

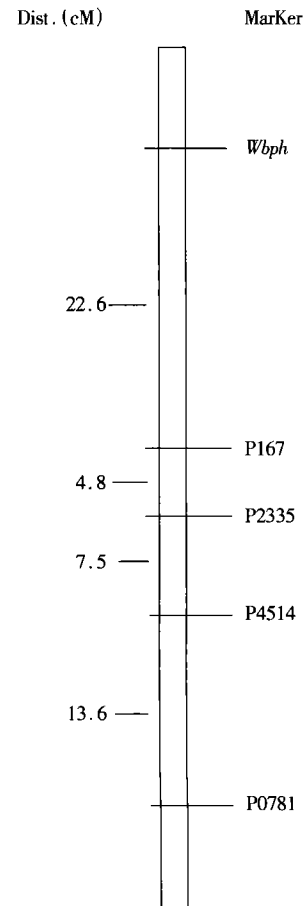
Mapping of putative sucking inhibitory gene to whitebacked planthopper by linkage analysis with CAPS markers

ZENG Dali^{1, 2)}, K Sogawa¹⁾, H Fujimoto¹⁾, Li Jiayang³⁾, and QIAN Qian²⁾,
¹⁾ Japan International Res Center for Agri Sci, Tsukuba, Japan; ²⁾ Key Lab for Rice Biology, CNRRI, Hangzhou 310006; ³⁾ Inst of Genetics and Development Biology, the Chinese Academy of Sciences, Beijing 100101, China

Resistance to whitebacked planthopper (WBPH) in Chinese japonica rice Chunjiang 06 (CJ-06) was mediated by sucking inhibitory and ovicidal mechanism. The ovicidal response was a common self-defense mechanism against WBPH in japonica. The ovicidal gene and its chromosomal position had already been identified. The sucking inhibitory nature of CJ-06 caused a definite non-preference behavior of WBPH in fields. A single dominant gene governed the sucking inhibition in CJ-06.

We preliminarily located the putative sucking inhibitory gene on rice chromosomes. About 250 F₂ plants from reciprocal crossing between CJ-06 and susceptible indica TN1 were phenotyped based on the weight of honeydews excreted by WBPH. Gravid WBPH females were individually confined into a parafilm sachet for a day, and each parafilm was quantified by weighing. F₂ plants on which WBPH females excreted more than 10 mg and less than 5 mg honeydews were phenotyped as susceptible and resistant, respectively.

Totally, 205 SSR and CAPS markers distributed over 12 chromosomes were screened for polymorphism between the resistant CJ-06 and susceptible TN1, and 82 markers were found to be polymorphic. Linkage analysis between the polymorphic markers and resistant/susceptible phenotypes showed that the putative sucking inhibition gene cosegregated with the CAPS markers P167, P2335, P4514, and P0718 on chromosome 11, and with the genetic distance of 22.6 cM, 27.4 cM, 34.9 cM, and 48.5 cM, respectively. Detailed CAPS of this gene is continuously progressing. □



Location of the vicinity of the sucking inhibitory gene for WBPH rice on chromosome 11.

QTL analysis of leaf photosynthetic rate and related physiological traits in rice (*Oryza sativa* L.)

TENG Sheng^{1, 3)}, QIAN Qian¹⁾, ZENG Dali¹⁾, Yasufumi Kunihiro⁴⁾, Hiroshi Fujimoto⁴⁾, HUANG Danian^{1, 3)}, and ZHU Lihuang²⁾, ¹⁾ Key Lab for Rice Biology, CNRRI, Hangzhou 310006; ²⁾ Inst of Genetics and Development Biology, the Chinese Academy of Sciences, Beijing 100101; ³⁾ College of Life Sci, Zhejiang Univ, Hangzhou 310029, China; ⁴⁾ Japan International Res Center for Agri Sci, Tsukuba, Japan

Photosynthesis is one of the most important factors that influence the biomass and yield. Recently, more attention has been paid to genetic study on rice photosynthesis and rice breeding for the physiological traits related to high efficient photosynthesis. Chlorophyll content, stomatal resistance, and transpiration rate were very important physiological traits related to photosynthesis. But until now, no genetic study on these traits has been reported. A DH population derived from anther culture of ZYQ8/JX17, a typical indica/japonica hybrid was developed,

the photosynthetic efficiency and its related physiological traits were quite different between ZYQ8 and JX17. In this study, QTL analysis of net photosynthetic rate, chlorophyll content, stomatal resistance, and transpiration rate were conducted and the utilization in rice breeding was explored by using the DH population.

Field experiment was conducted on the farm of CNRRI in 2000. DH lines and its parents were planted in a randomly complete block design with two replications. Chlorophyll content was measured by using