Influence of landscape structure and cropping system on microbial diversity and microbial interactions in vineyards

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Microbial diversity and microbial interactions support many ecosystem services, including the regulation of plant diseases. A current challenge is to robustly infer these microbial community properties from environmental DNA, and to assess their resistance and resilience to agricultural practices and other global change components. To meet this challenge, we first used an artificial microbial community to identify the bioinformatic approach best recovering microbial community properties from metabarcoding data. We then used this approach to assess the influence of landscape structure and cropping system (conventional *versus* organic) on microbial diversity and microbial interactions in vineyards. We focused on the fungal component of grapevine microbial communities as it includes major pathogens. Our results showed that bioinformatic pipelines using DADA2 to detect amplicon sequence variants were the most effective for recovering the richness and composition of the artificial fungal community. We also showed that fungal dispersal events from forest patches to adjacent vineyards hardly influence grapevine foliar fungal communities. In contrast, the cropping system had a major impact on grapevine foliar fungal communities. Community richness, diversity and evenness were significantly higher in organic plots at the time of sampling, and community composition differed significantly between cropping systems. Fungal association networks also differed, but the high turnover of associations among plots did not allow us to reveal ecological interactions between fungal species. These findings suggest that microbial association networks inferred from metabarcoding data can capture variations in ecosystem functioning but are not robust enough to monitor the disease regulation service provided by the plant microbiota.