

Population and Evolutionary Biology of Fungal Symbionts
Ascona
2007

Migration of the rice blast fungus *Magnaporthe grisea*

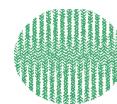
Marc Henri Lebrun
UMR 2847
CNRS-Bayer CS,
Lyon, FRANCE

Didier Tharreau, Jean Loup Notteghem
UMR BGPI
CIRAD-INRA-SupAgro.M
Montpellier, FRANCE

and soon **Elisabeth Fournier**



Bayer CropScience



INRA



Montpellier
SupAgro

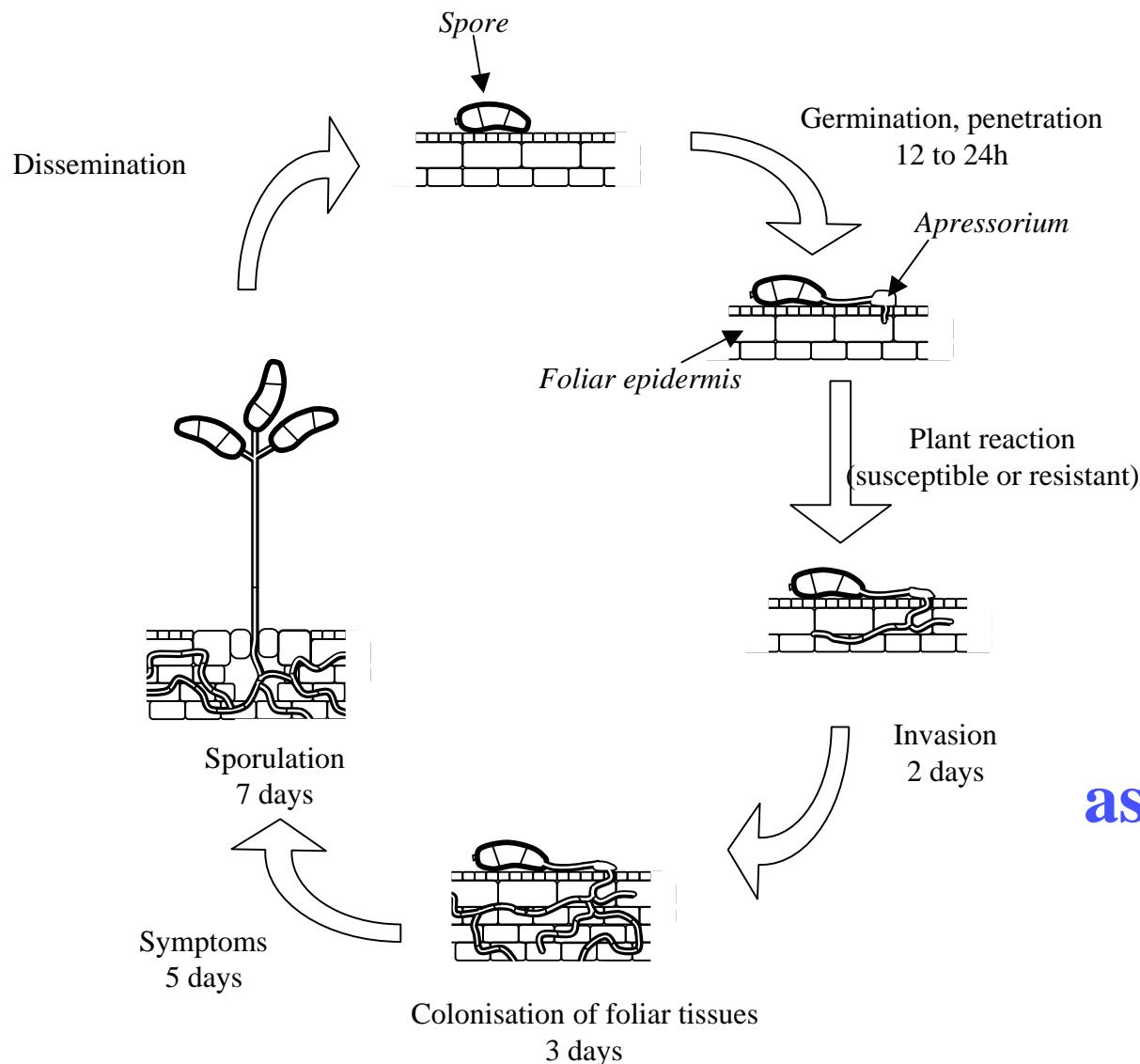
Introduction: Rice blast symptoms

Rice blast disease caused by the fungus *Magnaporthe oryzae*



Introduction: Rice blast cycle

Magnaporthe oryzae haploid Ascomycete fungus



