Mapping of natural nematode resistance in rice for use by West African farmers

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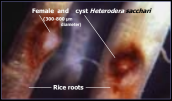
Introduction

Today, only about 1 ton/ha of rice is harvested in West Africa from rainfed lowland and upland areas mainly because of low soil fertility and pest and disease problems.
However, the potential of 3.7 tons/ha (world average) should be possible using pest and disease resistant high yielding rice varieties. Desirable genes for this are available in *Oryza sativa*, the Asian rice, and in *O. glaberrima*, the African rice, germplasm. Interspecific crosses between these have been achieved by WARDA (Jones et *al*.,1997) which combine the good traits of each species, but little is known of the genetics of those traits introgressed.

Incidence of Nematodes in West Africa

From pot and micropots experiments using culture inocula, nematologists in the past demonstrated that significant losses (> 50%) were caused by various species of nematodes *Meloidogyne spp*., *Pratylenchus brachyurus* and *Heterodera spp.* (Babatola, 1986; Plowright et *al*., 1999).



Heterodera sacchari (cyst nematode) against which no nematicide is efficient, is a known pest of upland rice, the predominant rice cultivation type in West Africa.

Description of the mapping populations

- Numerous tillers with droopy leaves at the vegetative stage (good for weed competition)
- Low yield, lodging and grain shattering at the reproductive stage
- Nematode resistant

African Rice
Oryza glaberrima
CG 14
(Ancestor 2)

X

Asian Rice
Oryza sativa
WAB 56-104
(Ancestor 1)

Interspecific introgression lines (BC_2F_6)
Oryza sativa/glaberrima
among which was the two Nematode resistant lines
WAB 450-IBP-160-HB (Parent 1.1)
WAB 450-11-2-BL1DR-DR1 (Parent 2.1)

Asian Rice
Oryza sativa
inbred lines
ITA 257 (ssp japonica) (Parent 1.2)
Bouake189 (ssp indica) (Parent 2.2)

- Fewer tillers with erected leaves at the vegetative stage
- Higher yield at the reproductive stage

105 F_4 families
76 F_3 families

Nematode testing at CABI:

For *Heterodera sacchari*: Two trials were carried out using two different isolates of *H. sacchari* : one from the Ivory Coast (RNC 71) and the other one from Ghana (RNC 65). In both cases, secondary juveniles (J_2s) and eggs were pipetted out and 100 J_2s and eggs were inoculated per plant on parents and their progenies (over 5 replicates). At harvest, 60 DAI, cysts and white females were washed from roots with a strong jet of water and elutriated 4 times onto a 250 µm sieve. Counts were done for the total number of females and cysts.

Molecular work at JIC:

Genetic maps of our two mapping populations have been initiated mainly with microsatellites markers using JOINMAP 3.0. To generate those genetic maps, 278 microsatellites markers (Temnykh et *al.* 2000) have been tested on the parental lines covering more than 300 loci. QTL analysis has been performed using QTL Café (http:// web.bham.ac.uk/G.G.SEaton/qtl_old/)

Phenotyping Results

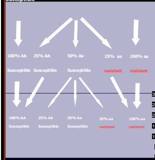
Single recessive gene model

First parent AA Susceptible × Second parent aa resistant

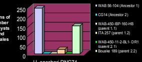
F1 100% Aa Susceptible

F2

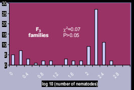
25% AA Susceptible — 50% Aa Susceptible — 25% aa resistant

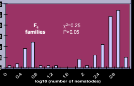


Results of *H.sacchari* RNC 71 (Ivory Coast) screening experiment on ancestors and parental lines



Distributions of frequencies among the 76 F_3 families and 105 F_4 families according to log_{10} (number of nematodes)

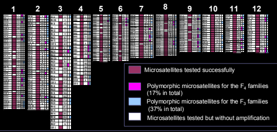




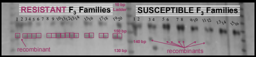
The 3 : 1 ratio over those two mapping populations suggests that, resistance towards *H.sacchari* is likely to be due to a single recessive gene.

Molecular Results

Genome coverage of our F_4 and F_3 families mapping work using microsatellites markers sorted per chromosome, according to their genetic distances on the Cornell's consensus genetic map 2001



Using Bulk Segregant Analysis on our F_3 families, a microsatellite marker on Chromosome 11 appears to be reasonably linked to the resistance but in a dominant way.



The construction of genetic maps is on going but is made difficult due to strong segregation distortions.

Future work…

- For both populations, to get a saturated map in the surrounding of the linked microsatellite marker using microsatellite markers or other kind of markers (like ESTs) in order to find a co-dominant marker segregating with our gene.
- Provide a gene tag to rice breeders to enable them to select their material efficiently for resistance to *H.sacchari*.

References

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Jones et *al*. (1997), Euphytica 92, 237-246.
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Abbreviations

DAI: Days After Inoculation
ESTs: Expressed Sequence Tags
J_2s: secondary juveniles
JIC: John Innes Centre
RM: Rice Microsatellite

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