RXam-1: a Xa21 cassava homologue associated to bacterial blight resistance in cassava



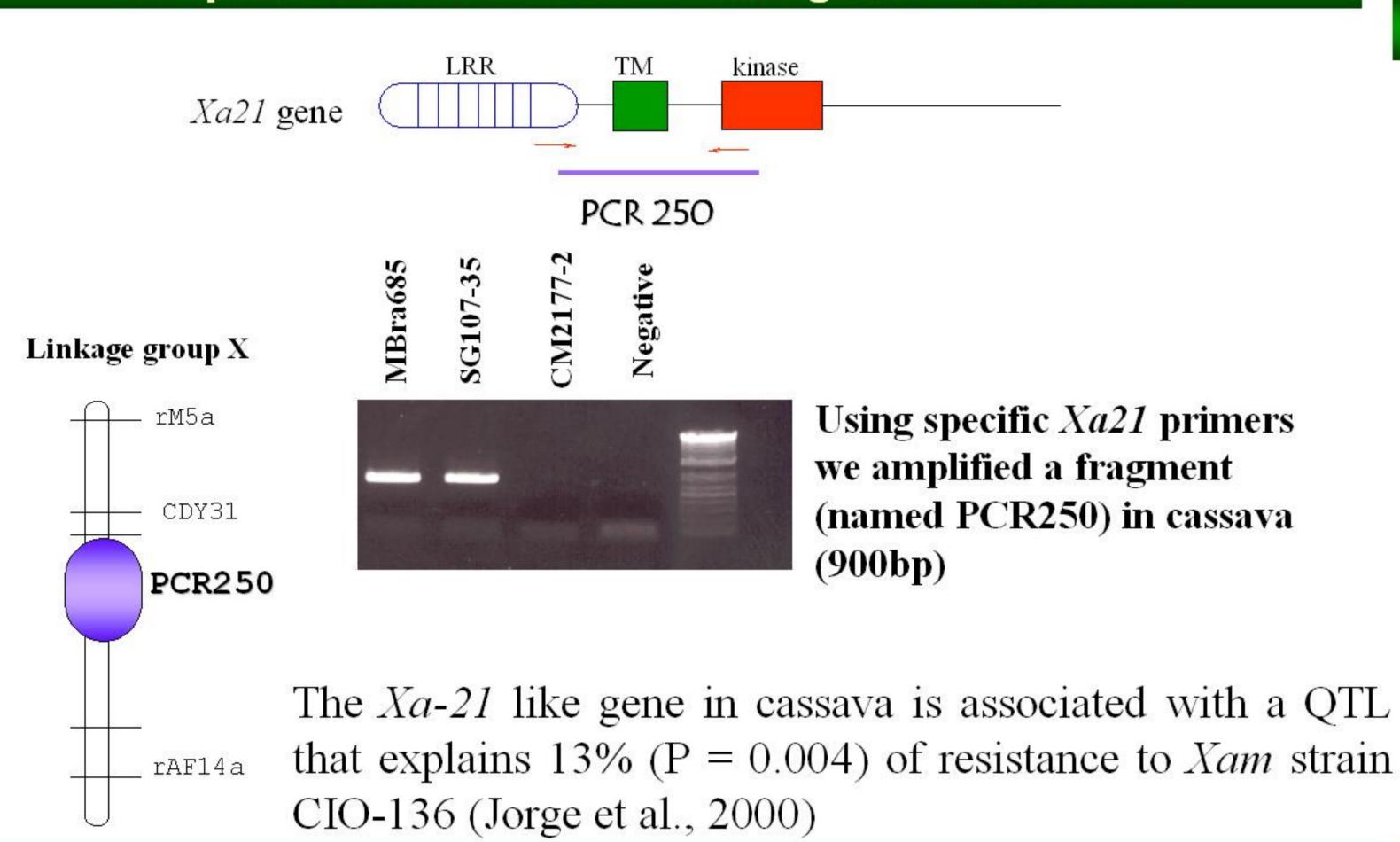
Lopez C., Cooke R., Delseny M., Tohme J., and Verdier V.

