MSc. Thesis Abstract

TRUONG QUOC ANH. 2007. Genetic analysis of resistance to bacterial blight of rice in a rice cultivar Asominori. MSc. Thesis. Kyushu University, Japan. 64 p.

Bacterial blight of rice (BB) caused by *Xanthomonas oryzae* pv. *oryzae* is one of the most destructive diseases of rice and widely distributes to the rice growing countries in the world. Rice yield losses due to BB in some areas of Asia can be as high as 50%. Recently, the incidence of this disease is frequently reported in Southeast Asia, especially in hybrid rice growing areas as in China. Since there is no bactericide effectiveness to the disease, introduction of resistant varieties is the most effective measure to control it. Currently, more than 20 resistance genes for BB have been identified. Some of them have been successfully incorporated into improved varieties. A rice cultivar Asominori conveyed a unique resistance to Japanese BB pathogen races. It showed not only qualitative resistance to some races but also quantitative resistance to other races. The resistance pattern was long recognized as genetic resource for rice breeding in Japan. The study aimed at analyze genetic basis of resistance to BB using recombinant inbred lines (RILs), and chromosome segment substitution lines (CSSLs).

The RILs derived from cross of Asominori / IR24 were used to genetically analyze. For QTL analysis, simple interval mapping (SIM) and composite interval mapping (CIM) methods were used by Window QTL cartographer version 2.0

A critical threshold value of the likelihood of odd (LOD) score was calculated by conducting 1,000-permutation test at significant level of 0.05.

Three Japanese representative BB strains of three races (T7174, T7133 and H75304) were used for inoculation and plants were inoculated at booting stage by leaf-clipping method

Frequency distribution of lesion length caused by race I and V showed bimodal segregation with 2 resistant and susceptible groups. The segregation fits a 1:1 ratio, indicating that the resistance of Asominori to both races I and V was under monogenic control. Linkage between resistance gene and DNA markers showed that the gene was located on chromosome 4. These agreed with the previous finding of resistance genes *Xa-1* and *Xa-12* from Kogyoku donor. The alleles at *Xa-1* and *Xa-12* loci from Asominori were tentatively designated as *Xa1-Aso* and *Xa12-Aso*, respectively.

Frequency distribution of lesion length to race III showed continuous variation. QTL analysis indicated that one QTL was detected on chromosome 4 near the region of *Xa1-Aso* and *Xa12-Aso* with LOD score of 10.4 and explained 48.5 percent of total variation. This suggested that only *Xa1-Aso* and *Xa12-Aso* region (hereafter-referred to*Xa1-Aso* region) on chromosome 4 affected to the resistance to race III

Since *Xa1-Aso* region on chromosome 4 affected qualitative and quantitative nature of the resistance of Asominori, a CSSL, IAS22 line, containing the chromosome segment of *Xa1-Aso r*egion of Asominori on chromosome 4 under genetic background, IR24 was used for further analysis. F_2 population from IAS22 / IR24 was inoculated by race I. Several F_2 plants showed homozygous; and heterozygous segregants for *Xa1-Aso* region were selected in F_3 generation. A total of 72 F_3 segregants from three heterozygous F_2 plants were used for mapping. The locus of *Xa1-Aso* was mapped between RM6089 and RM1153, with genetic distance of 7.9 cM and 5.8 cM, respectively. This linkage information is useful for marker-assisted selection of *Xa1-Aso* region in rice breeding and for fine dissection of the *Xa1-Aso* region. The F_4 progenies from the homozygous F_2 plants for *Xa1-Aso* region were selected to evaluate quantitative nature of resistance to race III. The selected F_4 plants (XF_4 1 and 2) showed also the shorter lesion development when inoculated by race III. Quantitative nature of resistance conveyed by Asominori to the

other Japanese race IV and Vietnamese races was also investigated using the F_4 progenies. Significant difference was not observed when compared with the susceptible check IR24.

The inheritance of qualitative resistance to Japanese BB pathogen races I and V conveyed by Asominori agreed with that by a resistance donor Kogyoku. The resistance to races I and V appeared to be controlled by *Xa1-Aso* and *Xa12-Aso* on chromosome 4, respectively. SSR markers sandwiching *Xa1-Aso* and *Xa12-Aso* region should be useful for marker-assisted selection in breeding program. QTL analysis and comparison of lesion development using CSSLs suggested that only *Xa1-Aso* and *Xa12-Aso* region on chromosome 4 affected the quantitative nature of resistance of Asominori to race III. This phenomenon in which both qualitative and quantitative natures of resistance is controlled by the same region should be considered for further development of BB resistance genes in future breeding program.