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Modelling approach to design innovative spatial strategies to control black leaf streak disease

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Abstract

Black leaf streak disease (BLSD), due to the airborne ascomycete *Pseudocercospora fijiensis*, is the main constraint of banana production for exportation by damaging leaves and impacting fruit ripening and yield. In any producing country in the world cultivating very susceptible varieties, the disease is managed by frequent aerial applications of fungicides (about 50 in Costa Rica). Due to fungicide resistance and considering environmental impacts, such frequent fungicide strategies are not durable. As experiments are difficult to implement at the scale of a production basin (e.g. several hundred hectares), modelling is a key approach to identify innovative scenarios to reduce the use of pesticides while efficiently and sustainably controlling the disease. In this study, we assess the efficacy of different spatiotemporal strategies to reduce pesticide use. These strategies, chosen with banana producers, are either directly based on fungicide applications (reduction of application frequency, spatial coverage, or dose), or based on the deployment of resistant cultivars (increase in spatial coverage, resistance efficiency, choice of target pathogen traits). To test these strategies, we adapted a published mathematical spatially-explicit model called *landsepi* (Rimbaud et al., 2018) to simulate BLSD epidemics in a real agricultural landscape. The adaptation of the *landsepi* model is undergoing and consists in modifying plant growth and epidemiological parameters. Using this model, we plan to compare the yield and epidemiological control provided by the simulated control strategies in a real 300-ha banana production basin. More than 11,000 simulations are currently running and will help identify the most promising strategies to test in the field.

Reference

Rimbaud L, Papaïx J, Rey J-F, Barrett LG, Thrall PH (2018) Assessing the durability and efficiency of landscape-based strategies to deploy plant resistance to pathogens. PLoS Comput Biol 14(4): e1006067. https://doi.org/10.1371/journal.pcbi.1006067