asexual reproduction

After Romain Berruyer, CIRAD

Rice -rice blast interactions follows the *Gene for Gene* theory

		Plant	
		R/R or R/s	s/s
Pathogen	AVR		
	vir		

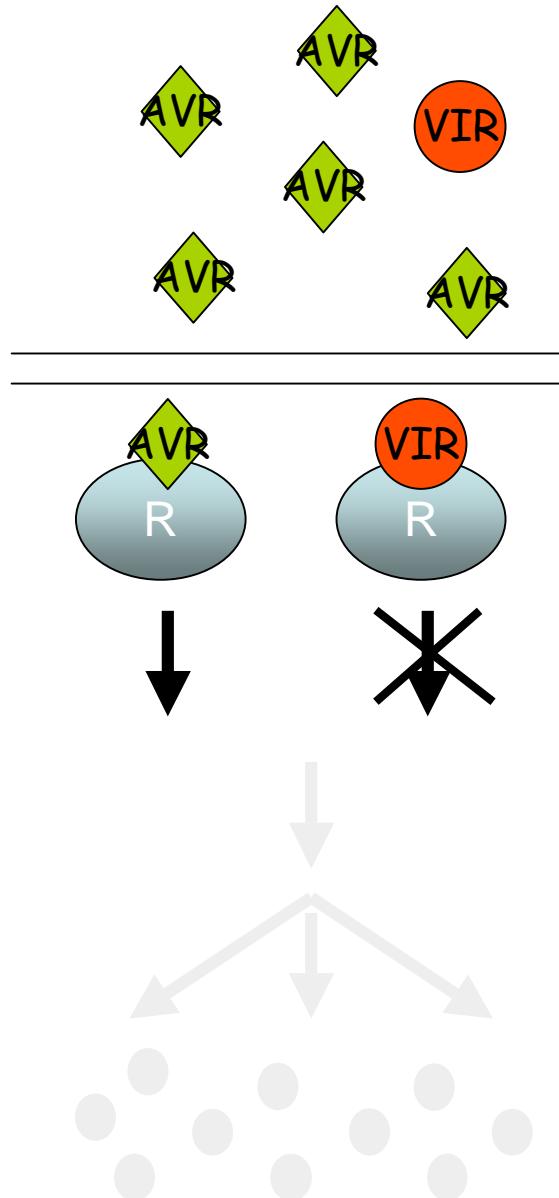
Silué et al, 1992, Phytopathology

Introduction: Resistance Breakdown

Resistance breakdown common and rapid

Varieties	69	70	71	72	73	74	75	76	77	78	79	80	81	82
IR8	O	X												
Cica4			O	X										O release, X resistance breakdown
IR22			O	X										<i>F. CORREA, CIAT, Colombia</i>
Cica6					O	X								
Cica7							O			X				
Cica9							O	X						
Cica8									O		X			
Metica1												O	X	

