

# Simulation model to assess the efficacy of host partial resistance: case of black leaf streak disease on banana

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## INTRODUCTION

- Few epidemiological models exist combining plant and epidemic development and integrating two (asexual and sexual) modes of pathogen reproduction. None exists for the Black leaf streak disease (BLSD), the most severe foliar disease of bananas, due to the heterothallic ascomycete fungus *Mycosphaerella fijiensis*.
- Previous studies have shown that partial resistance of banana may act on the 3 of the 4 main steps of the BLSD infectious cycle (Figure 1) : infection, lesion growth and sporulations.
- The aims of this study are to propose a simulation model of banana/*M.fijiensis* pathosystem at plant scale, to evaluate the impact of partial resistance components on the BLSD severity and to estimate epidemic cycle parameters with dynamical experimental data.

## THE MODEL

- A mechanistic model** was developed in discrete time (1 day step) at plant scale. It describes both banana development and BLSD process over several crop cycles and under optimal epidemiological conditions. The spatial unit of the model is 1mm<sup>2</sup> of lesions.
- Two submodels** (Figure 2):
  - a **deterministic model** of banana growth with simplified architecture; 10 parameters are implied.
  - the **complete detailed epidemic cycle** integrating stochasticity into the reproductive process of the pathogen; 19 parameters are implied.

Example of formalization:  
[1] Number of infections on the part of leaf (c) of leaf (l) in t :

$$Infection_{l,c}(t) = \frac{vacant\_area_{l,c}(t)}{total\_area_{l,c}(t)} IE \cdot exp^{-b \cdot l} (A_{l,c}(t) + S_{l,c}(t))$$

- The **main output** of this model is the BLSD severity (i.e.% necrotic area).

## SIMULATIONS

- The **prior knowledge of parameters** based on available data issued from field and controlled experiments, expert opinion and literature, were used to realize simulations over several crop cycles (Figure 3).

**Difference of variety susceptibility**  
**= different values of IE, IP, LG, ASC and SSC epidemic parameters**

- Results show that:**
  - the highest level of BLSD severity is on the susceptible variety with the highest LG.
  - the lowest level is on the partial resistant variety with the lowest IE.

