Best talk / PhD student

Cropping system shapes foliar fungal networks of grapevine.

Charlie Pauvert[1], Jessica Vallance[2,3], Laurent Delière[2], Marc Buée[4], Corinne Vacher[1]
1BIOGECO INRA, Univ. Bordeaux, 33615 Pessac, France.
2INRA, UMR 1065 Santé et Agroécologie du Vignoble, ISVV, F-33882 Villenave d'Ornon, France.
3Université de Bordeaux, Bordeaux Sciences Agro, UMR 1065 SAVE, F-33175 Gradignan, France.
4INRA, UMR 1136 Interactions Arbres/Micro-Organismes, F-54280, Champenoux, France.
* charlie.pauvert@inra.fr

Microbial networks support many ecosystem services, including disease regulation. A current challenge is to reconstruct these networks from environmental DNA, and to assess their potential adaptation and resilience to environmental disturbances. Here, we investigated the impact of the cropping system on foliar fungal networks of grapevine. Fungal association networks were reconstructed from metabarcoding data in three organic plots and three conventional plots, after 30 having selected the best bioinformatic pipeline using a fungal mock community (about 200 fungal strains) as standard. A total of 120 networks were inferred for each plot by varying the network construction parameters in SparCC. Whole-network and node-level topological properties were computed and compared between cropping systems. The dissimilarity between networks was calculated and partitioned into the dissimilarity due to both turnovers of associations and species. We showed that foliar fungal α-diversity was significantly higher in organic plots at the time of sampling, and that the community composition significantly differed between cropping systems. Erysiphe necator, a major foliar fungal pathogen of grapevine, was significantly less abundant in organic plots than in conventional plots, and its centrality in the association networks was higher. The dissimilarity of networks between cropping systems was mainly due to changes in associations rather than changes in species composition and this result was robust to variations in network construction parameters. This latter finding highlights the importance of monitoring changes in microbial association networks, in addition to changes in microbial community α-diversity and composition.

References

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Keywords: network inference, microbial networks, fungal pathogen, metabarcoding, phyllosphere, grapevine, organic farming