Dispersal processes underlying the recent pandemic caused by the plant pathogenic fungus *Mycosphaerella fijiensis*

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**CONTEXT & OBJECTIVES**

How plant pathogenic fungi spread is the first question to consider for understanding the emergence of diseases caused by such organisms.

The ascomycete fungus *Mycosphaerella fijiensis*, causing the black leaf streak disease of banana, is an example of a recent pandemic in agriculture and a good model to address this question in the case of an aerial plant pathogen. The pandemic started around 1960 from the South-East Asia and *M. fijiensis* has spread to almost all banana producing areas for the last 40 years.

Previous studies of genetic structure of populations have highlighted a higher genetic diversity in South-East Asia, and high levels of genetic differentiation between and within continents, suggesting that founder events have accompanied the pandemic (Carlier et al., 1996; Rivas et al., 2004 Mol. Ecol.).

A further investigation of the dispersal processes underlying the pandemic is now required.

**Objectives:**
- To infer historical and demographic events (bottlenecks, admixture) undergone by invading populations
- To reconstruct global routes of dissemination and clarify dispersal modes of the pathogen

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**PHYLLOGEOGRAPHY STUDY AT GLOBAL SCALE**

- **Molecular phylogenetic analysis**
  - 120 *M. fijiensis* individuals
  - 8 sequence-based nuclear markers
  - Phylogenetic tree reconstructed by the maximum likelihood method
  - Low level of intraspecific polymorphism
  - Markers of old events of introductions
- **Explorative population genetics analysis**
  - 23 populations (~700 individuals)
  - 21 microsatellite markers

These different analysis were congruent and suggested strong hypotheses:
- An only successful introduction in AFRICA, probably associated with a bottleneck, explaining emergence of an homogeneous group comparatively to the other continents
- A pattern of genetic admixture in AMERICA, possibly due to multiple introductions
- Asian origins for all these introduction events certainly from transport of infected plant materials

**Perspective:** test different scenarios and estimate parameters using ABC (Approximate Bayesian Computation) method

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**SPATIAL GENETIC ANALYSIS AT LOCAL SCALE**

- **Along a 300-km-long transect**
  - (Halketty et al., 2010 Mol. Ecol.)
  - 10 Populations (~290 individuals)
  - 19 microsatellite markers
  - Diversity and differentiation indices, Clustering analysis (STRUCTURE)
- **On a 50x50 km area**
  - (Rieux et al., 2011 Mol. Ecol.)
  - 2D sampling (105 sites, 570 individuals)
  - 17 microsatellite markers

- The Cameroon situation, an example of a recently (~1980) colonized area
- A genetic discontinuity was detected at the middle of the transect (between sites 5 and 6)
- An isolation by distance analysis detected the above discontinuity suggesting gradual dispersal through ascospores
- The genetic discontinuity was sharp delimiting 2 populations. No landscape features matched this discontinuity = colonization trace (e.g. through gene surfing)
- No isolation by distance ⇒ high effective population size in *M. fijiensis* is suspected

**Perspective:** estimate dispersal from allelic clines detected between the 2 populations