Genetic diversity and population structure of Moniliophthora roreri in cocoa producing areas in Guatemala

José A. Ruiz-Chután[1, 2], Julio E. Berdúo-Sandoval [1], Luis Montes[1], Marie Kalousová [2], Bohdan Lojka [2], Carlos E. Villanueva-Gonzalez [2], Amílcar Sánchez-Pérez [1]

Introduction

Moniliasis, caused by *Moniliophthora roreri*, is one of the most devastating cocoa diseases in the western hemisphere. From its centre of origin in the Magdalena Valley, Colombia [1], the pathogen has spread to eleven countries, including Guatemala, causing severe production losses [2]. Despite reports of the dispersal of *M. roreri* to Central America from a single clone [3], the pathogen's genetic diversity has not been studied in Guatemala, and the biological evolution of the pathogen is unknown. The main objective of this study was to assess the genetic diversity and population structure of *M. roreri* in Guatemala to better understand the colonization process of the pathogen in the country.

Methodology

From five cocoa-producing areas (Figure 1), we obtained 69 *M. roreri* isolates. DNA was extracted from the isolates and fingerprinted with AFLP and the fragments were visualised using polyacrylamide gel electrophoresis. Data analysis – genetic diversity indexes (GenAlEX[4]), clustering analysis (Structure [5] DAPC [6] PCA [7])

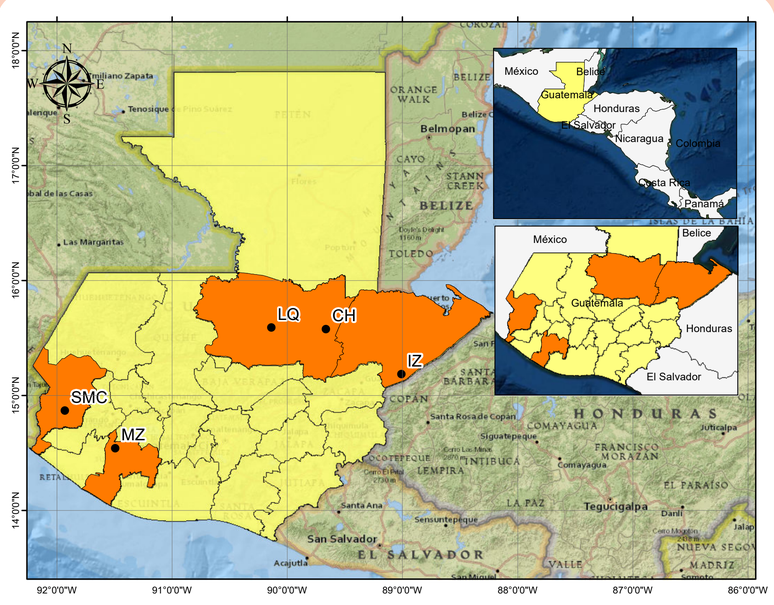

Figure 1. Collecting sites

Table 1. Measures of genetic diversity of five populations of *M. roreri*.

Population	Region	N	Polymorphic loci	PLP	Na	Ne	I	*Hj*
LQ	Southwestern	15	15	10.71	0.80	1.232	0.027	0.143
CH		13	16	11.43	1.15	1.243	0.072	0.172
IZ		15	23	16.42	0.95	1.195	0.067	0.136
MZ		12	19	13.57	1.30	1.272	0.052	0.188
SMC		14	14	9.29	1.30	1.360	0.071	0.226
Mean		13	17.4	12.28	1.10	1.259	0.0578	0.173

N= population size, PLP= proportion of polymorphic loci, Na= number of alleles, Ne= Effective number of alleles, I= Shannon's diversity index, *Hj*= Nei's genetic diversity index