Introduction: Population evolution



Understanding Resistance breakdown

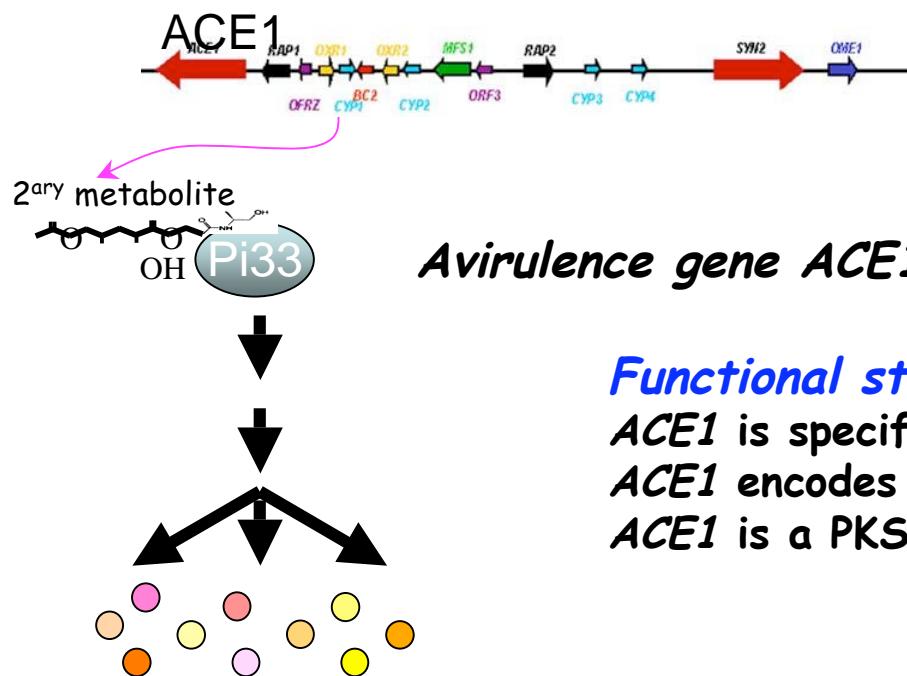
Virulent strains emerge
Different mechanisms (lab studies)
Point mutation, insertion, deletion,
recombination
Few examples in natural populations

How virulent strains appear and spread in the field?

Identify and characterize alleles of avirulence genes
in natural populations

ACE1/Pi33: our model system for specific interactions

	Plant	Pathogen
<i>ACE1</i>	<i>Pi33</i>	<i>pi33</i>
Pathogen	<i>ACE1</i>	<i>ace1</i>



Avirulence gene ACE1 cloned

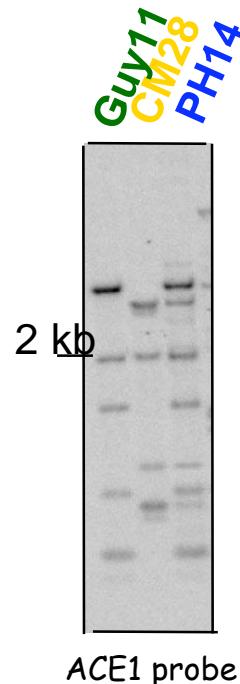
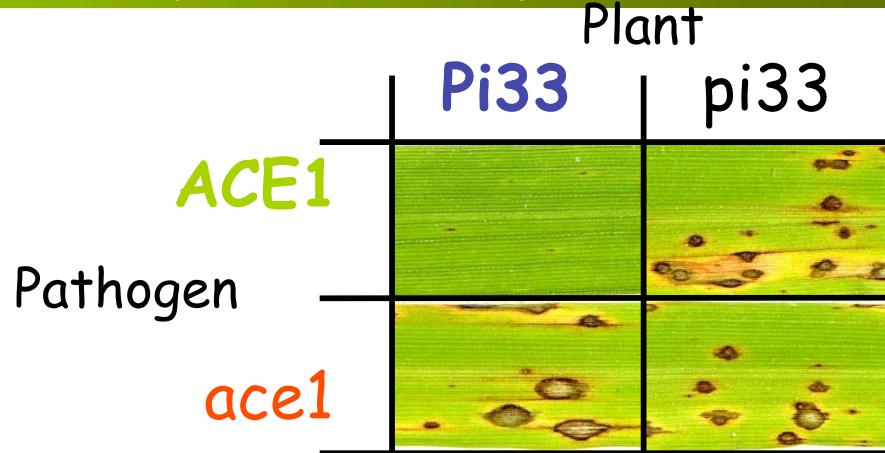
Functional studies

ACE1 is specific of the infection

ACE1 encodes a big, non secreted protein

ACE1 is a PKS/NRPS, 2^{ary} metabolite biosynthesis enzyme

ACE1/Pi33 : our model system for specific interactions



Avirulence gene ACE1 cloned

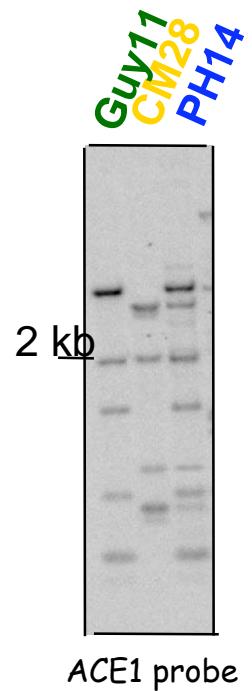
Population studies

Identification and characterization of *ACE1* alleles
in a worldwide collection (55 countries, 3,500 strains)
by RFLP, then PCR

