

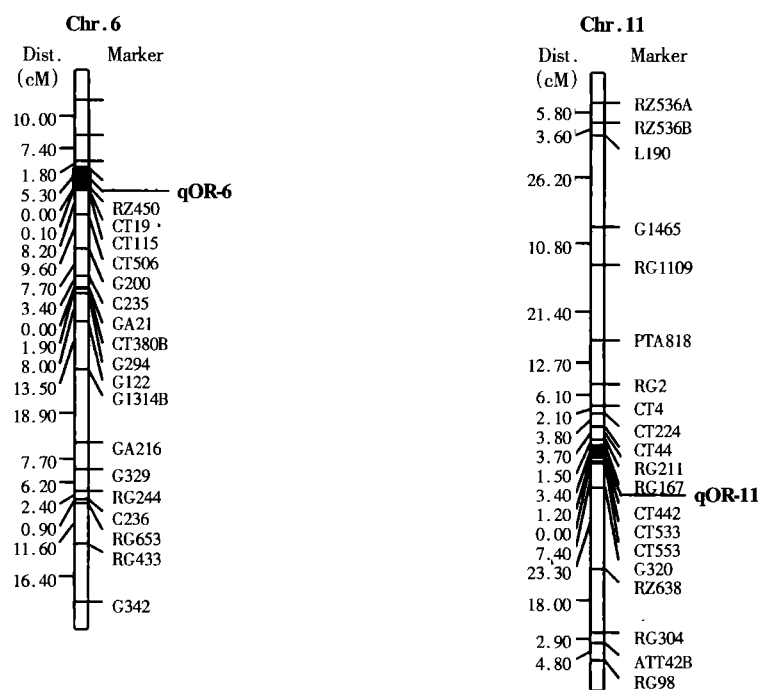
QTLs for ovicidal response to whitebacked planthopper in rice

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Japanese japonica rice commonly provides with an ovicidal resistance against the whitebacked planthopper (WBPH). Similarly, ovicidal activity was also found to play a significant role in a stable field resistance to WBPH in some Chinese japonica rice. Rice varieties with ovicidal resistance characterized by watery lesions and subsequent necrotic symptom in the leaf sheaths oviposited by WBPH. Based on the ovicidal symptom, the ovicidal QTLs on the rice chromosomes were analyzed by using a doubled haploid (DH) population of 122 lines derived from a cross between a non-ovicidal indica variety Zaiyeqing 8 (ZYQ 8) and an ovicidal japonica variety Jingxi 17 (JX 17). There was a significant difference in WBPH egg mortality between the two varieties. Average egg mortality was 36.5% in ZYQ 8, and 72.8% in

JX 17.

Each DH line was transplanted into a 1 m² plot with 6 × 7 plants in CNRRI farm on Jun 21, 2001, and exposed to be oviposited by WBPH immigrants. The ovicidal symptom in each DH line was graded by 0 - 3 scales according to the intensity of ovicidal symptom on Jul 6, 2001. ZYQ 8 and JX 17 were graded 0 and 2, respectively. The number of DH lines graded at 0 was 12, at 1 was 32, at 2 was 42, and at 3 was 36. Based on a RFLP linkage map consisting of 127 DH lines, the QTLs for ovicidal symptom were detected by using the software Mapmaker/QTL 1.1b. A major ovicidal QTL was located at the position between CT201 and RZ450 on the short arm of chromosome 6. Its LOD peak score was 5.60, and explained 20.7% of phenotypic variance of ovicidal symptom. This ovicidal allele was from JX 17. Another minor QTL with LOD scores of 2.96 was found between RG167 and CT442 on chromosome 11. Its ovicidal allele was contributed by ZYQ 8. □



Locations of ovicidal QTLs on the rice chromosomes.

Intervals between markers in centi-Morgans (cM) on the left of each chromosome. Ovicidal QTLs indicated on the right of chromosome.

Detecting QTLs for rice panicle length under different N levels

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Rice panicle length is a quantitative trait controlled not only by genetic factors but also by environment conditions, especially by nitrogen supply level. It is supposed that genes of rice panicle length could be fully expressed under sufficient N supply and be restricted by low N stress. Determination of QTL × N-level interaction associated with the rice panicle length would be helpful for revealing the genetic basis of rice N efficiency at low N level. This study was to identify QTLs for rice panicle length in a doubled haploid (DH) population under two N levels, and to search for evidences on the genetic basis of nitrogen