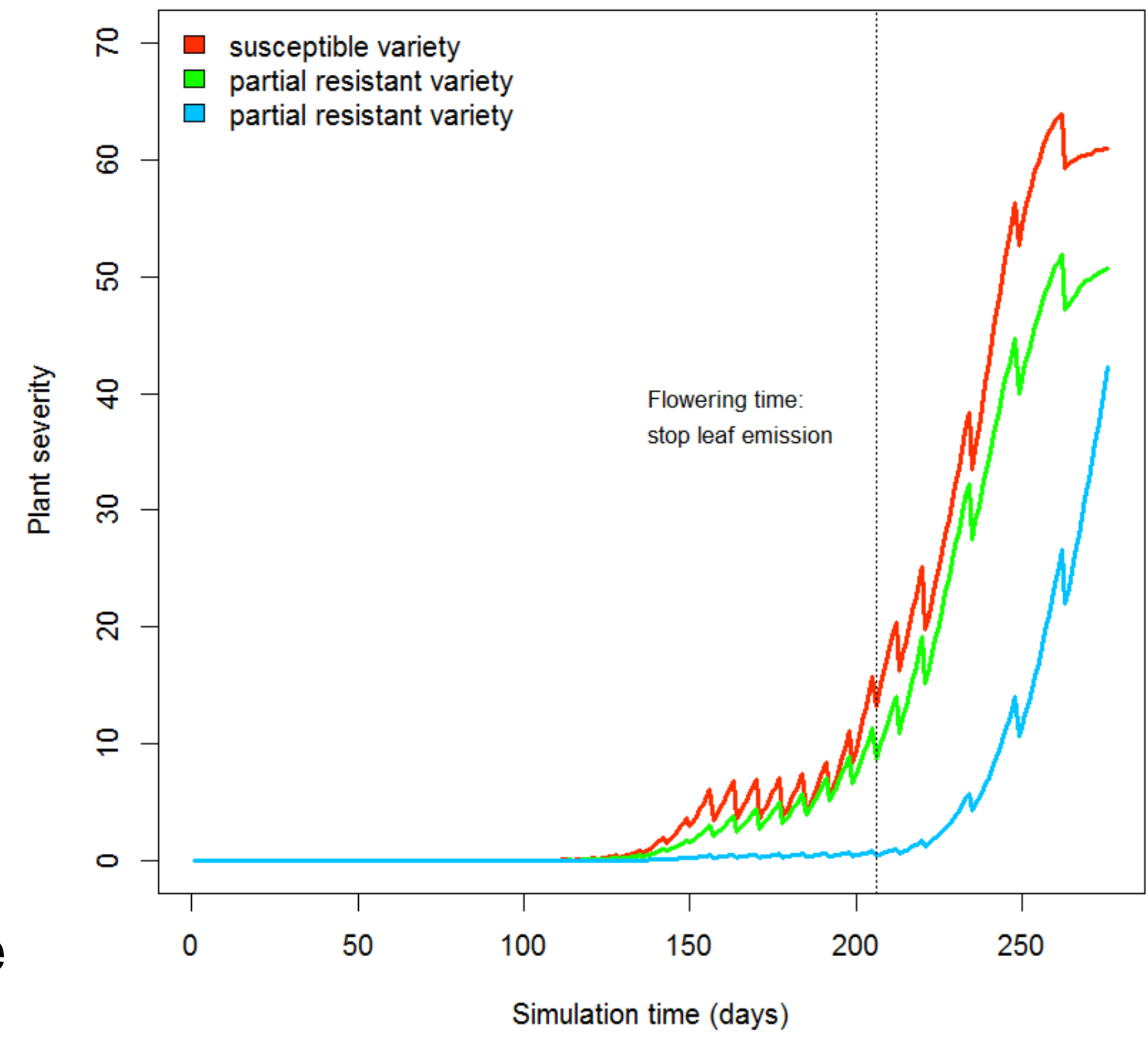
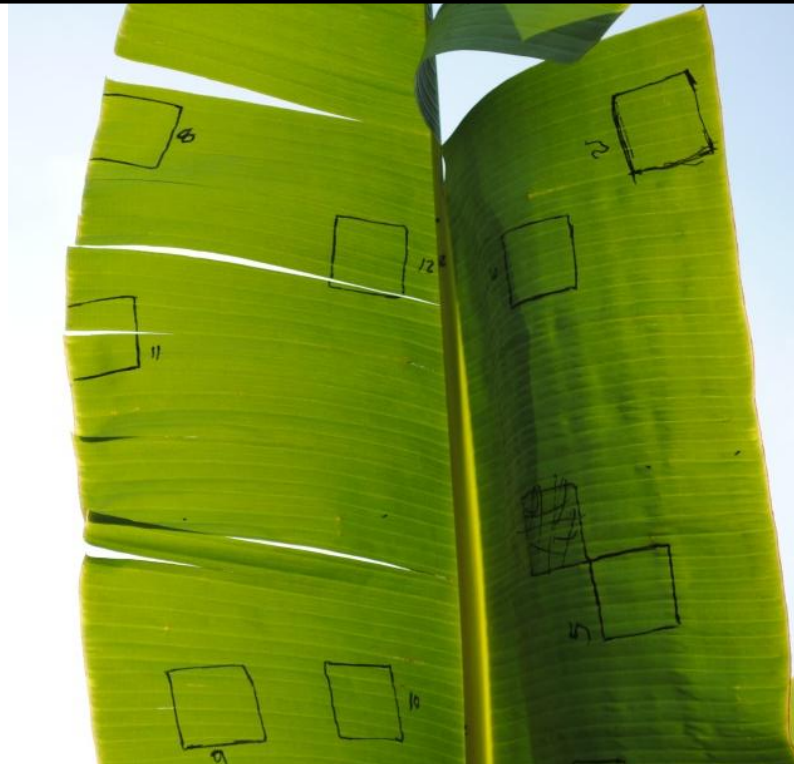


Figure 3. Simulated BLSD severity kinetic on 3 different varieties differing on epidemic cycle parameters during one crop cycle

## MODEL CALIBRATION

- Inference on the epidemic parameters is being performed by Bayesian methods using available and newly collected data.
- Newly collected data:** Kinetics of number and size of lesions on 3 leaves during their complete life. Leaves were divided in zones and BLSD spots were drawn during 3 months and analyzed using image analysis software



- Bayesian framework:** MCMC methods such as Metropolis within Gibbs algorithm (Robert and Casella, 2010)
- $$\pi_m(\theta_m | data) \propto L(data | \theta_m) \cdot \pi^0(\theta_m)$$
- $$L(data | \theta_m) = \prod_t \prod_l \prod_c \frac{\exp(-(severity_{l,c}(t) - severity_{l,c}(t)^*)^2 / 2\sigma^2)}{\sqrt{2\pi\sigma^2}}$$
- Where  $severity_{l,c}(t)^*$  are the severity values predicted by the model and  $\pi^0(\theta_m)$  are priors, based on available data.