UMR5096, LGDP, CNRS-Université de Perpignan- IRD, 52 Av Paul Alduy, 66860 Perpignan Cedex, France Centro Internacional de Agricultura Tropical CIAT, Cali-Colombia AA6713

The rice gene Xa21 represents a class of resistance genes (R-gene) conferring resistance to Xanthomonas oryzae pv oryzae. Xa21 encodes a receptor like-kinase consisting of LRRs in the putative extracellular domain.

Cassava is a major tropical food crop providing food and income for about 600 million people in the world. Cassava Bacterial Blight (CBB), caused by *Xanthomonas axonopodis* pv. *manihotis* (*Xam*), is a major disease for the crop and is endemic in Africa and Latin America. The use of varietal resistance is the most realistic way to control the disease. We have identified and characterized an homologue of *Xa21* (*RXam-1*) in cassava. *RXam-1* is associated to one QTL that confers resistance to *Xam* strain CIO-136.

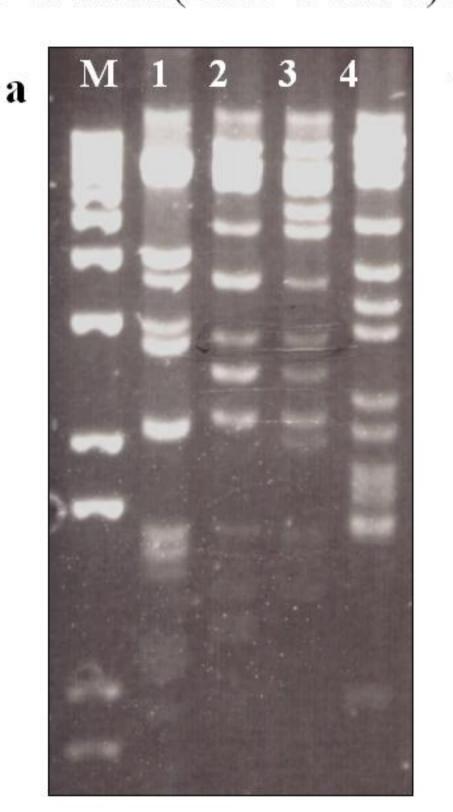
Amplification of a Xa21- like gene in cassava

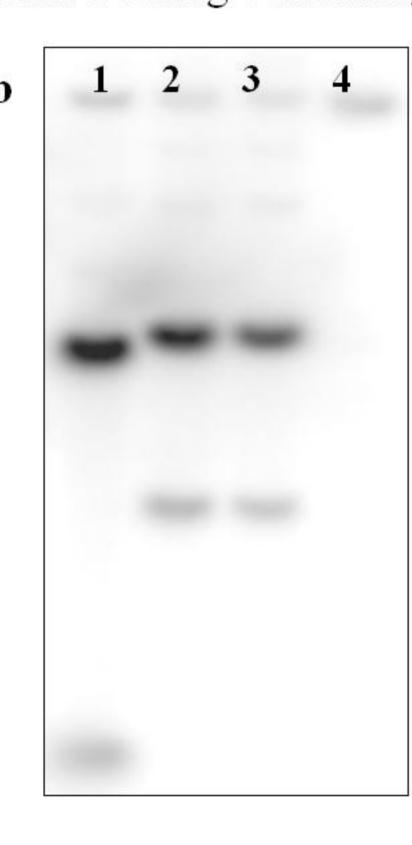


Screening a cassava BAC library

Four BAC clones (1 to 4) were detected in the cassava BAC library (var. TMS3001 susceptible to *Xam* CIO-136 strain)