ACE1: rare emergence and long distance migration

Identification and characterization of *ACE1* alleles

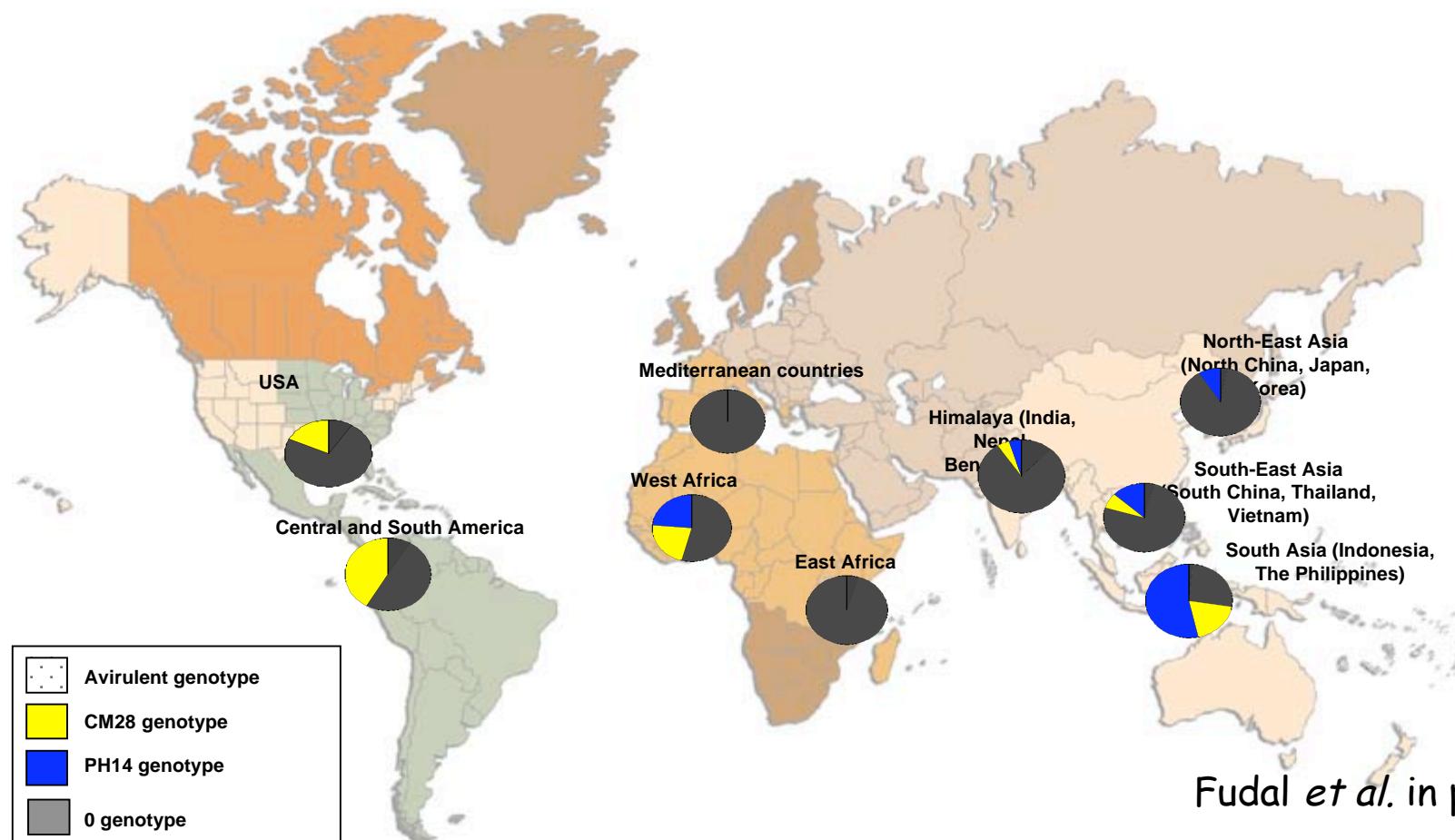
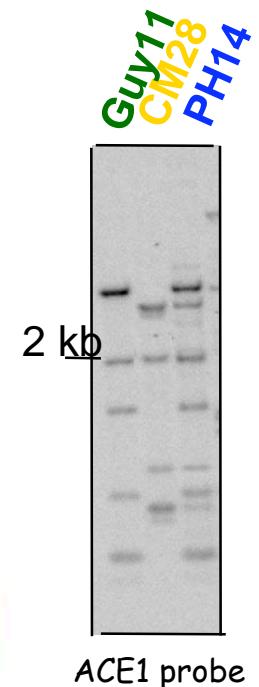
3 virulent genotypes with 2 dominant
1 complex event (duplication/deletion)



