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## Genetic Diversity and Population Structure of *Moniliophthora Roreri* in Cocoa Producing Areas in Guatemala

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### Abstract

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, the pathogen has spread to eleven countries, including Guatemala, causing severe production losses. Despite reports of the dispersal of *M. roreri* to Central America from a single clone, the genetic diversity of the pathogen has not been studied in Guatemala, and the biological evolution of the pathogen is unknown. To clarify this aspect, 69 isolates of *M. roreri* obtained from four cocoa-producing departments were analysed, and genetic diversity was evaluated using the molecular marker AFLP. We identified a low level of genetic diversity by the Shannon index (0.0578) and the proportion of polymorphic loci (12.28 %). The overall genetic diversity ( $H_t$ ) was 0.1289, and the mean genetic diversity within populations ( $H_w$ ) was 0.1310. Molecular analysis of variance showed a variance between regions, populations and within populations of 3 %, 6 % and 91 %, respectively, indicating a weak genetic structure. The Bayesian clustering analysis implemented in STRUCTURE revealed that the most likely number of genetic groups in the data was two, although we did not observe geographical differentiation. The low genetic diversity identified is congruent with reports of the colonisation process of *M. roreri* in Central America through a single haplotype. However, given the high mutation rate of *M. roreri*, we suggest constant monitoring of its evolution, quarantine practices that limit its dispersion. We also recommended evaluations of cocoa clones tolerant to the new *M. roreri* genotypes preventing increased losses to Guatemalan producers.

**Keywords:** AFLP, AMOVA, gene flow, moniliasis