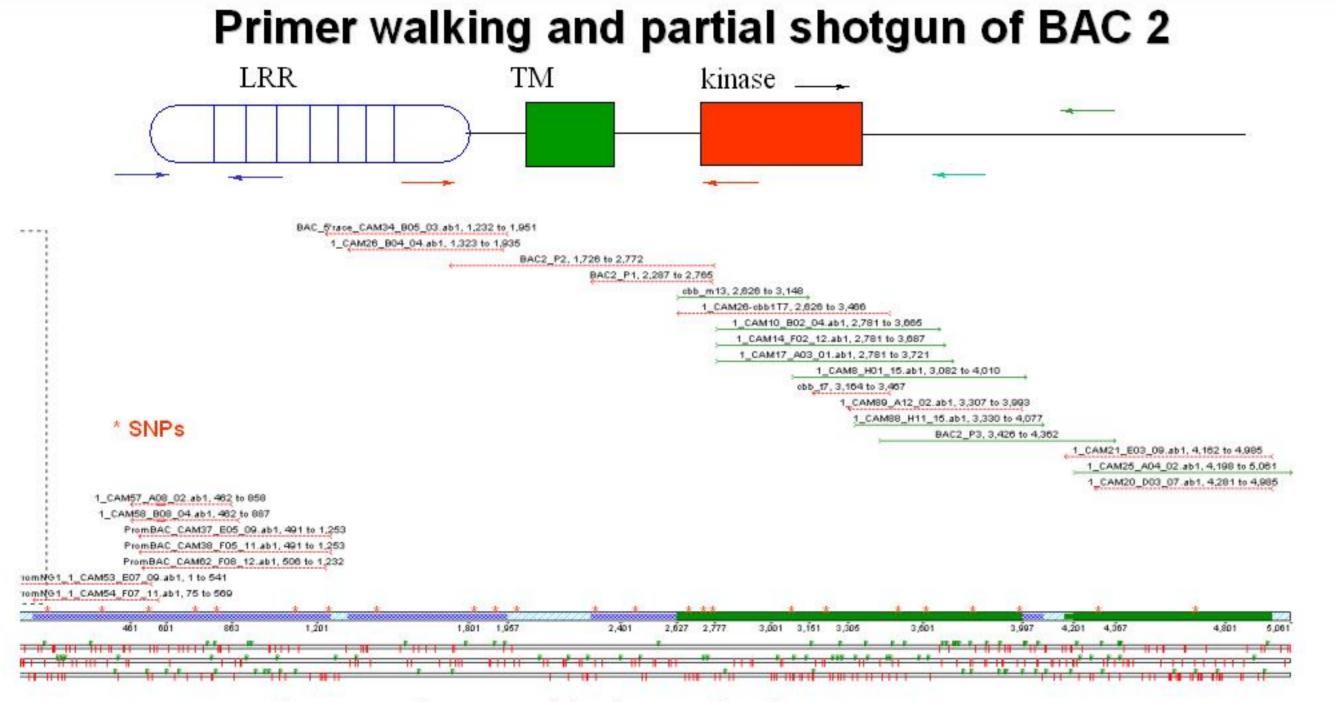
Fingerprinting analysis showed that one of them may represent a false positive Two of them (BAC 1 and 2) form a contig containing 2 copies of PCR250





Fingerprinting analysis
a) BACs were
digested with *Hin*dIII.
b) Southern-blot analyses *Hin*dIII BACs digested
were hybridized with
PCR250 as probe.0

