





Combining field epidemiological information and genetic diversity to understand *Phytophthora megakarya* dispersion in young cocoa plantations in Cameroon

Ndoungué Djeumekop MM, Blondin L, Herail C, Ten Hoopen GM, and Neema C





Cacao tree and P. megakarya

Black pod rot due to *Phytophthora* spp <u>In Africa:</u> *P. palmivora* and *P. megakarya*

<u>P. megakarya:</u>

- Most aggressive species (80 to 100% losses)
- Original host(s) unknown
- Free water, high humidity and relatively cool conditions
- 5 clonal lineages in Africa

P. megakarya genetic diversity in Africa



(Mfegue, 2012)

Reproduction and Infection cycle of P. megakarya

(Gregory et al, 1981; Griffin et al., 1981; Mfegue, 2012)



Main dispersion mechanism: rain splashing

Reproduction cycle

Infection cycle

Objective

Understanding the origin of primary infections and their subsequent spread in cacao plantations can help to improve disease management

Integration of population genetics and plant disease epidemiology can deliver relevant information about dispersal mechanisms

Study progression of first *P. megakarya* infections and their genetic diversity in young cocoa plantations through disease monitoring with SSR markers

Experimental site

- 4 cacao plantations established in 2006
- 3 villages: Bakoa, Kedia and Ngat
- On soil free of *P. megakarya*
- Known cacao germplasm associated with specific crops
- In different environments

Focus here on Kedia



Data collection and analysis

Farm monitoring from 2009 to 2016

- Weekly observations on each tree for presence/absence of pod infection
- Analysis of disease progression

Collection of P. megakarya strains

• Isolation of *P. megakarya* from cacao pods, soil and water samples

Genetic characterization of P. megakarya strains

• Genotyping with 14 microsatellite markers and analysis using GenAlEx

Disease progression in Kedia



Genetic diversity in Kedia

MLGs distribution in experimental plot and its surrounding environment

Total number of MLGs observed on pods, soil and water



MLG 11 (65 %)

Exp. Plot: experimental plot **SE**: surrounding environment

Discussion and conclusion

- Primary infections of *P. megakarya* can originate from neighboring cacao plantations or water
- One clone of *P. megakarya* (MLG 11), primary responsible for disease epidemics

Establishment of cacao plantations away from flood prone areas and preventing infections from neighboring cacao plantations

Acknowledgements



And of course our Farmers !









PCP Agroforesterie Cameroun Pôle de compétences en partenariat