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Identification of resistance sources and mapping of resistance QTLs to African strains of *Xanthomonas oryzae* pv. oryzae causing Bacterial Leaf Blight in rice

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Xanthomonas oryzae pv. *oryzae* is the causal agent of bacterial leaf blight (BB) and is considered as the most important disease of rice in irrigated environment (Fig.1) The disease was reported in Africa in the 80s, since then it is increasing in importance. The use of varietal resistance has proven to be very efficient in Asia in controlling the disease but selection and deployment of resistant varieties are still lacking in Africa. Recently we reported differences between Asian and African strains of *X. oryzae* pv. *oryzae and* the existence of three new races (A1,A2,A3).

The objectives are to identify sources of resistance to *Xoo* African strains among *O.glaberrim*a germplasm, to conduct a QTL analysis using the reference population IR64xAzucena to further identify genes controlling BB resistance in rice. Throughout the project we are using GCP products (genetic resources, markers). NARS capacities are strengthened through the transfer of skills.

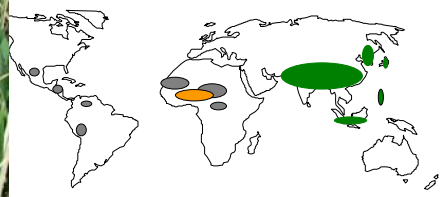

Fig.1 Symptoms and geographical distribution of BB

Materials and methods

Evaluation of O. glaberrima accessions

28 accessions of African cultivated rice *Oryza glaberrima* (source: GCP *iBridges project)* were selected and screened for BB resistance using two African *Xoo* strains (MAI1 and BAI3 originating respectively from Mali and Burkina-Faso) representing two *Xoo* African races (A1 and B3) (Figs 2, 3 & 4).

QTL mapping

The reference IR64xAzucena RI population made of 172 lines was obtained from IRD. A standardized method for BB resistance screening was used. At least 5 plants per genotype and 2 leaves per plant were inoculated with each strains (BAI3 and MAI1). QTL mapping analysis was done using ANOVA.

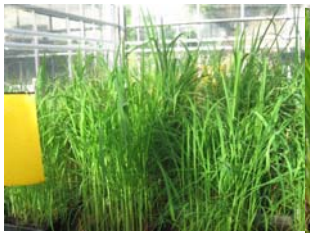

Fig.2 Plants in greenhouse

Fig.3 Leaf clipping inoculation

Plants were grown under controlled conditions (28°C and 80% humidity) in greenhouse (Fig.2) at IRD (France). Leaf clipping inoculation (Fig.3) were performed on 5 week-old plants with bacterial at an OD of 0.2 Phenotypic evaluations were done 3 weeks after inoculation by measuring the leaf lesion length (Fig.4) using the following scale: 0-5cm: Resistant (R), 5-10cm: Moderately Resistant (MR) 10-15cm: Moderately Susceptible (MS) >15cm Susceptible (S)

Results

***O. glaberrima :* a source for BB resistance?**

The two African *Xoo* strains tested were found to provoke different reactions on the *O. glaberrima* accessions. *Xoo* MAI1 induced 14 reactions classified as MR/R while *Xoo* BAI3 only one (TOG5672). As observed with BAI3, most all the *O. glaberrima* accessions were highly susceptible (Fig.5). On the contrary, CG14, TOG6308 and TOG6356 showed a high level of resistance to *Xoo* strain MAI1.

Fig.4 Scale used

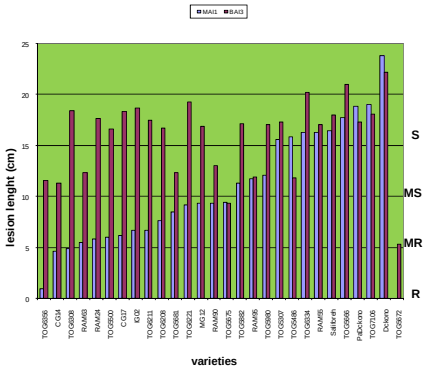

Fig.5 Reaction of 28 *O. glaberrima* accessions for BB resistance

New QTLs for BB resistance

IR64 shows a high level of resistance while Azucena is highly susceptible to both strains (BAI3 and MAI1). QTL mapping based on ANOVA evidenced five putative QTLs common to *Xoo* strains (MAI1 and BAI3), located on chromosomes 1, 4, 7, 10 and 11 respectively with a major QTL on chromosome 7 (29.8 % of total variance) (Fig.6). 2 additional QTLs were strain-specific (chromosome 3 for BAI3 and chromosome 8 for MAI1). Most of the QTLs reported here are different from those previously known however some colocalized with existing QTLs or *Xa* genes (chr 4 & 11) (Fig.6).

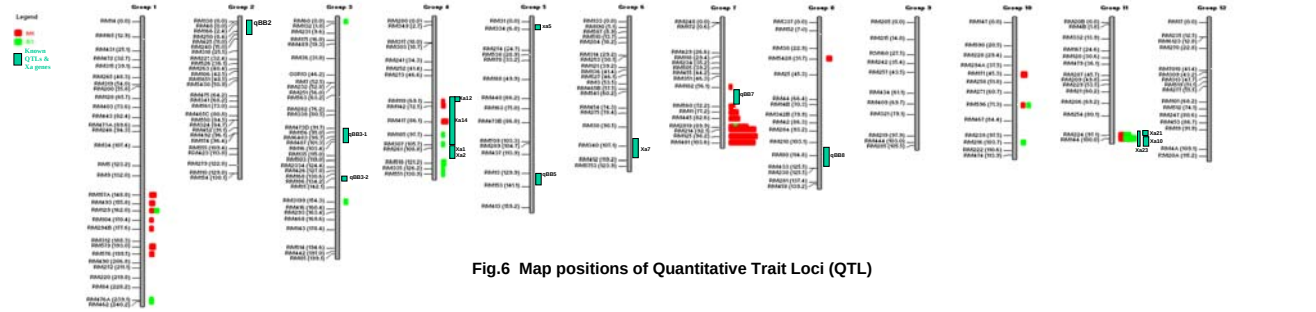

Fig.6 Map positions of Quantitative Trait Loci (QTL)

Conclusions and perspectives

- ***O. glaberrima* accessions were evaluated for BB resistance with new *Xoo* strains isolated in West Africa. Potential donors for BB resistance to specific *Xoo* strain were identified. Evaluation with 2 other *Xoo* strains (corresponding to race A2 strain BAI4) and Phil race2 (PXO86) is on going.**
- **The reference map population IR64xAzucena (172 lines) was evaluated for R to BB (2 African strains). Two additional *Xoo* strains are being evaluated. New QTLs were found on the reference map suggesting the existence of new R genes. Perspectives are to dissect the most significant QTL through recombination and to perform a detailed phenotypic analysis.**
- **We are increasing capacities of NARS (Generation fellowship awarded to GD). Activities in this project are strongly linked to existing activities under Generation Challenge Program (SP5 for training, SP3: iBridges, low cost gene marker, NERICA projects...)**