Partial BAC sequence



Schema of assembled contig from BAC2

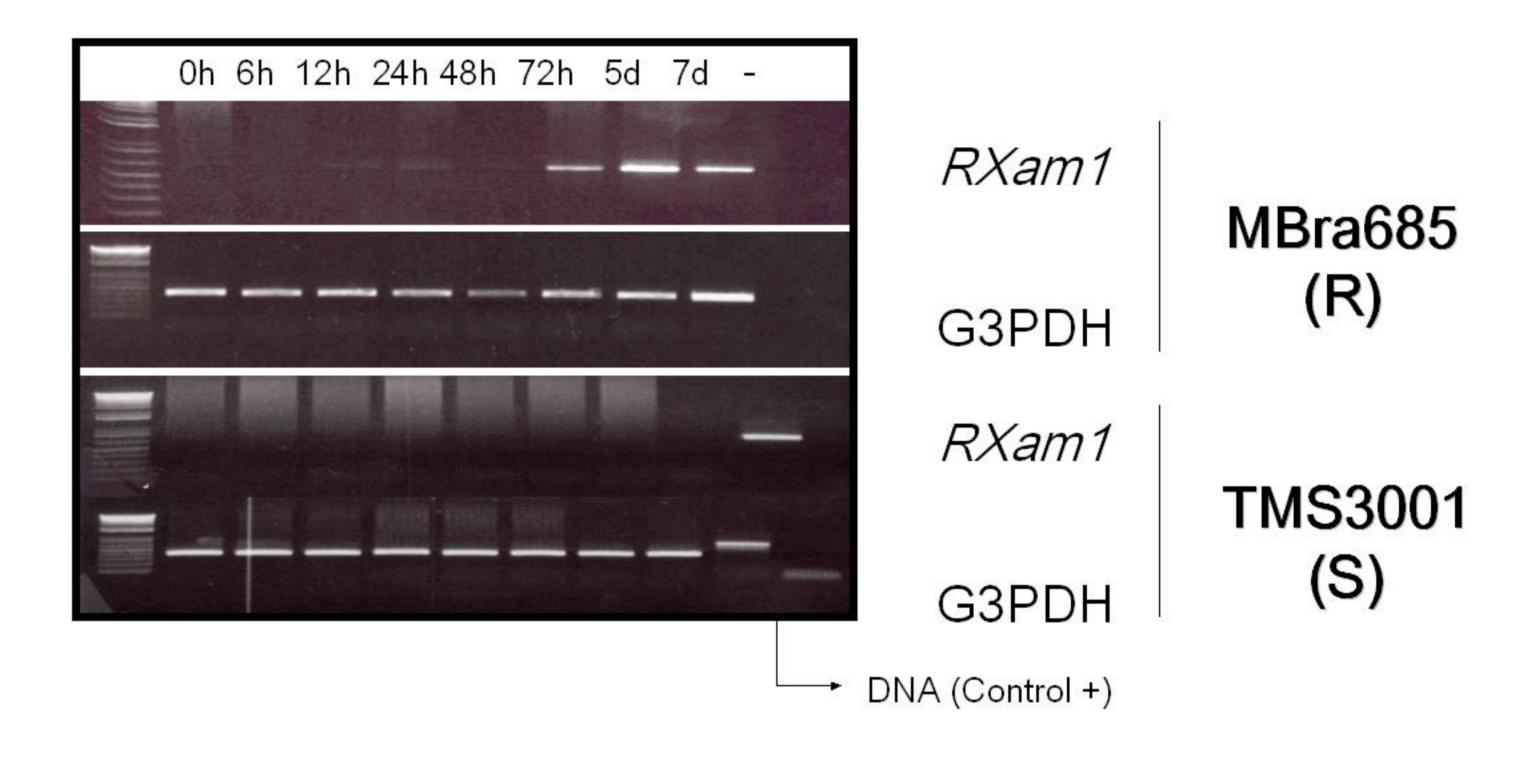
Sequence analysis of RXam-1

Comparative analyse of RXam-1 sequences obtained from TMS3001 (S) and MBRA685 (R)