ACE1: rare emergence and long distance migration

Identification and characterization of *ACE1* alleles

3 virulent genotypes with 2 dominant
1 complex event (duplication/deletion)
1 unique apparition event
intercontinental distribution ← migration



Fudal *et al.* in preparation

ACE1: rare emergence and long distance migration

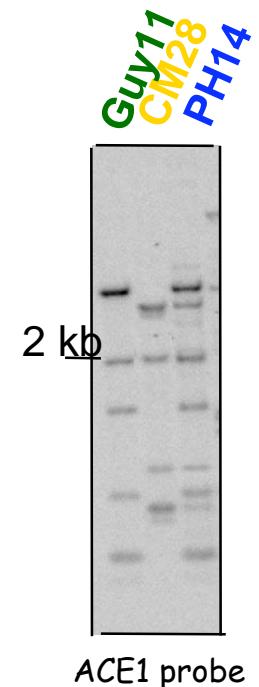
Identification and characterization of *ACE1* alleles

3 virulent genotypes with 2 dominant

1 complex event (duplication/deletion)

1 unique apparition event

intercontinental distribution ← migration



- emergence of *ACE1* Vir. is rare in the field
- intercontinental migration of Vir. strains occurred

Fudal *et al.* in preparation

Couch *et al.* Genetics 2005

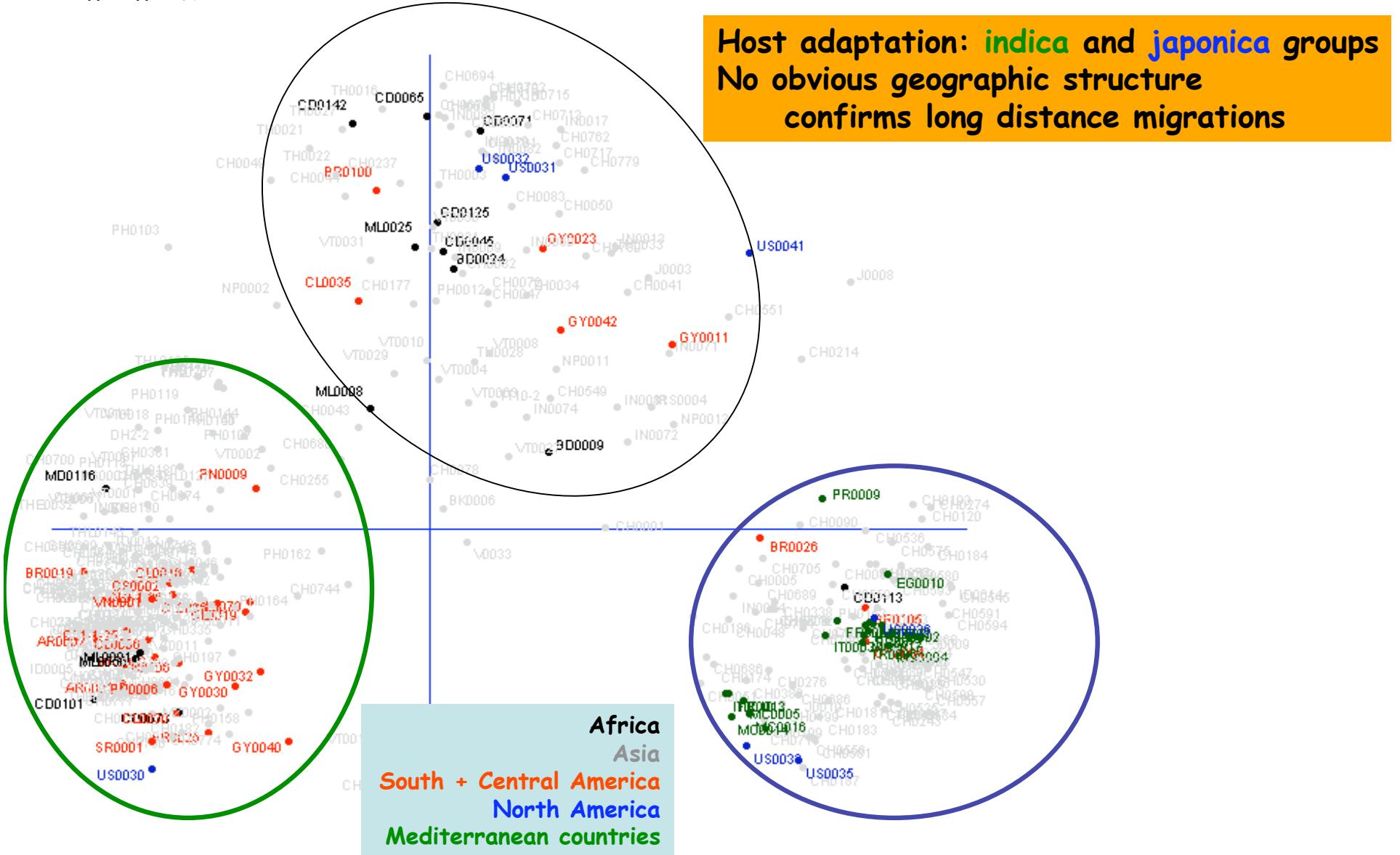
Fudal *et al.* Fungal Genetics and Biology 2005