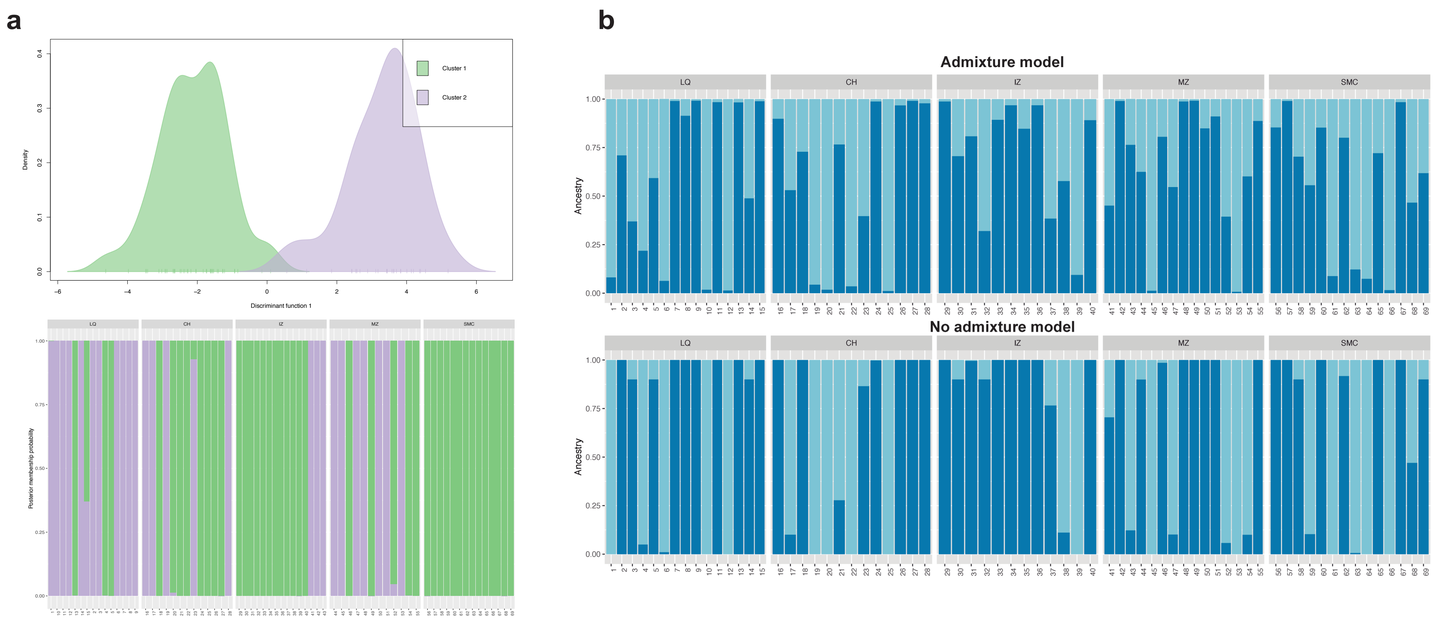

Figure 2. a) Population genetic structure based on a Discriminant Analysis of Principal Components (DAPC). b) Assignment of probabilities for the 69 isolates of *M. roreri* in each group inferred by STRUCTURE.

Results

The results showed that population structure could be composed of two genetic clusters (Fig 2a, 2b). However, a weak structure was observed (Fig 3a, 3b). The population SMC, MZ and CH showed high diversity, whereas population LQ and IZ presented lower levels of genetic diversity (Table 1). Molecular analysis of variance (AMOVA) showed a variance between regions, populations and within populations of 3%, 6% and 91%, respectively. Nonetheless, Phi statistics were not significant (Figure 4).