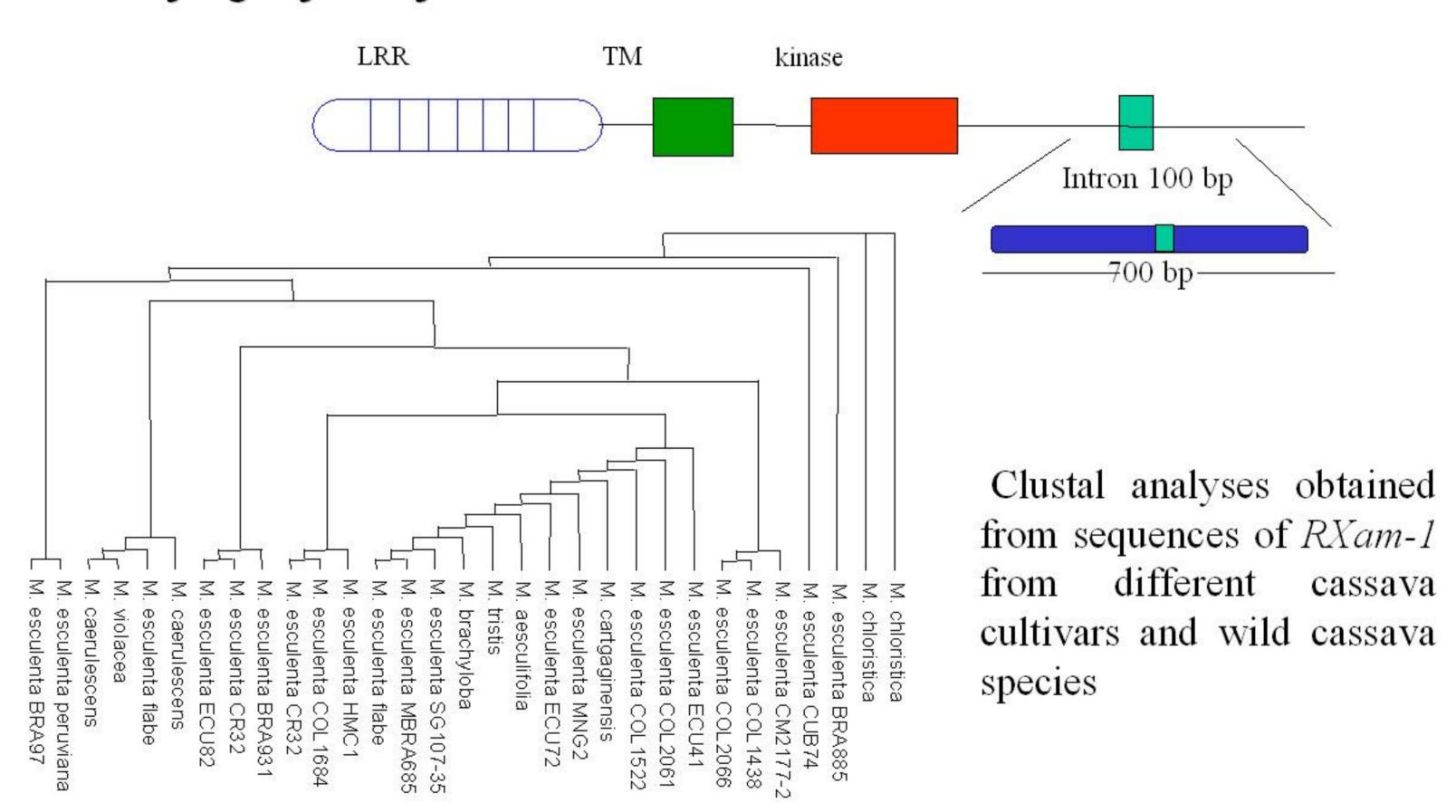
	Sequenced region	Complete ORF	Identity to Xa21	LRR domain	Ser/thr kinase domain
TMS3001 (BAC2)	4.6 kb		34%	Yes	Yes
MBRA685	3.5 kb	Yes	35%	Yes	Yes

Expression and phylogeny analysis

Expression of RXam-1 is induced after infection by Xam CIO-136 in the resistant cultivar but not in the susceptible one



Phylogeny analysis of RXam1



High similarity among different cassava cultivars and wild species

Highlight the importance of RXam-1 gene function

Perspectives

- •To isolate and characterize the RXam-1 promotor for further plant genetic transformation with RXam1
- Functional analysis of RXam1 using a cassava transformation system and/or silencing (VIGS)
- Correlate the sequence polymorphism observed with resistance level of different cassava cultivars to *Xam* CIO136