

A simple sequence repeat- and single-nucleotide polymorphism-based genetic linkage map of the brown planthopper, *Nilaparvata lugens*

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The first genetic linkage map for brown planthopper (BPH, *Nilaparvata lugens*), a major insect pest of rice, was developed. The linkage map was constructed by integrating linkage data from two backcross populations derived from three inbred BPH strains. The consensus map consists of 474 simple sequence repeats, 43 single-nucleotide polymorphisms, and 1 sequence-tagged site, for a total of 518 markers at 472 unique positions in 17 linkage groups.

Keywords: *Nilaparvata lugens*, brown planthopper, genetic linkage map, SSR, SNP

Background

Brown planthopper (BPH, *Nilaparvata lugens*) is the most important insect pest of rice that decreases rice yield by direct feeding on rice or virus transmission of rice diseases. While various insecticides and host-plant resistance to BPH have been applied for controlling this insect pest, emergence of new populations that developed insecticide resistance or adaptation to resistant rice varieties in the fields is the critical threat for BPH management. Understanding the genetic basis and identifying responsible genes for these agriculturally important traits in BPH are necessary for future BPH management strategies. A genetic linkage map of BPH based on molecular markers could provide a valuable tool for genetic analysis of BPH.

Results and Discussion

1. Inbred lines were established for three BPH strains with different genetic backgrounds (Hadano-66, Chikugo-89, Koshi-10). Two backcrossed populations were generated and used as the basal materials for developing molecular markers and genetic linkage maps.
2. SSR (simple sequence repeat) markers and SNP (single nucleotide polymorphism) markers were designed by analyzing genomic sequences and EST (expressed sequence tags) of BPH.
3. SSR and SNP markers that are polymorphic between inbred lines were selected and their individual genotypes in backcrossed populations were detected. Recombination values between markers were calculated to determine linkage groups and generate a genetic linkage map. The linkage map contains 474 SSR markers (including 100 previously reported markers by Jing *et al.* 2011) and 42 SNP markers (Fig. 1).
4. The sex-linkage group was identified by exploiting X-linked and Y-specific markers.
5. Molecular marker database for BPH was constructed and released to the public.

Future prospects

1. Our genetic linkage map and molecular markers for BPH are essential resources for genetic analyses of genes controlling agriculturally important traits of BPH, such as insecticide resistance and virulence to the resistant rice varieties.
2. The discrepancy in the number of linkage groups (17) obtained by genetic analysis and the actual number of BPH chromosomes (15) will be resolved using additional molecular markers.

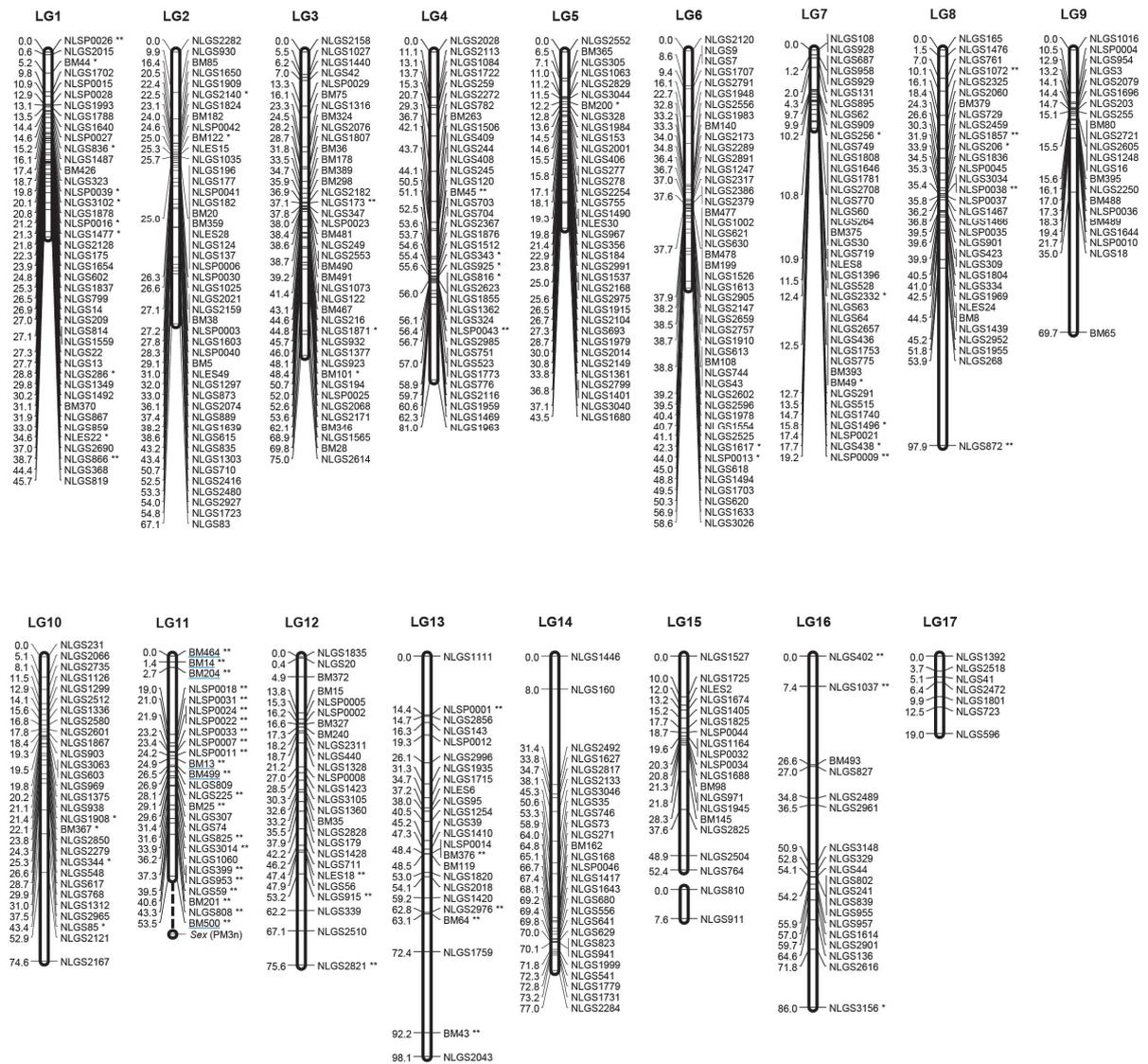


Fig. 1. Genetic linkage map of the brown planthopper with 518 markers. NLGS and NLES represent SSR markers, NLSP represents SNP markers and BM represents previously reported SSR markers.

Collaborators

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