World population structure confirms migration

World population structure preliminary study

500 isolates (reference isolates = maximum genetic diversity)

15 ms markers



What is the quantitative importance of migration at different scales?

Pop. Genetics: measure migration = measure gene flow

Migration	High	0
Gene flow	High	0
Populations	identical	100% different
Differentiation	No	Yes
Fst value	0	1

Evaluating migration : development of new markers

Appropriate genetic markers required

- identification of alleles for each locus
- no null allele

→ Development of new markers for rice blast

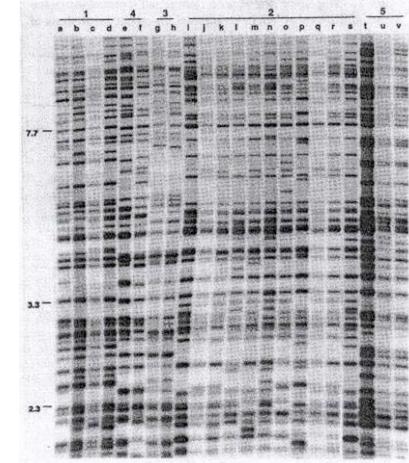
Microsatellite markers commonly used for pop. genetics

Genome sequence available

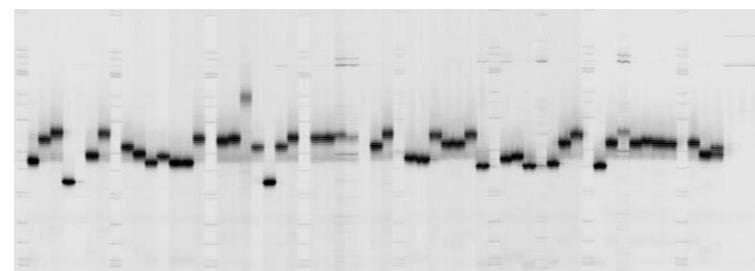
→ ca 1,500 microsatellite sequences

- 300 primer pairs designed and tested
- 130 microsatellite markers mapped
- 18 markers chosen for pop. studies

MGR fingerprinting



ms marker



Kaye et al Fung. Genet. Biol. 2003
Kaye et al. in preparation

Evaluating migration : local scale

Differentiation at a local scale

4 sites in Madagascar

Distance between sites: < 20 km

	L Mangalaza	L Manandona	U Belazao	U Andrano
L Mangalaza		0.01	0.04	0.30
L Manandona	NS		0.09	0.30
U Belazao	S	S		0.26
U Andrano	S	S	S	

