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Type of presentation:

Oral presentation

Title:

Identifying microbiota patterns important for plant protection using machine learning in synthetic community experiments

Authors:

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Abstract (300 words maximum): :

Plant-associated microbiomes contribute to host phenotypes such as resistance to biotic and abiotic stresses. While beneficial candidate strains contributing to such host phenotypes can be tested individually, strain performance may vary in different biotic contexts. Therefore, the identification of beneficial strains within a microbiome can provide valuable insight into their potential to impact plant health. We developed an experimental and analytical approach to explore properties relevant for a microbiota-conferred host phenotype, here plant protection, in a synthetic community context. We screened 136 randomly assembled synthetic communities (SynComs) of five strains, followed by classification and regression analyses as well as empirical validation. We identified strain identity as the most important predictor of pathogen reduction, with machine learning algorithms improving performance compared to random classifications (94-100% versus 32% recall) and non-modelled predictions (0.79-1.06 versus 1.5 RMSE). Validation experiments confirmed three strains as the main drivers of pathogen reduction individually and in combination, and two additional strains that conferred protection in combination. Beyond the specific application presented in our study, we provide a framework that can be adapted to identifying features relevant for microbiota function in other biological systems. Additionally, further investigation of function and abundance of these driver strains in their natural microbiota contexts will drive our understanding on applicability of potential biotic interventions in agricultural systems

and beyond.

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