Molecular epidemiology of *Xanthomonas campestris* pv. *manihotis* causal agent of cassava bacterial blight

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Abstract

In order to detect and assess genetic and evolutionary relationships among strains of Xc pv. manihotis a comparison of strains of distinct geographical origin, representing 18 countries, was performed using a range of assays including restriction fragment length polymorphism (**RFLP**) analysis. The probes used were: 16+23S rRNA genes from *E.coli* and three restriction fragments from the chromosomal or plasmid DNA of Xc pv. manihotis.

Hybridization with the probe corresponding to the rRNA genes allowed the distinction of four RFLP groups. Subgroups were identified based on hybridization profiles with the three others probes.

Genetic variability of Xc. pv. manihotis was extensive in strains from the area of origin of the host plant and limited elsewhere. These results are in agreement with the hypothesis of the recent introduction of the pathogen to these latter areas and suggests that the African strains have not yet diversified genetically at the chromosomal level.

Our results indicate that RNA and DNA probes are useful tools for epidemiological studies and in following the genetic evolution of strains.

Keywords: Xanthomonas campestris pv. manihotis, cassava, RFLP, rRNA probe, DNA probe.

I. INTRODUCTION

Cassava (*Manihot esculenta*), family *Euphorbiaceae* is a root stock crop native from South and Central America. Portuguese traders introduced it to West Africa in the sixteenth century and to East Africa in the eighteenth century (SILVESTRE & ARRAUDEAU, 1983). It became one of the most important tropical food in countries of Tropical Africa.

Cassava bacterial blight (C.B.B) caused by Xanthomonas campestris pv. manihotis is one of the most important diseases of cassava. The disease was first reported in Brazil in 1912 (BONDAR, 1912) but has also been observed in Colombia and Venezuela (LOZANO & SEQUEIRA, 1974), as well as in most of African (MARAITE & MEYER, 1975) and Asian countries (BOOTH & LOZANO, 1978).

Cassava originated from South America and its related bacterial pathogens could have been propagated to others countries through the cuttings and seeds. To be able to detect and assess evolutionary relationship among pv. *manihotis* a comparaison of strains was developped using a wide range of assays.

II. MATERIAL AND METHODS.

X.c. pv. manihotis collection.

The bacterial strains used in this study, their geographical origin and their sampling collecting places are listed in Table 1.

Physiological characteristics.

Different phenotypic features were examined: the *in vitro* susceptibility to 20 antibiotics was determined, the utilization of carbon sources (19 tested), and the amylase activity according to described methods (GROUSSON et *al*, 1990).

Phytopathogenicity test.

Pathogenicity of all strains was tested on cassava plants, Congo's cultivar PMB, multiplied from cuttings. The stem inoculation was done according to previously described methods (MARAITE et al, 1981).

