

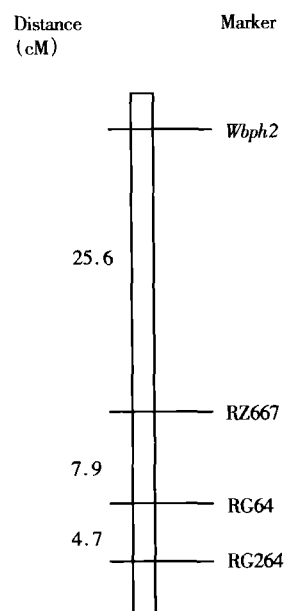
Tagging the gene *Wbph2* in ARC 10239 resistant to the white-backed planthopper *Sogatella furcifera* by using RFLP markers

LIU Zhiyan¹⁾, LIU Guangjie¹⁾, K SOGAWA²⁾, and ZHENG Kangle¹⁾, ¹⁾ CNRRI, Hangzhou 310006, China; ²⁾ Japan International Res Center for Agri Sci, Tsukuba, 305-8686, Japan

Gene tagging is the base of marker-assisted breeding for insect resistance in rice. Five genes (*Wbph1*, *Wbph2*, *Wbph3*, *Wbph4*, and *Wbph5*) were identified to be responsible for the resistance to the whitebacked planthopper. The gene *Wbph2* in ARC 10239 was clarified as a dominant resistant gene to *S. furcifera*. In present study, ARC 10239 and susceptible Minghui 63 were selected as parents to make a cross for gene tagging.

Restriction fragment length polymorphism (RFLP) markers were used as probes to survey the bulked DNAs from homozygous susceptible lines. DNA from parents, pooled sample, and F₂ were digested with four restriction enzymes: *Bam*H I, *Dra* I, *Eco*R V, and *Hind* III. One hundred and twenty-nine RFLP markers distributed over the 12 chromosomes were screened. Six positive probes were used to assay the 142 F₂ individuals. It was found that *Wbph2* were linked to the marker RZ667 on the chromosome 6 with a distance of 25.6 cM (LOD = 4.5) (see figure). Further screening of the adjacent probes indicated that RG64 and RG264 were also linked to *Wbph2* with the distance of 27.8 cM (LOD = 4.32) and 36.4 cM (LOD = 2.56), respectively. Therefore, the gene

Wbph2 was mapped on rice chromosome 6. □



Mapping *Wbph2* on rice chromosome 6.

Geographic distribution of mating type and female fertile isolates in *Magnaporthe grisea* of China

SHEN Ying¹⁾, JL NOTTEGHEM²⁾, YUAN Xiaoping¹⁾, ZHAO Xinhua¹⁾, and D THARREAU³⁾, ¹⁾ CNRRI, Hangzhou 310006, China; ²⁾ INRA, UFR de Biologie et Pathologie Vegetales, 2 Place Viala, 34060 Montpellier; ³⁾ International Center for Cooperation in Agronomic Research Development, TA 73/09, 34398 Montpellier, Cedex 05, France

Population studies of *Magnaporthe grisea* have brought new insight on old controversies. This species include pathogens of rice, causing the rice blast, and of other grass hosts. It has been demonstrated that isolates collected from rice are pathogenic to rice and to a limited number of grass hosts. The genetic structure of the *M. grisea* populations showed that a sexual reproduction was predominant in most rice growing areas. Being a hermaphroditic heterothallic ascomycete, sexual reproduction of *M. grisea* required isolates of both mating types. Moreover, it also required the existence of female fertile isolates. Thus, the first step to find sexual reproduction in the field was to look for the presence of strains of both mating types and of female fertile ones. Female fertile isolates collected from rice was very rare. Thus, further investigation was made for testing the hypothesis of sexual reproduction by population genetics studies.

Three hundreds and seventy-eight isolates of *M. grisea* were collected from 17 provinces/cities and autonomous regions in China. Each isolate was tested for mating type with two Mat 1.1 and two Mat 1.2 fertile (hermaphroditic) standard

isolates. Among them, 24.8 % were Mat1.1, 39.2 % were Mat1.2, and the remains did not produce perithecia with any of the 4 fertile testers. In most provinces, both mating types existed. In three provinces, only one mating type was found. Almost all the isolates had very low fertility, as they were in general female sterile and male sterile. Hermaphroditic isolates recovered at low frequencies (6 % -11 % of the total analyzed isolates) in four provinces (Guangdong, Guizhou, Hunan, and Zhejiang). Higher frequencies were recorded in Yunnan (14.3 %) and Hubei (66.7 %).

A large number of field isolates and highly fertile standard tester strains of known mating type was required to determine the frequency of each mating type in natural populations of *M. grisea*. This study confirmed the low fertility of *M. grisea*