## CONCLUSION / PERSPECTIVES

- We built a specific simulation model combining the banana growth and the complex epidemic cycle of *M.fijiensis*. First sensitivity analyses suggest that lesions growth has the main effect on BLSD severity. Experimental field data and the use of a Bayesian framework will enable us to estimate epidemic cycle parameters and their uncertainties. This model will be helpful both for geneticists by allowing to test the efficacy of partial resistance and for agronomists by identifying the most efficient cultural practice in disease control.

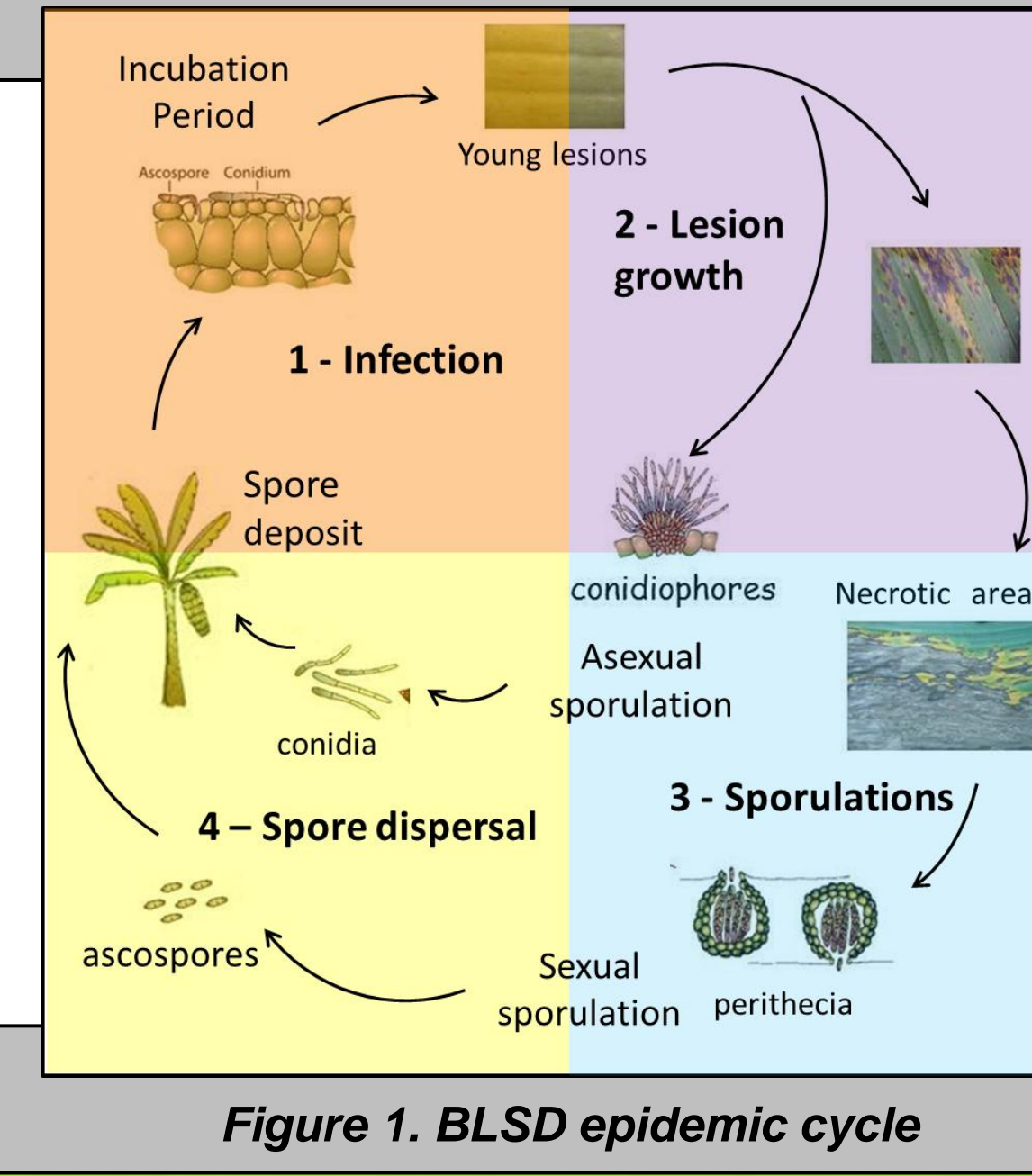


Figure 1. BLSD epidemic cycle

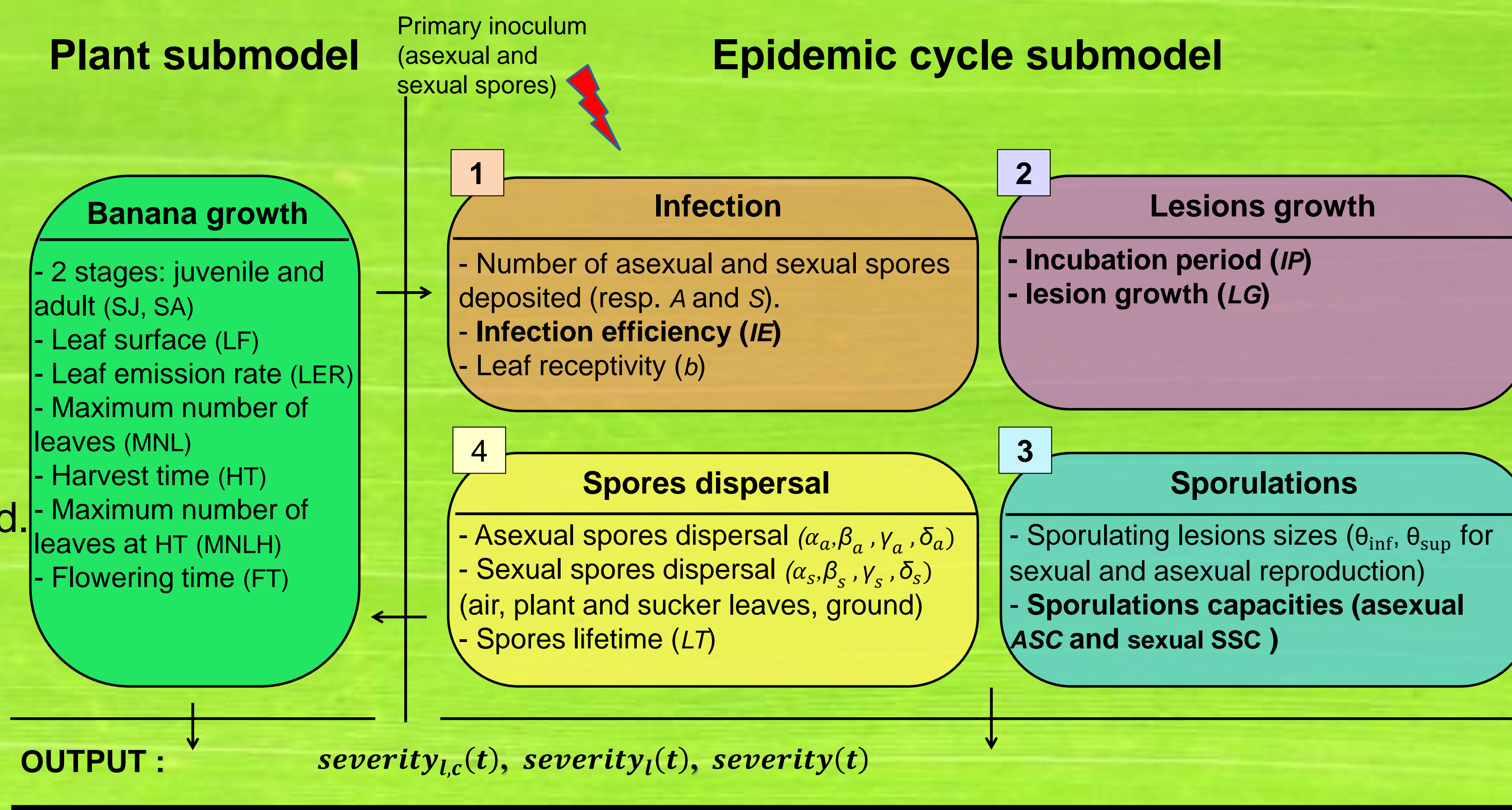


Figure 2. Overview of the banana/*M.fijiensis* model and the articulation of different submodels

## SENSITIVITY ANALYSIS

- We performed a sensitivity analysis to quantify the impact of 5 epidemic parameters and their interactions on the decomposition of the disease severity variance (Figure 4).
- We used **FAST method** to calculate the global sensitivity indices (Saltelli et al., 2000) from 200 simulations for each parameter.

