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Grapevine Trunk Disease Microbiomes Shaped by Region and Genetics, Portuguese Study Finds

Research reveals environmental and genetic factors drive microbial diversity in diseased vines, offering clues for future disease management strategies

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Researchers in Portugal have found that the composition of the microbiome in grapevine trunks affected by trunk diseases is strongly influenced by both the grapevine's genetic background and the region where it is grown. The study, published in Scientific Reports, analyzed 97 symptomatic grapevines from two popular Portuguese cultivars, Touriga Nacional and Aragonez (also known as Tempranillo), across eight major wine-producing regions. The research team used next-generation sequencing to examine both fungal and bacterial communities present in the trunks of these vines.

Grapevine trunk diseases (GTDs) are a significant threat to vineyards worldwide, causing wood decay, reduced yields, and eventual vine death. These diseases are caused by a complex group of fungi that colonize woody tissues, including the trunk, arms, and sometimes roots. Once symptoms such as wood necrosis, dead arm, striped leaves, and dieback appear, infected plants often need to be removed to prevent further spread.

Despite efforts by growers to manage GTDs through chemical treatments, improved sanitation, pruning practices, and biocontrol agents, losses remain high. Understanding how the microbiome—the community of microorganisms living inside the plant—changes in response to disease could help develop new strategies for disease control.

The study found that the region where vines were grown had a major impact on the types of microbes present in diseased trunks. Environmental factors unique to each region appeared to shape which bacteria and fungi thrived inside the plants. The grapevine's genotype also played a key role: Touriga Nacional showed more pronounced changes in its trunk microbiome compared to Aragonez when affected by disease.

Researchers collected sawdust samples from symptomatic trunks and sequenced both fungal and bacterial DNA. They discovered that three fungal families—Phaeomoniellaceae, Togniniaceae, and Botryosphaeriaceae—dominated the samples. These families include genera such as Phaeomoniella, Phaeoacremonium, Neofusicoccum, Diplodia, and Botryosphaeria, all known to be associated with GTDs like

Esca and Botryosphaeria dieback. Most vines were co-infected with pathogens from both disease groups.

The study also looked at other factors such as vine age and rootstock but found that these had less influence on microbiome diversity than region or cultivar. However, they did observe that different combinations of these factors led to distinct microbial communities within the trunk.

In addition to cataloging which microbes were present, the researchers examined how these organisms interacted. They found evidence that some microbial genera may compete with GTD pathogens inside the trunk. This suggests that certain endophytic microbes—those living harmlessly within plant tissues—could potentially be harnessed as biocontrol agents to suppress disease-causing fungi.

The findings highlight the complexity of plant-microbe interactions in vineyards and suggest that both environmental conditions and grapevine genetics must be considered when developing strategies for managing trunk diseases. The research provides new insights into how regional differences and plant features shape the internal microbial landscape of grapevines suffering from GTDs.

This large-scale study is one of the first to examine how multiple factors—including region, cultivar, age, and rootstock—influence the microbiome of diseased grapevine trunks using advanced DNA sequencing methods. The results could inform future efforts to breed more resilient grapevines or develop targeted microbial treatments for GTDs.

The work was carried out by a team of scientists from Portugal and other European countries who specialize in plant pathology and microbiology. Their research adds important knowledge about how grapevine health is linked to its internal microbial community—a topic of growing interest as vineyards face increasing challenges from disease and changing climate conditions.