

14. The distribution and mapping of QTL for resistance to brown planthopper infestation in rice

Y. Q. LIU¹, C. C. SU¹, L. JIANG¹, J. HE¹, C. PENG¹, H. WU¹, L. L. LIU¹ and J. M. WAN^{*1, 2}

1) State Key Laboratory of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing 210095 China

2) Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081 China

Tel.:+86-25-84396516, Fax: +86-25-84396516

* Corresponding author (e-mail: wanjm@njau.edu.cn)

The brown planthopper (BPH) *Nilaparvata lugens* Stål is one of the most destructive insect pests of rice (*Oryza sativa* L.) throughout Asian rice-growing countries. The use of genetically resistant cultivars has proven to be a more economical, efficient and environmentally friendly means to combat this pest. The exploitation of quantitative resistance has been suggested as a better way of achieving durable resistance (Heinrichs 1986; Bosque-Perez and Buddenhagen 1992). Either way, there is a need for further sources of genetic resistance.

We screened 515 rice landraces originating from Vietnam and China for the reaction to brown planthopper (BPH) infestation. Most of the resistant selections were *indica* types from Vietnam and Guangxi province, China (Fig. 1, 2).

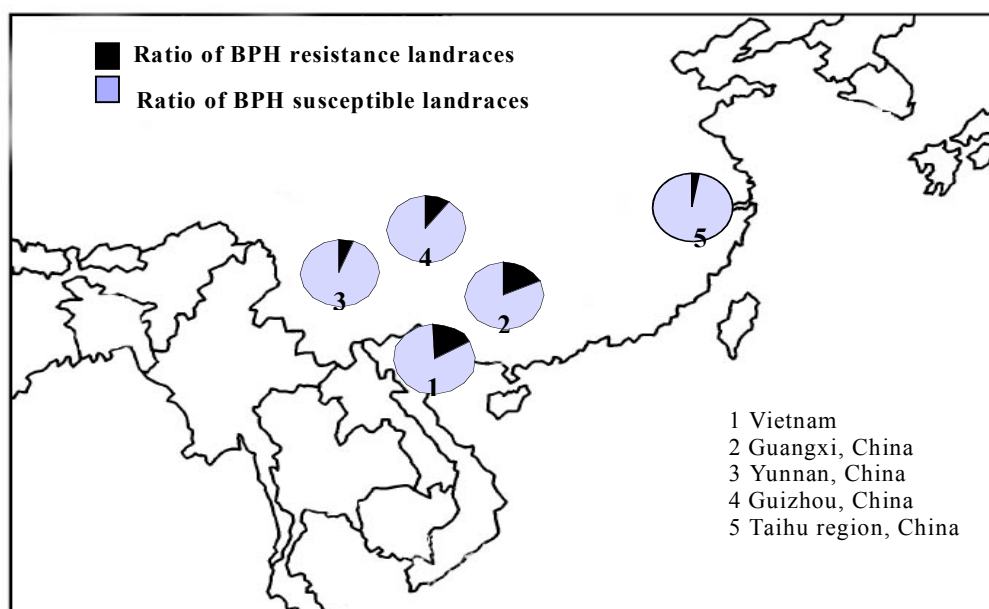


Fig.1. Geographical distribution of BPH resistance in a collection of rice landraces.

