

2. Genetics of Host Resistance and Pathogen Variability of Rice Bacterial Blight

Seong-Ho Choi

Crop Environment and Biotechnology Division, National Crop Experiment Station, RDA, Suwon 441-100, Korea

Bacterial blight of rice caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is one of the most important diseases in most rice growing countries. Although the disease had been reduced in Korea since late 1980s, it has become more serious in recent years. Since host resistance is the most effective way to control the disease, researches on the host resistance and pathogenic variation have been emphasized most significantly. Development of resistant cultivars to the disease has also been one of the major targets in rice breeding program in Korea.

Genetics of rice resistance and Xoo virulence interaction was well established. So far more than 25 major resistance genes have been identified and designated mainly to the Japan, Philippines and Chinese Xoo strains. Most countries where the disease is a problem have their own differential system to classify the virulence of the pathogen. Near isogenic lines containing a single major gene were developed in several countries, which will be useful to establish an international differential system as well as for resistance breeding. Resistance spectrum of most genes was race or isolate specific.

Breakdown of resistance gene *Xa4* was reported by severe disease incidence and virulent race population build-up in Philippines. The mechanism of the resistance breakdown was understood as a virulence change of Xoo population structure from host selection as well as occurrence of a new virulent strains by genetic mutation. This aroused the importance of durability of host resistance, which accelerated QTL researches on resistance.

The gene-for-gene concept between resistance gene and avirulence gene in bacterial blight was well verified by the molecular genetics between *Xa10-avrXa10* and *Xa7-avrXa7* combination; that is, resistance of rice plant to Xoo was determined by the interaction with the Xoo avirulence genes and breakdown of the resistance was occurred by mutation of the complement avirulence gene in Xoo. So far two avirulence genes *avrXa7* and *avrXa10*, and two resistance genes *Xa1* and *Xa21* have been cloned and characterized in Xoo and rice, respectively.

Interestingly, loss of avirulence function of the *avrXa7* accompanied reduction of virulence to the susceptible cultivars, suggesting that the resistance gene *Xa7* might be durable. This hypothesis was tested in field experiment and verified by significantly less disease in rice lines having *Xa7* compared to the other varieties having resistance gene *Xa10* or *Xa4*. This results suggested that durable resistance genes could be identified and selected from major genes through evaluation of Xoo avirulence gene function on

the basis of gene-for-gene concept.

In Korea, the Xoo population showed unique virulence spectrum compared to the Philippines Xoo population. Although most Philippine Xoo strains were avirulent to *Xa21*, most Korean Xoo strains were compatible to the resistance gene. The Korean Xoo population could be classified into only five races by the current Korean BB differential system. However, when the near isogenic rice lines having more number of resistance genes were used, Korean Xoo population was classified into 18 pathotypes.

Recently, near isogenic lines having *Xa1*, *Xa2*, or *Xa3* have been developed in Korean cultivars. Gene pyramiding using the three resistance genes has been tried recently in Korea. However, based on the wide spectrum of virulence of the Korean Xoo population, other resistance gene sources than the three would be required in resistance breeding program in Korea. Besides, the current status of genetic analysis of Korean rice cultivars to bacterial blight is very poor. Therefore, characterization of Xoo population in virulence, analysis of the origin of the resistance genes in Korean rice cultivars, and identification of durable resistance genes are deemed necessary to increase the efficiency of host resistance to control the bacterial blight disease in Korea.

E-mail: shchoi@rda.go.kr