NS / S = Fst value not significantly/significantly different of 0

L / U = Lowland / Upland agrosystems

3 sites in France

Distance between sites: < 20 km

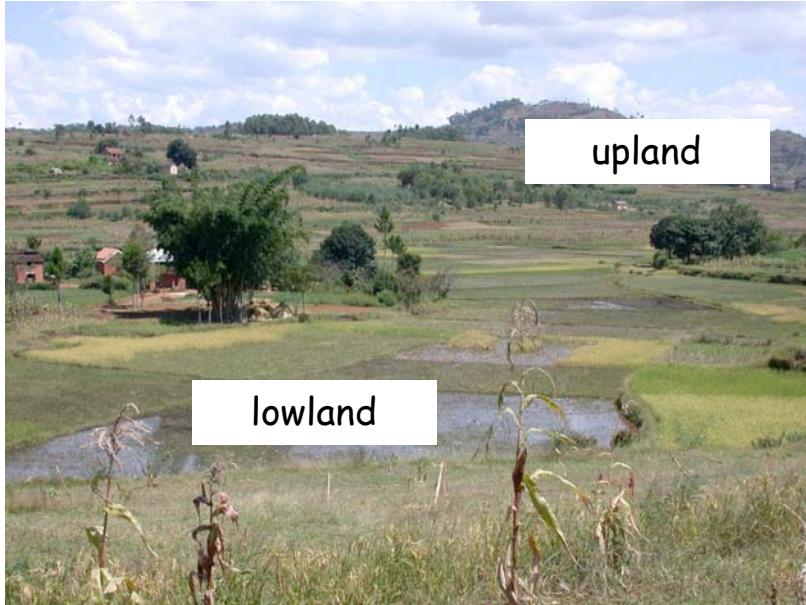
	Furane	Vigne	Gd Manusclat
Furane		0.590	0.094
Vigne	S		0.603
Gd Manusclat	NS	S	



Differentiation at local scale:

- evidence for short distance migration
- in agreement with short distance spore dispersal (1-5 m)

Evaluating migration : effect of selection?



**Two agrosystems: lowland vs upland
One site in Madagascar**

	2004	2005
Fst value	0.13	0.04
	S	S

CULTIVARS	STRAINS																							
	From lowland						From upland																	
	MD398	MD802	MD803	MD804	MD1025	MD728	MD730	MD731	MD751	MD1030	MD1032	MD791	MD798	MD801	MD989	MD990	MD994	MD997	MD1004	MD1007	MD1010	MD1013	MD1016	
Daniéla	R	.		S	R	R	R	R	MR	R	R	S	S	S	S	S	S	S	R	S	MR	MR		
Fofifa133	R	R	MR	R	R	R	R	R	S	R	MR	S	S	S	S	S	S	S	S	S	S	S		
Fofifa154	R	R	MR	R	R	R	R	R	S	R	MR	S	S	S	S	S	S	MR	S	MR	S	S		
Fofifa152	R	R	R	R	R	R	R	R	S	R	MR	S	S	S	S	S	S	S	S	S	S	S		
Fofifa159	R	R	R	R	R	R	R	R	MR	R	R	S	R	S	S	R	S	S	MR	S	S	S		
Fofifa161	R	R	R	R	R	R	R	R	MR	R	R	R	R	R	S	S	S	S	MR	S	R	R		
Fofifa62	R	R	.	R	R	R	R	R	S	R	R	S	S	S	S	S	S	S	MR	R	S	MR		
Fukunishiki	MR	MR	R	R	MR	R	R	MR	S	S	MR	S	S	S	S	S	S	S	S	S	S	S		
K3	R	MR	MR	R	MR	MR	R	R	S	R	R	R	R	R	S	S	R	R	R	S	S	R		
Nerica4	R	R	R	R	R	R	R	R	MR	R	MR	S	MR	S	S	MR	S	S	MR	MR	MR	MR		

Differentiation at local scale = limited migration + selection

Evaluating migration : Regional and intercontinental

Differentiation at different scales

Regional

2 sites in Indonesia (Indramayu and Sukabumi)