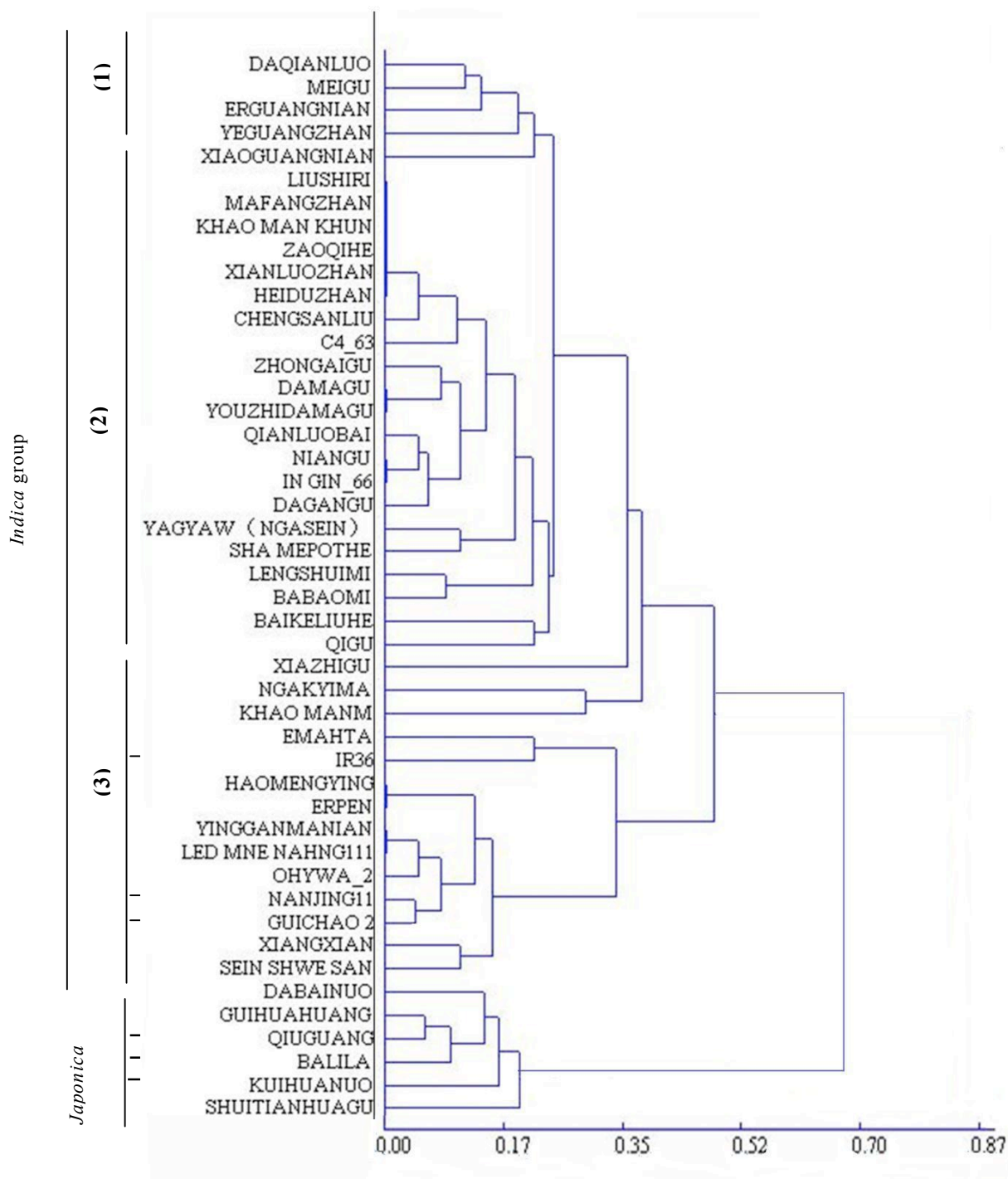


Fig. 2. Genetic diversity of 40 BPH resistant landraces based on their genotype at 47 SSR loci. *indica* check, *japonica* check, (1), (2), and (3) - three sub-clusters within the *indica* group.

We created an F₂ population from the cross between a BPH resistant Vietnamese landrace YAGYAW and the susceptible cultivar Cpslo17, and this was used to construct a genetic map, which allowed us to determine the genetic basis of BPH resistance. We

mapped four quantitative trait loci (QTL) and they were located on chromosomes 2, 4, 7 and 11, designed as *QBPH2*, *QBPH4*, *QBPH7*, and *QBPH11*. The individual QTL accounted for between 8.7% and 16.5% of the phenotypic variance, with the resistant alleles at all four QTL deriving from YAGYAW (Fig.3, Table 1). Compared with previous research, *QBPH2* may be a novel source of BPH resistance. The linkage information derived in the present study between SSR markers and the BPH resistance QTL provides the necessary tools to undertake marker-assisted selection for BPH resistance in rice.