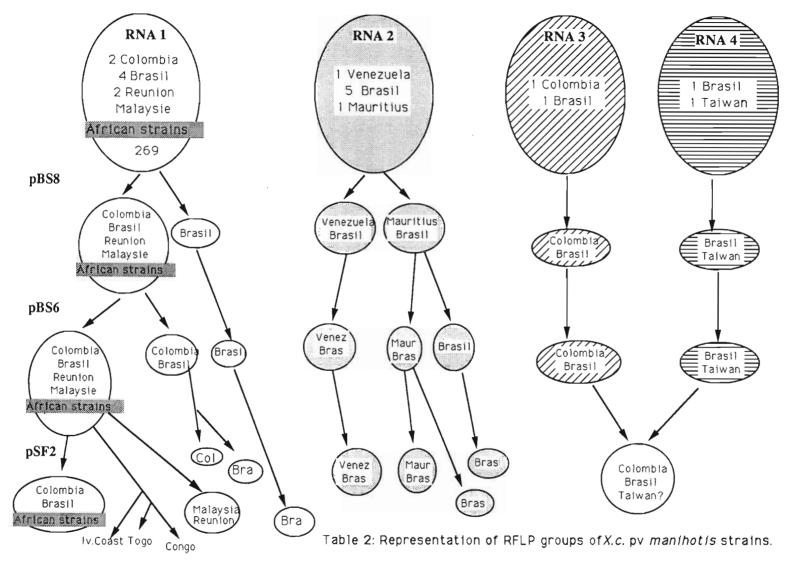
Strain no * and in other collection	Place and	year of isolation	Isolated y	Strain no * and in other collection	Place and year of isolation		
CFBP1851,CIAT1111	Colombia	1974	Lozano.J	HMB6, LMG 767	Zaïre	1973	
LMG 776, NCPPB2443, HMB72,0		1970	Lozano.J	HMB9, LMG 768, NCPBB3O58	Duni	»	
ORST1, CIAT1060, CFBP1849		1970	Lozano.J	LMG 769, NCPPB3O59, HMB10		»	
ORST2, CIAT1061, CFBP1850 Venezuela		1971	Lozano	LMG 766, HMB3		»	
ATCC 23380, HMB68,NCPPB1159 Brazil		1941	Burkholder	ORST44		1979	
IMB 70, NCPBB1160, LMG5273		1941	Drumond Hipolito	ORST45		»	
MB 55a,NCPBB1834*, LMF784		1965	Robbs C.	ORST46		»	
RST7, CFBP1854		1973	Neto J.R.	ORST47		»	
HMB23, LMG770		1973	Pereira A.	ORST48		»	
ORST3, CIAT 1120, CFBP1852		1974	Lozano.J	ORST49		»	
ORST5, CFBP1855		1974	Neto J.R.	ORST50		»	
ORST6, CFBP1856		1976	Neto J.R.	ORST51		»	
IMB79, LMG778		1978	Takatsu.A.	ORST52		>>	
LMG777, HMB78		1978	Takatsu.A.	ORST53		»	
MG779, HMB80		1978	Takatsu.A.	ORST54		»	
HMB25, NCPBB3060, LMG 771 Nigeria		1976	Maraite H.	ORST186		1987	
ORST42	2	1978	Daniel J.F	ORST187		»	
ORST43		1978	«	ORST39	RCA	1977	
CFBP1857, ORSTOM A202.1		1978	*	ORST40		»	
CFBP1858, ORSTOM A203.1		1978	«	ORST41		»	
CFBP1859, ORSTOM A205.1		1978	«	LMG 5287, NCPPB 3161	Cameroon	1976	
CFBP1860, ORSTOM A207		1978	«	HMB27, LMG629		1977	
ORST34	Benin	1982	Daniel J.F	LMG780, HMB81	Uganda	1979	
ORST35		1982	«	LMG782, HMB93		»	
ORST36		1982	«	LMG783, HMB148	Kenya	1979	
ORST37		1982	«	LMG5288, NCPPB 3194	Niger	1978	
ORST38		1982	«	LMG765	Malaysia	1980	
CFBP1944	Ivory Coast	1979	Ridé M.	1			
MG5249, HMB203	- <i>y</i> •	1981	Maraite H.	LMG774, HMB60	Taïwan	1978	
ORST55		1984	Daniel J.F				
DRST56		1984	<i>«</i>	HMB71, NCPBB1161, LMG775	Mauritius	1946	
ORST (198 strains) C	ongo	1977-1991	Daniel J.F]			
			Boher B.	CFBP2624	Reunion	1986	
			Verdier V.	CFBP2635		1987	
ORST (29 strains)	Годо	1987-1991	Boher B.				

ATCC : Americain Type Culture, Rockville, Maryland, USA. CFBP : Collection Française de Bactéries Phytopathogènes, Angers, France.

NCPPB : National Collection of Plant Pathogenic Bacteria, Harpenden, U.K. HMB : H. Maraite's Bacterial Collection, LOUVAIN La Neuve, Belgium.

