

学 位 論 文 要 旨	
氏 名	Constantine Sakala Busungu Athanas Kwilasa
題 目	Genetic analysis of resistance to bacterial blight ( <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> ) in rice (イネにおける白葉枯病菌 ( <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> )に対する抵抗性の遺伝解析)
<p>Rice (<i>Oryza sativa</i>) is one of the most important food crops in the world, feeding 50% of world population daily. Bacterial blight disease caused by <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (<i>Xoo</i>) is one of the most destructive diseases inflicting rice. Developing resistant cultivars is generally regarded as the most effective and economical means of controlling this disease, which is based on study of resistant genes against <i>Xoo</i>.</p> <p>In this thesis, I report the genetic analysis of the <i>Xoo</i> resistance of XM14 line. This line was obtained by the mutation induction of an Indica cultivar IR24, which is susceptible to six Philippine <i>Xoo</i> races and six Japanese <i>Xoo</i> races, using N -methyl-N-nitrosourea. XM14 shows resistance to all the races tested: one Philippine <i>Xoo</i> race and six Japanese <i>Xoo</i> race. I inoculated Japanese <i>Xoo</i> race II to the F<sub>2</sub> population from the cross between XM14 and IR24. The ratio of resistant plants: susceptible plants fitted 1: 3, which suggested that a single recessive gene of XM14 controlled resistance to the <i>Xoo</i> race.</p> <p>Approximate chromosomal location of the resistance gene was determined using F<sub>2</sub> plants from the cross between XM14 and a Japonica cultivar Koshihikari, which is susceptible to Japanese <i>Xoo</i> races. Because the distribution of lesion length was continuous, I adopted the analysis using extreme recessive phenotype proposed by Zhang <i>et al.</i> (1994). Ten plants with shortest lesion length were genotyped for 116 DNA markers covering the whole rice genome, with the result that the gene was located close to centromeric region on chromosome 3.</p> <p>IAS16 line carries IR24 genetic background with a Japonica cultivar Asominori chromosome 3 segment, on which the above resistance gene locus was thought to be located. 194 F<sub>2</sub> plants from the cross between XM14 and IAS16 showed a discrete distribution. The linkage analysis using 6 SSR markers and 12 INDEL markers revealed that the gene is located very close to the centromeric region of chromosome 3. The gene identified in XM14 was new, and named <i>XANTHOMONAS ORYZAE</i> PV. <i>ORYZAE RESISTANCE 42</i> (<i>XA42</i>). <i>Xa42</i> is a susceptible wild type allele, whereas <i>xa42</i> is a resistant mutated allele.</p> <p>Then, a high-resolution mapping of <i>xa42</i> was performed using 13,000 F<sub>2</sub> plants from the cross between XM14 and IAS16, F<sub>3</sub> lines from selected F<sub>2</sub> recombinants, 2 SSR markers, 12 INDEL markers, 3 CAPS markers and 2 dCAPS markers, with the result that the candidate <i>xa42</i> region was narrowed down from 578 kb, which had been obtained in the initial mapping, to 57 kb.</p> <p>In addition to resistance against multiple <i>Xoo</i> races, XM14 line shows brown spots like lesion mimic mutants in its leaves. This line also has a smaller stature than the original cultivar IR24. In <i>XA42</i> gene segregating F<sub>3</sub> lines from the cross between XM14 and IAS16, homozygotes of <i>xa42</i> allele were consistently resistant to six Japanese <i>Xoo</i> races used. They also showed brown spots, and significantly short stature compared with the other genotypes, suggesting that <i>xa42</i> gene exhibits pleiotropic effect.</p> <p>Because <i>xa42</i> gene is resistant to multiple <i>Xoo</i> races, it will be very useful in resistance breeding programs.</p>	