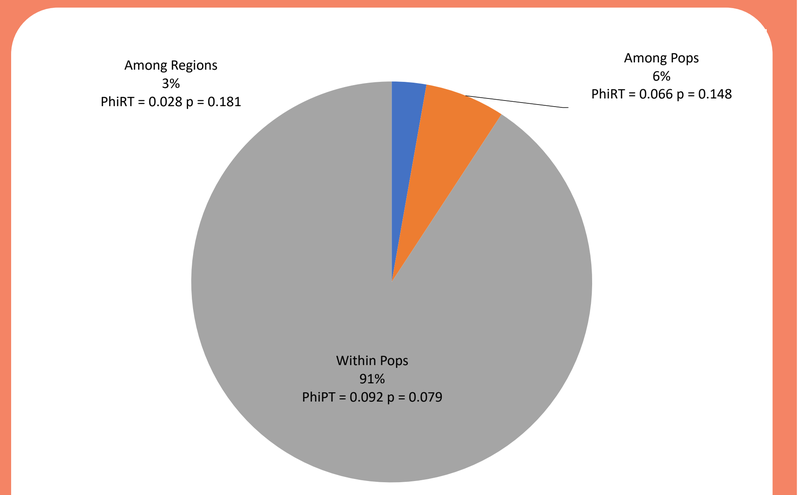

Figure 4. Percentage of molecular variance and Phi statistics

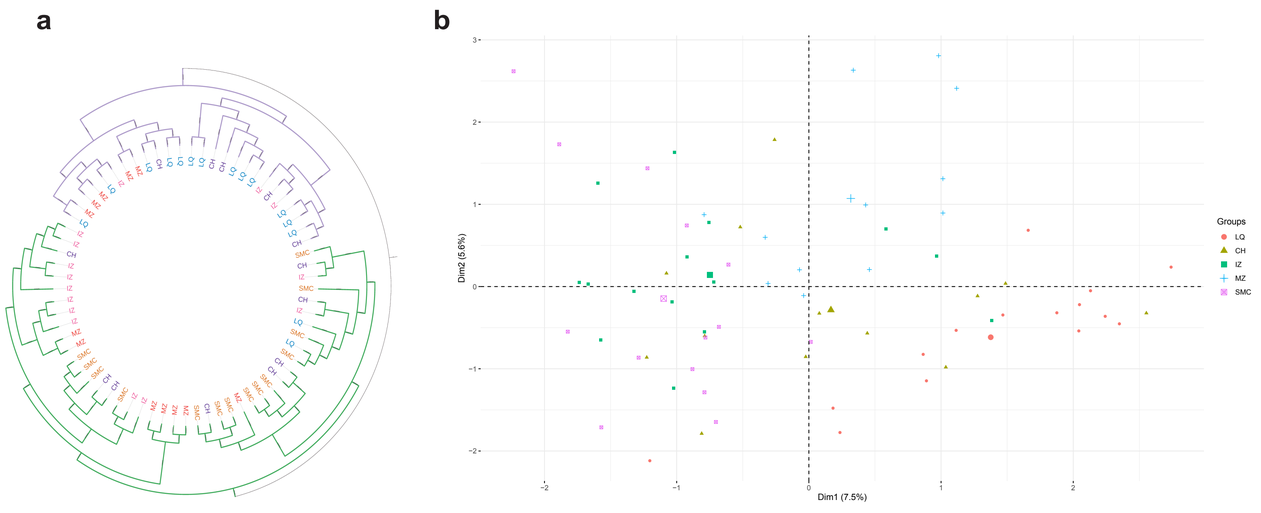

Figure 3. *a)* Dendrogram constructed with UPGMA showing the genetic relationship of the 69 isolates of *M. roreri. b)* Principal Components Analysis (PCA) of the five analysed *M. roreri* populations in Guatemala based on a dataset of AFLP. PCA dim 1 and 2 represent 7.5% and 5.6% variation, respectively.

Conclusions

The low genetic diversity and lack of population structure are consistent with a recent introduction and invasive phase of the pathogen in the country that can generate new and increasingly virulent genotypes. We suggest the constant monitoring of the biological evolution of the pathogen, quarantine practices that limit the dispersion of the pathogen to a minimum, and evaluations of different cocoa clones tolerant to the new genotypes of *M. roreri*.

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1 Dirección General de Investigación, Universidad de San Carlos de Guatemala

2 Czech University of Life Sciences Prague, Faculty of Tropical AgriSciences

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