated-pest-management vineyards, where AMF community composition shifted across phenological stages [7], and AMF community diversity buffered grapevine growth losses under severe black foot disease pressure [8] and differentially affected nutrient uptake across rootstocks [9]. Across the studies reviewed, optimal AMF benefit consistently coincided with moderate-to-low soil phosphorus availability and reduced fungicide input, underlining that chemical management strategy, not only soil chemistry, governs realized mycorrhizal benefit.

Plant growth-promoting rhizobacteria complement this picture through biological nitrogen fixation, phosphate solubilization, siderophore production and phytohormone synthesis [10], and bacterial taxa involved in nitrogen and phosphorus cycling were shown to co-occur with beneficial Pseudomonas and Bacillus populations in Pinot Noir rhizospheres under integrated pest management [7]. At the functional-gene level, metagenomic profiling of warm-climate vineyard soils found that organic management enhanced the predicted potential of nitrogen- and phosphorus-cycling enzymes relative to conventional management, even though overall bacterial functional redundancy buffered part of this difference [2] — indicating that management effects on the microbiome are often more detectable at the functional than at the purely taxonomic level.

Comparisons of cover cropping and whole-system management again show that realized microbial-diversity benefit is not guaranteed by management label alone. A review concluded that increasing inter-row plant functional diversity (legumes, C3/C4 grasses, non-leguminous forbs) increases soil microbial diversity and suppresses soil-borne pathogens, whereas frequent tillage, herbicide use and copper-based fungicides erode these gains [11]. Yet a ten-year Rheingau field trial found that fungal community composition, not overall richness, differed between integrated and organic/biodynamic management [12], a Friulian organic-versus-conventional comparison detected no significant difference in overall alpha- or beta-diversity despite shifts in specific phyla linked to soil organic matter [13], and — outside viticulture — a 21-year cropland experiment found that organic farming increased microbial richness mainly where organic fertilizer quality and quantity were high [14], while a geography-and-management survey of ten Italian vineyards found that location explained far more of the variance in soil microbiome composition than management practice itself [15]. Taken together, these partly divergent results caution that the diversity benefit of "organic" or "cover-cropped" management is real but strongly conditional on local soil, climate and input-quality context, rather than a fixed, transferable effect size.

Rhizosphere and soil microorganisms also connect below-ground agronomy to above-ground product quality through microbial terroir. Soil microbiota were shown to be a principal source of the microorganisms recovered on grape berries at harvest [16], and region-specific grape microbiome composition was subsequently linked to the fermentation-relevant metabolome and to distinguishable wine chemical profiles [17]. A global survey spanning 200 vineyard sites on four continents confirmed that soil microbiome composition reflects viticultural terroir at a global scale [18], while a high-resolution study of the Vino Nobile di Montepulciano appellation showed that even the twelve sub-zones of a single denomination carry distinguishable microbial signatures [19] — evidence that supports treating the vineyard microbiome as an oenological, and not merely agronomic, variable.

Finally, the soil microbiome contributes directly to phytosanitary management. Native Trichoderma populations isolated from vineyard soil displayed antibiosis and mycoparasitism against Phaeoacremonium minimum, a key grapevine trunk disease pathogen; Trichoderma abundance correlated

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positively with soil iron content and lower pH, and was reduced under intensive chemical spraying regimes [20]. This parallels the AMF-mediated suppression of the trunk-disease-associated fungi Cadophora and Roesleria reported in the Czech metagenomic survey [6], indicating that nutrient-cycling and disease-suppressive functions of the vineyard microbiome are mechanistically linked rather than independent management targets.

Conclusion.

The evidence reviewed supports a microbiome-informed, staged approach to vineyard soil management. Preserving and inoculating with locally adapted AMF should be prioritized in phosphorus-limited or water-stressed vineyard blocks, since realized benefit depends strongly on soil phosphorus status and on limiting fungicide frequency [4,5,6]. Functionally diverse inter-row cover cropping should be adopted primarily where it can be paired with reduced tillage and reduced copper/fungicide input, because diversity gains are conditional on these complementary practices rather than guaranteed by cover cropping alone [11,12,13]. Because location and local management history explain more of the variance in vineyard microbiome composition than any single practice in isolation [14,15], microbiome-based recommendations cannot be transferred uncritically between regions and require local metagenomic characterization before large-scale adoption. Where soil-derived biocontrol agents such as native Trichoderma are present, fungicide regimes should be timed and dosed to conserve rather than eliminate them [20]. Finally, because rhizosphere and soil microbial composition measurably contribute to grape and wine chemical identity [16,17,18,19], vineyard soil microbiome management should increasingly be considered not only an agronomic input-reduction strategy but also a lever relevant to regional wine typicity and quality differentiation.

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