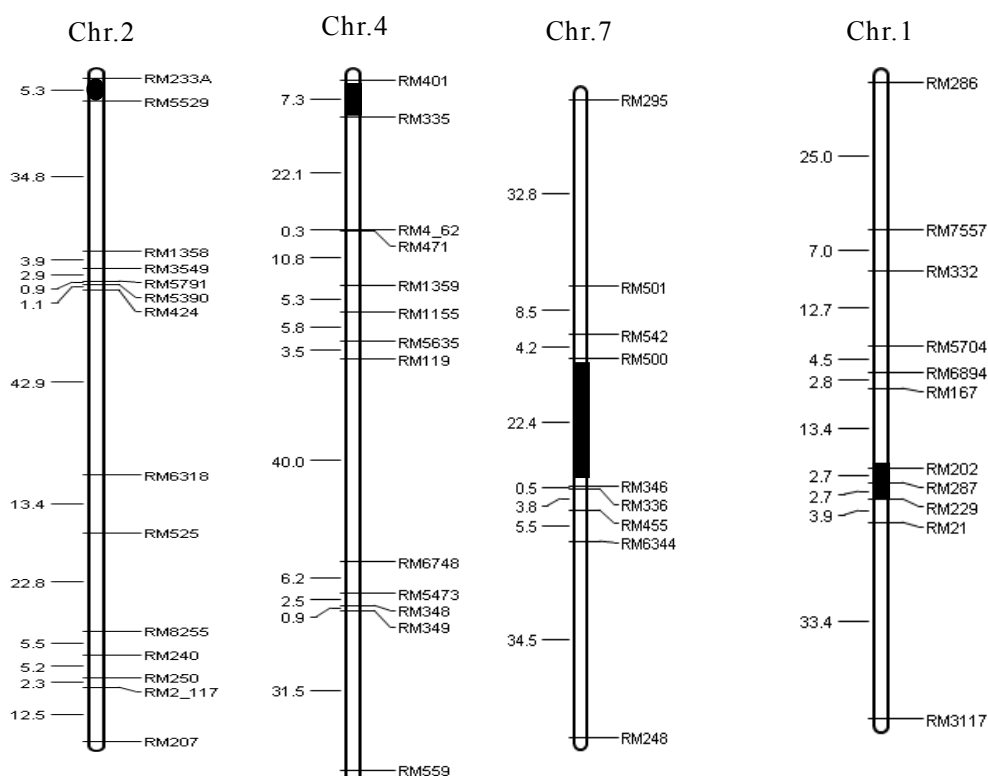


Fig.3. The frequency distribution of BPH-resistant $F_{2:3}$ lines derived from the cross YA x Cpslo17. The black bar on each chromosome represents the QTL location.

Table 1 QTL associated with resistance to BPH mapped in the cross YA x Cpslo17.

QTL	Interval	Chromosome	LOD score	PVE(%) ^a	Additive effect	Dominance effect
<i>QBPH2</i>	RM233A-RM55	2	2.6	11.9	-1.45	0.93
<i>QBPH4</i>	RM401-RM335	4	5.5	16.5	-1.59	0.73
<i>QBPH7</i>	RM500-346	7	3.1	9.2	-0.87	1.61
<i>QBPH11</i>	RM202-RM229	11	3.1	8.7	-1.59	-0.92

a) Percentage of phenotypic variance explained (%)

References

- Heinrichs E.A. 1986, Perspectives and directions for the continued development of insect resistant rice varieties. *Agric Ecosyst Environ* 18:9–36.
- Bosque-Perez N.A., Buddenhagen I.W. 1992, The development of host-plant resistance to insect pests: outlook for the tropics. In: SBJ Menken, J H Visser & P Harrewijn (eds), *Proceedings 8th International Symposium Insect-Plant Relationships*, Dordrecht: Kluwer Academic Publishers, pp. 235-249.