Simulation Model of a Tropical Foliar Epidemic Disease at Plant Scale: Case of Black Sigatoka on Banana

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Black sigatoka (BS), caused by the fungal pathogen *Mycosphaerella fijiensis*, is considered as the most destructive foliar disease of banana and plantains. Controlling BS is essential to the export production because of the important damages caused to fruit quality. The main current control consists in frequent aerial fungicide applications and deleafing, which is not a safe and durable solution. To overcome this practice, CIRAD has set up a banana breeding program to create BS partial resistant varieties. However evaluation of resistances efficacy puts constraints in time (long crop cycle) and space (numerous experimentals plots to set up). To help in resistant hybrid selection, a mechanistic simulation model of BS was designed. This model aims to better understand the pathosystem and to identify the most effective resistance components. The model was developed in discrete time at plant scale. It describes, without spatialization and in optimal climatic conditions, the development of the lesions during several crop cycles. Two sub-models are defined: the first one describes simply the growth of the banana in a deterministic way (9 parameters); the second one describes the complete and detailed epidemic cycle by integrating stochasticity (12 parameters). Infectious cycle data were collected in both controlled and natural infestation conditions on susceptible and resistant cultivars. Data used for the model calibration were collected over a period of three months on the same kind of cultivars. The estimation of the model parameters was realized in a bayesian framework using MCMC (Markov Chain of Monte Carlo) methods such as the Metropolis-within-Gibbs algorithm. First result of sensitivity analysis allow to quantify the epidemiological impact of each resistance components.