

Development of diagnostic molecular markers for rapid identification of *Xanthomonas oryzae* pv. *oryzae* and *X. oryzae* pv. *oryzicola*

Jillian M. Lang¹, John Hamilton², Genaleen Diaz¹, Marie Anne Van Sluys³, Ned Tisserat¹, C. Robin Buell², & Jan E. Leach¹;

¹Colorado State University, Fort Collins, CO, USA; ²The Institute for Genomic Research, Rockville MD, USA;

³Universidade de São Paulo, SP, Brazil



X. oryzae pv. *oryzicola* on rice



<http://cpgr.tigr.org>

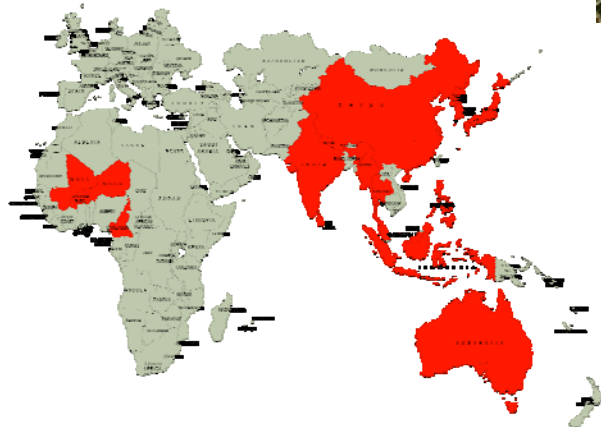
Geographically Diverse
Xoo & Xoc DNA



X. oryzae pv. *oryzae* on rice

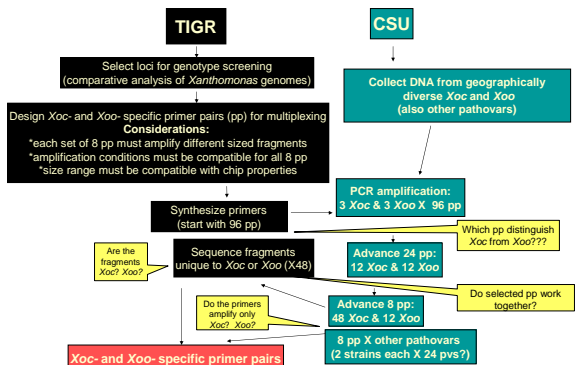
Abstract

Xanthomonas oryzae pv. *oryzae* (Xoo) and *X. oryzae* pv. *oryzicola* (Xoc) cause bacterial blight and leaf streak of rice, respectively. *X. oryzae* pv. *oryzicola* has not been reported in the USA and is currently on the USDA select agent list. Although symptomatology is distinct, the two pathogens are difficult to differentiate from each other based on cultural or biochemical diagnostic methods. Thus, there is need for molecular-based tools to diagnose these pathogens. Genomic analysis tools available in the Comprehensive Phytopathogen Genomics Resource (<http://cpgr.tigr.org>) were used to identify over 150 primer pairs with the potential to distinguish *X. oryzae* pv. *oryzae* from *X. oryzae* pv. *oryzicola*. Each primer pair was screened against well-characterized isolates of each pathovar using conventional and multiplex polymerase chain reaction (PCR). Robust primers were tested against a larger number of isolates including geographically diverse strains of both pathogens, several other *Xanthomonas* species and pathogens, and other bacterial plant pathogens. An extensive set of primers were identified that distinguish *X. oryzae* species and each pathovar.



- Our collection consists of over 80 Xoo & 40 Xoc strains from over 17 different countries worldwide, highlighted here
- We rely on our collaborators to share only Xoc DNA because it is a restricted organism in the USA

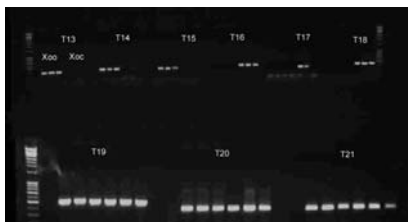
Pipeline to develop diagnostic primers



Results

	# Strains Tested (Xoo, Xoc & other pathogens)	# Primer Pairs Tested	# Specific Primer Pairs
Xoo	38	35	13
Xoc	25	28	9
Xoo + Xoc	26	28	18

Gel image of primer screening



T13-T15 Xoo specific

T16-T18 Xoc specific

T19-T21 Xoo & Xoc specific

Future Research

- Continue screening all primer pairs against more geographically diverse strains and other pathogens to identify a confident set of diagnostic primers to release for public use
- Investigate possible connections between monocot vs. dicot and vascular vs. non-vascular pathogens using our primer pairs
- Use primers to study variation and phylogenetics of geographic populations

Email: cpgr@tigr.org