LMG : Laboratorium voor Microbiologie Gent culture Collection, Gent, Belgium. ORST : Collection du Laboratorie de Phytopathologie, ORSTOM, Brazzaville, Congo.

CIAT : Centro International de Agricultura Tropical, Cali, Colombia. * : Pathovar reference strain.



RFLP analysis.

Total genomic DNA isolation, endonuclease digestion, electrophoresis and Southern blot were done according to previously described methods (BERTHIER et al, 1992). Hybridization was made with different probes. Acetyl Amino Fluorene labeled ribosomal 16+23S RNA genes from *E. coli* (Eurogentec, Liege, Belgium) hybridized with the genomic DNA of bacteria. The rRNA - rDNA duplexes were detected using the anti-AAF monoclonal antibody (GRIMONT et al, 1989).

The DNA probes used in this study were: **BS6** (7kb-*Eco*RI) and **BS8** (8kb-*Eco*RI), two restricted fragments from the chromosomal DNA (Xc. pv manihotis strain CNBP1851-CIAT1111) and **pBsF2** derivated from the 13kb-*Hin*dIII fragment of plasmid DNA cloned in the bluescript vector plasmid. DNA probes were labeled *in vitro* by using a random priming kit with ³² P deoxycytidine triphosphate (Multiprime Amersham).

III. RESULTS

RFLP patterns.

Using the rRNA probe, the distinction of 4 RFLP groups among the 290 strains tested could be possible. Strains from South America were heterogenous and gave different patterns, on the contrary no polymorphism was noticed in African strains (Table 2).

Hybridization profiles with DNA probes could differentiate 6 groups with BS8 probe and 8 groups with BS6 probe, each group representing strains with identical RFLP pattern (Table 2). Polymorphism could be noticed in South American strains which are represented in groups mentioned above. In contrast, no polymorphism was observed in African strain with BS8 and BS6 probes suggesting that these regions are well conserved into the genome.

Variability among RFLP patterns of African strains was only noticed with the plasmid DNA probe pSF2.

Pathogenic characteristics.

Variability among pathogenic characteristics exists but was not related with the geographical origin of strains.

Phenotypic features.

Same results were obtained for two of the three phenotypic features tested (sensitivity to antibiotics and utilization of carbon sources). Starch hydrolysis was observed for all strains but two groups were differentiated. All African Reunion and Malaysian strains showed a low amylase activity similar to that found in 3 Brasilian and Colombian strains.

IV. DISCUSSION

Based on numerical analysis of protein gel electrophoregrams and, 267 phenotypic features, VAN DEN MOOTER et al, (1987) and VAUTERIN et al, (1991) indicate that the py manihotis strains constitute a phenotypically and genetically homogeneous group. In this study, using the RFLP analysis, small changes in DNA organization were observed. Genetic variability of pv manihotis was more extensive in strains from the area of origin of the host plant and more limited in those coming from elsewhere. Among African strains homogeneity was observed with the probe corresponding to the rRNA genes and thus was confirmed with genomic probes used in this study. In our previous data based on plasmid DNA study we have indicated the hypothesis of one common geographic origin within strains of Xc. pv. manihotis (VERDIER, 1988). The results presented here agree with the hypothesis of the recent introduction of this pathogen from South America to the other countries, and suggest that African strains are not already diversified at chromosomal level. Using the DNA plasmid fragment as a probe, this study revealed that DNA polymorphisms exist in African strains. Plasmids are mobile elements which easily perform genetic exchange in bacterial strains (COPLIN, 1989; EBERHARD, 1990). Presence of essential pathogenicity genes on these plasmid fragment was previously demonstrated (VERDIER et al, 1989).

RNA and DNA probes used here were particularly useful in our epidemiological studies, providing information on the genetic population structure of these pathogens and its ability to identify clonally related individuals.

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