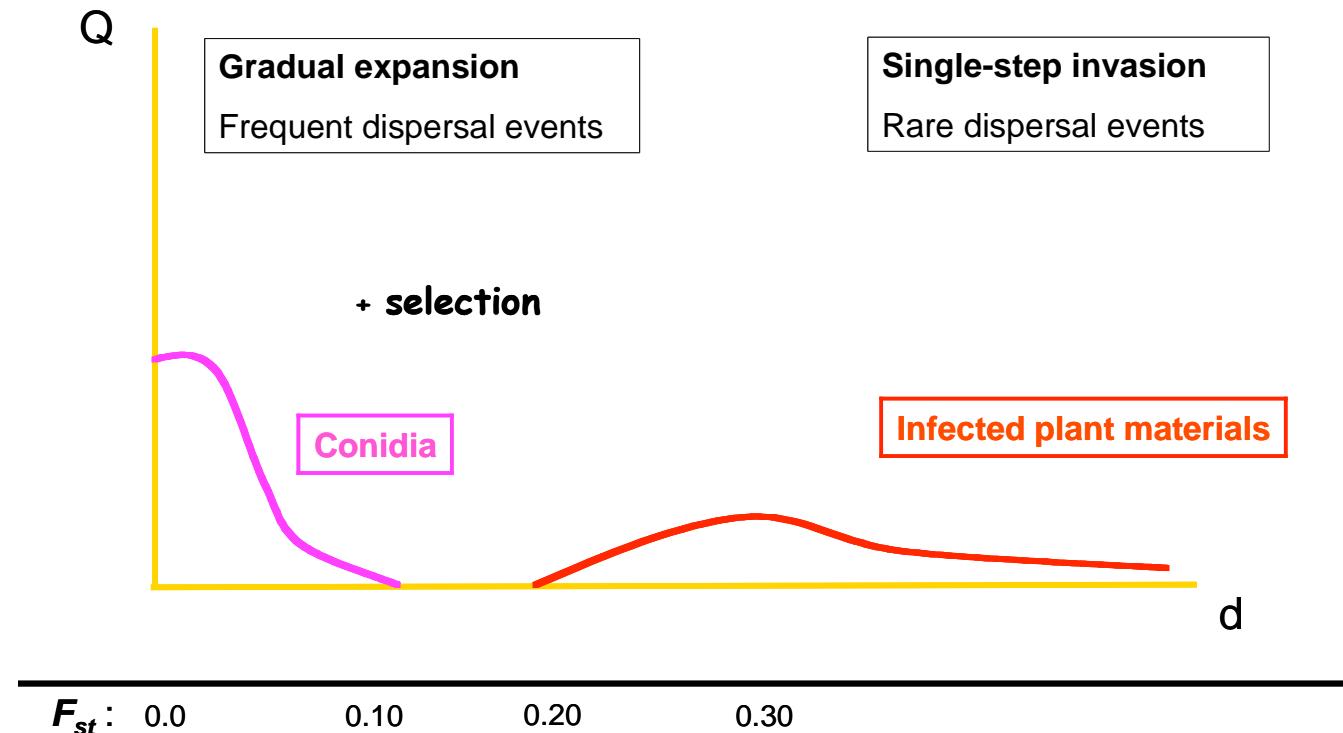
Distance between sites: 200 km

Fst = 0.19 S

Intercontinental

	Europe France + Spain	Asia Indonesia	Africa Madagascar
Europe		0.45	0.60
Asia	S		0.41
Africa	S		

Differentiation at regional and intercontinental scales
are also in agreement with limited migrations
Contradiction with ACE1 results ?



After Jean Carlier, CIRAD

Differentiation evaluations indicate limited migration (consistent with short distance movement of spores)

But :

- long distance migration is possible, probably by transportation of infected seeds
- in absence of recombination, selection by host resistance can also generate differentiation at local scale

To confirm preliminary studies on differentiation and migration with more populations

To trace intercontinental migrations with "phylogenetic" markers

To measure migration at local scale by epidemiological studies in the field

To measure the relative importance of migration and selection on differentiation

In collaboration with:

Manuel Aguilar, Mercedes Castejon
Dodelys Andriantsimialona
Dwinita Utami
M. Santoso

CIFA, Sevilla, Spain
Fofifa, Antsirabe, Madagascar
Icabograd, Bogor, Indonesia
Research Institute for Rice, Subang, Indonesia

