

# Characterization and evolution of pathogenic *Phytophthora megakarya* populations on cocoa in Cameroon (1986-2002)

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Figure 1. Number of *P. megakarya* genotypes isolated from cocoa at each survey site.

**In Cameroon, the predominant pathogenic *Phytophthora* species on cocoa, *P. megakarya*, causes almost 50% pod losses on average. This species is only found in Africa. It comprises two populations, one in West Africa, the other in central Africa (figure 1). In order to gain a clearer understanding of the different mechanisms involved in the development of this pathogen in Cameroon, depending on geographical origin and environmental conditions, the structure of isolated populations was studied.**

## Material and methods

Over three periods, 360 strains were isolated from pods:

- 1986 – 1991: 135 strains,
- 1994 – 1996: 146 strains,
- 1999 – 2002: 79 strains.

After isolation, the *P. megakarya* strains were purified and added to the CIRAD collection in Montpellier. The mating type of each strain was determined by *in vitro* comparison with compatible strains available in the collection. Molecular characterization of the strains was carried out by RAPD (Random Amplified Polymorphism DNA) using the protocol developed by Nyassé, in 1999.

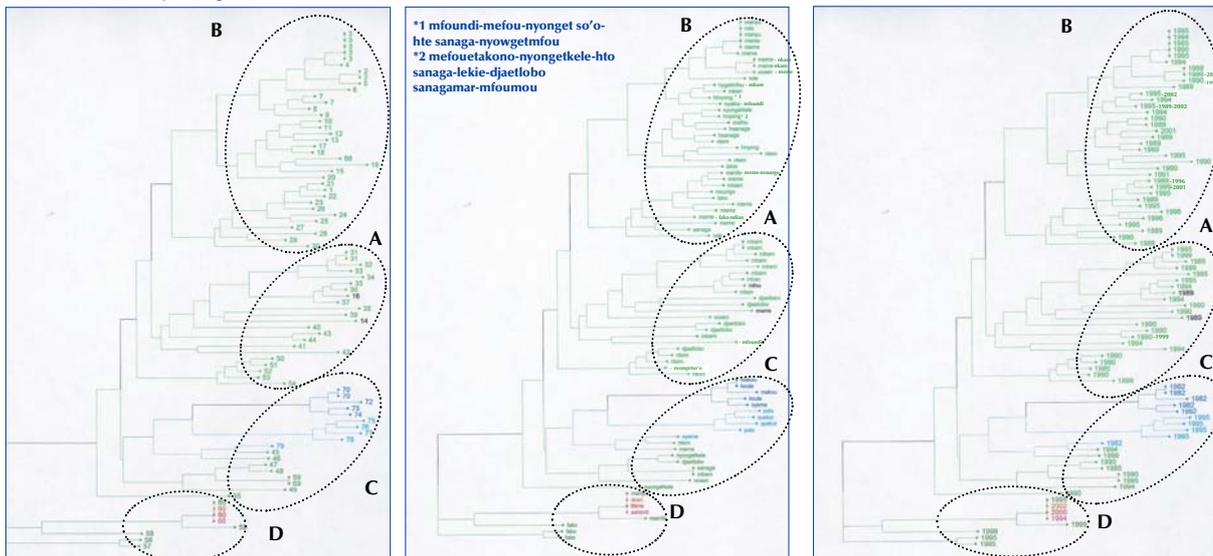
- 9 primers were studied: OPM4, OPM6, OPM7, OPM17, OPR4, OPR5, OPR6, OPR11, OPR14.
- 56 markers were selected.

## Results

The different RAPD genotypes revealed in Cameroon are shown in figure 2, their geographical origins and the years of their isolation are indicated in figures 3 and 4.

- 62 *P. megakarya* genotypes were characterized. All were of the A1 mating type, apart from genotypes 14 and 42.
- In Cameroon, 4 groups of genotypes were separated.
  - ✓ Group A mostly occurred in Mbam (Centre region) and in the South (Dja and Lobo, Ocean and Ntem), but these genotypes have become less and less characterized since 1994.
  - ✓ Group B was the most geographically represented group, with three sub-groups: the first existing in the West and Centre, the second in the Centre-East, and the third mostly in the West. These genotypes have become increasingly characterized since 1994.
  - ✓ Group C was related to strains from Gabon and São Tomé, and occurred in the Centre-South and South (Gabonese border).
  - ✓ Group D belonged to the population of West African strains, and this group was isolated on the Nigerian border and in the Fako region.

Figure 2 to 4. Classification in 4 groups of *P. megakarya* strains isolated in Cameroon (green) and compared to those from Gabon (pale blue), São Tomé (dark blue) and West Africa (Ivory Coast: brown; Togo; Ghana: violet), based on their genotype obtained by RAPD (figure 2), on their geographical origin (figure 3) and on the isolation year (figure 4).



Genotype	Year of <i>P. megakarya</i> strain isolation		
	1986-1990	1994-1996	1999-2002
Barombi-Kang (West region)			
1	-	-	*
2	*	*	*
3	-	*	*
4	-	*	*
5	*	*	-
21	-	*	-
24	-	*	-
25	-	*	-
Mengang (Centre-West region)			
7	-	*	*
8	*	*	*
11	-	-	-

Table 1. Characterization of *P. megakarya* genotypes isolated from cocoa pods at two IRAD research stations in Cameroon.



Photo. Cocoa pod attacked by *P. megakarya*.

## Discussion and conclusion

Through this study, it was possible to monitor the evolution of *P. megakarya* strains over time. Given the mostly clonal reproduction system (A1 mating type) of the 4 groups of strains existing in Cameroon, the structure of these pathogen populations between 1986 and 2002 was found to be highly stable. However, at Barombi-Kang for example, some genotypes (1, 2 and 3) gradually adapted to the environmental conditions at that station and took over from the other genotypes (4, 5, 21, 24 and 25) which existed up to 1996 (table 1). Genotype 2 has persisted since 1986 on cocoa clones susceptible to black pod; however, since 1999, genotype 1 has been characterized on clones judged to be resistant. Consequently, during resistance screening tests on cocoa clones at that station, it will be important only to use genotypes 1, 2 and 3, which have most effectively adapted to environmental conditions in that region.

At Mengang, use of genotypes 7 and 8, which have persisted at that station since 1986, should be recommended in screening tests.

To complete the investigation of *P. megakarya* genetic diversity in Cameroon, it seems necessary to study this pathogen on the other African Sterculiaceae, which are also host plants for this pathogen, and to more effectively define the possibility of those strains adapting to cocoa. In 1999, genotype 8 was isolated on kola intercropped with cocoa (Centre region).



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