LANDSCAPE GENETICS AND GENE FLOW IN THE BANANA PATHOGENIC FUNGUS *MYCOSPHAERELLA FIJIENSIS*

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Among the different evolutionary forces driving population genetics, gene flow related to dispersal plays a major role in local adaptation processes. However, up to now very few studies on plant pathogenic fungi have attempted to decipher gene flow patterns at the scale of a production area.

The causal agent of the black leaf streak disease on Banana crops, *Mycosphaerella fijiensis*, can be considered as a good biological model to study the adaptive potential of plant fungal pathogens: populations show relative demographic stability and panmixia so that most methods of population genetics can be properly applied. For gene flow analysis, we focussed on small farming production units which are scarcely distributed among large producing areas and rarely subjected to fungicide spraying. Previous population genetic studies of *M. fijiensis* allowed us to define the spatial scale to be considered and warned us about the effect of some putative barriers for gene flow analysis.

Here we aimed at taking into account landscape in our population genetic analysis to i) delineate pathogen populations and determine the nature and importance of the barriers to gene flow and ii) assess *M. fijiensis* dispersal pattern within a continuous population. Around 850 isolates were sampled in a referenced area in Cameroon and genotyped using 22 microsatellite markers. The effect of landscape features on gene flow was investigated using a population genetics method explicitly taking spatial location of samples into account (Landscape genetics). Two distinct populations were detected across a 50x50 km area, but no landscape feature matches the observed genetic discontinuity. Within the largest of the two pathogen populations, the dispersal pattern of *M. fijiensis* was examined using the continuous model of isolation by distance. The observed dispersal pattern is further discussed in the light of simulation results predicting dispersal patterns according to some realistic demographic scenarios for this plant pathogenic fungus.