**Main effect** = First order index, influence of one parameter independently of the others.

**Interactions** = Total index, influence of the parameter in combination with the others

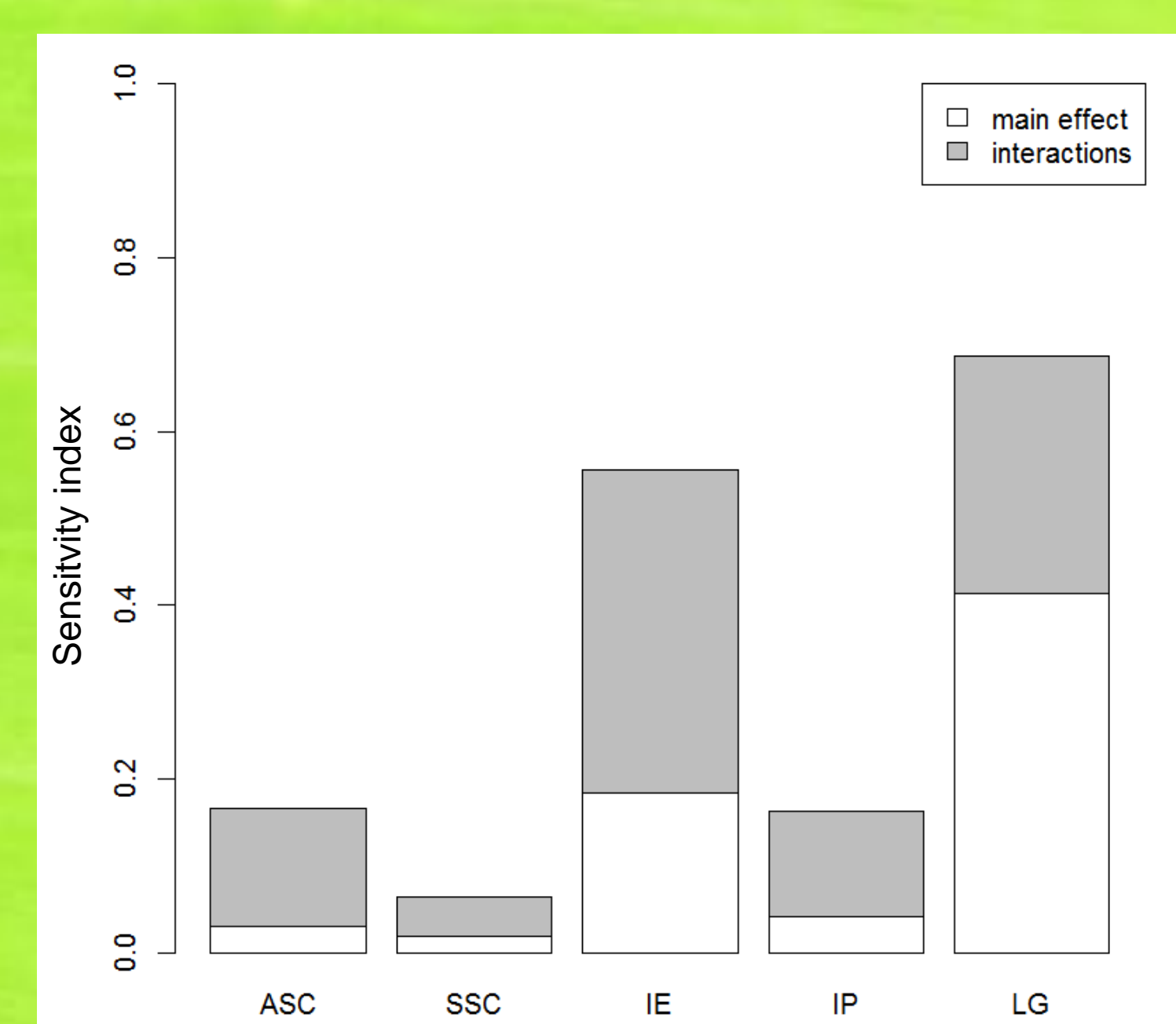


Figure 4. Evaluation of first order and total sensitivity indices on 5 epidemic cycle parameters.

- LG and IE** parameters have the highest first order indexes (resp. 0,41 and 0,18), explaining the largest part of severity variance.
- ASC, SSC and IP** have no significant influence (index < 0,1)