

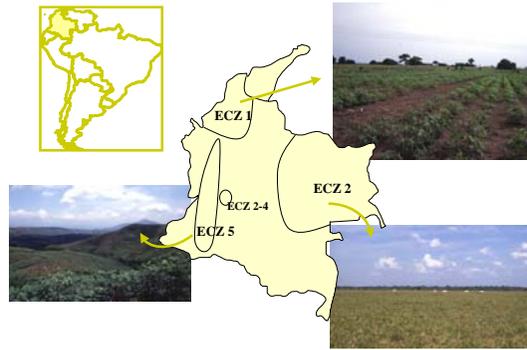
Population dynamics of *Xanthomonas axonopodis* pv. *manihotis* populations in Colombia from 1996 to 1999

S. Restrepo, C. M. Vélez, and V. Verdier

Biotechnology Research Unit, CIAT and Institut de Recherche pour le Développement (IRD), A.A. 6713, Cali, Colombia.

INTRODUCTION

Cassava Bacterial Blight (CBB), caused by *Xanthomonas axonopodis* pv. *manihotis* (*Xam*) is a major disease of cassava, (*Manihot esculenta* Crantz). The most realistic way to control the disease is the use and deployment of resistant cultivars. The change in the pathogen population structure may result in the overcoming of the deployed resistance as it was recently observed in Africa. The spatial and temporal context in which plant-pathogen associations occur is very important in determining the evolution of host-pathogen interactions. RFLP analysis was used to assess the population structure and genetic diversity of 643 strains of *X. a.* pv. *manihotis* collected between 1996 and 1999 in Colombia. Temporal changes and population dynamics were addressed by comparing samples from four years in six locations spanning four different edaphoclimatic zones (ECZs).



Spatial distribution of the *Xam* populations in the different ECZs in Colombia



Symptoms induced by *Xanthomonas axonopodis* pv. *manihotis*.



RESULTS AND DISCUSSION

Over the 5-year period, 42 different haplotypes were found in 6 different sites. The total genetic diversity was 0.7 in Colombia. A very large part of the total variation was within populations showing a high level of polymorphism at the field level. A large part of variation was also ascribed to differences among ECZs confirming the geographical differentiation of the diversity found in 1995-1996.

Source of variation	Variance component	%of total
Among ECZs	1.29	29.3
Among sites/within ECZs	0.53	12
Within sites	2.57	58.7

Genetic diversity in *Xam* was being maintained from year to year. AMOVA analysis ascribed most of the total variation to differences among the years that differences within a year.

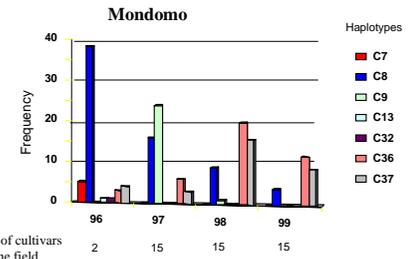
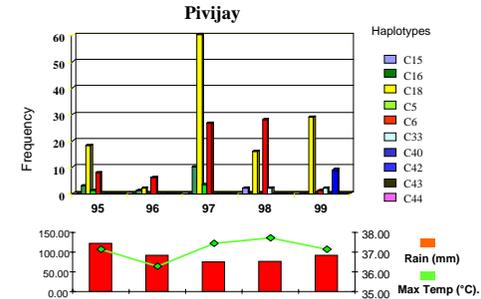
% Variation ascribed to Year of collection (among/within)					
Cajibío	Mondomo	Villavicencio	Carimagua	Pivijay	Stdr Quilichao
ECZ5	ECZ5	ECZ2	ECZ2	ECZ1	ECZ2-4
0/100	36/64	20/80	3/97	17/83	40/60

Chi-square tests showed that differences in haplotype frequencies over the 5-year were statistically significant, except for Cajibío, indicating that the populations of *Xam* at the site level were unstable.

Site	ECZ	Year	H _{year}	H _{SITE}	X ²
Pivijay	1	1995	0.58	0.69	118.8 (0.001) ^a
		1996	0.56		
		1997	0.56		
		1998	0.52		
		1999	0.46		
Carimagua	2	1995	0.83	0.87	113.5 (0.001)
		1996	0.83		
		1997	0.78		
		1998	0.78		
Villavicencio	2	1995	0.81	0.80	201.1 (0.001)
		1996	0.91		
		1997	0.64		
		1998	0.62		
Mondomo	5	1996	0.46	0.73	120.1 (0.001)
		1997	0.65		
		1998	0.69		
		1999	0.69		
Cajibío	5	1995	0.26	0.22	2.7 (0.446)
		1996	0.15		
		1998	0		
Stdr Quilichao	2-4	1996	0.30	0.58	66 (0.001)
		1997	0.26		
		1998	0		

^a The chi-square value was significant at the 5% level.

Several evolutionary forces interact to structure the populations of plant pathogens. Migration of strains between fields located in the same ECZ has been a very important factor to maintain the high levels of *Xam* diversity within the ECZs. Genetic drift might play a role in Pivijay (ECZ1) after the El Niño phenomenon in 1997. During 1997, the environmental conditions were not conducive for CBB development. Our results suggested that the host also played a role in causing pathogen differentiation. In Mondomo, population change and diversity was higher with the introduction of new cultivars.



Different pathotypes were defined in ECZs 2, 1 and 5 (11, 10 and 1 respectively) from 1995 to 1998. Some pathotypes were found in all years. New pathotypes appeared in 1997 in ECZ2 after the introduction of new cultivars and in 1998 in ECZ1 after El Niño.

ECZ	Pathotype	95	96	97	98
2	C-1	—	—	—	—
	C-2	—	—	—	—
	C-3	—	—	—	—
	C-4	—	—	—	—
	C-5	—	—	—	—
	C-6	—	—	—	—
	C-7	—	—	—	—
	C-8	—	—	—	—
	C-9	—	—	—	—
	C-10	—	—	—	—
	C-11	—	—	—	—
1	C1-1	—	—	—	—
	C1-2	—	—	—	—
	C1-3	—	—	—	—
	C1-4	—	—	—	—
	C1-5	—	—	—	—
	C1-6	—	—	—	—
	C1-7	—	—	—	—
C1-8	—	—	—	—	
C1-9	—	—	—	—	
C1-10	—	—	—	—	

CONCLUSIONS

The *Xam* population has shown a high degree of genetic diversity and the role of different evolutionary forces in structuring pathogen population was assessed.

The next step is to determine the prevalence and distribution of virulence characteristics and to use the knowledge on the dynamics within the bacterial population to predict the incidence of the disease and diversity of the pathogen using GIS and geostatistics.

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$$H = [n/(n-1)](1 - X_i^2)$$

where X_i is the proportion of the i th distinct *pthB* haplotype, and n is the number of strains.

Significance testing for differences in haplotype frequencies over the years in each site or ECZ was performed by a chi-square analysis.

Analysis of molecular variance (AMOVA) was used to estimate variance components for RFLP haplotypes, partitioning the variation among individuals within and among sites, ECZs and years. The analysis was undertaken with the ARLEQUIN program (Excoffier *et al.*, 1992).