

学 位 論 文 要 旨	
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題 目	Study on Sheath Blight Resistance and Yielding Capacity by Phenotype and QTL Analysis in Rice Line 32R (イネ系統 32R における表現型と QTL 解析による紋枯病抵抗性と多収性改善に関する研究)
<p>Sheath blight disease, caused by <i>Rhizoctonia solani</i> Kuhn, is one of the most important diseases of rice. Despite extensive searches of the rice germ plasm, major genes, which give a complete resistance to the fungus, have not been identified. The use of resistant rice cultivars is a powerful tool to reduce the use of environmentally destructive pesticides. Sheath blight disease severity of the rice can be affected by environmental and chemical factors, and the epidemic area of sheath blight disease is also increasing because of climate change.</p> <p>The objective of this study is to determine the genetic components of yielding capabilities and Quantitative trait loci (QTL) of sheath blight disease resistance rice line 32R. Rice line 32R is a well-documented source of durable and broad-spectrum resistance to sheath blight disease. Rice line 32R was developed from the indica cultivar Tetep by crossing with the japonica cultivar CN4-4-2 by using classical breeding techniques. CN4-4-2 is the progeny of Chugoku 45 and Nipponbare</p> <p>The rice line 32R, having the poor yielding capacity, crossed with Nipponbare produced 12.5 t/ha yield in the F₁ progeny with an ideotype plant structure. The high yielding capacity is due to the improved performance of culm length, panicle length, number of tiller, tillering angle, Rubisco content in leaf, nonstructural carbohydrate (NSC), dry matter accumulation (DMA), leaf area and number of filled grain per panicle. The mid parent and better parent heterosis was 42.3 and 29.8% for grain yield, respectively. Multiple regressions showed that number of filled grain per panicle, panicle length and leaf area contributed 83.0, 28.4 and 29.9 % of its effort to the grain yield, respectively in F₁ progeny.</p> <p>QTL analysis of the sheath blight disease resistance using simple sequence repeat (SSR) markers was conducted in F₂ population derived from the crossing of 32R with Nipponbare (susceptible to the sheath blight). Sheath blight resistance in F₂ population and its cross parents were studied using syringe inoculation method. Seven QTLs for the sheath blight resistance (<i>qSBR1</i>, <i>qSBR3</i>, <i>qSBR4</i>, <i>qSBR5</i>, <i>qSBR7</i>, <i>qSBR8</i> and <i>qSBR9</i>) were identified in chromosome 1, 3, 4, 5, 7, 8 and 9, respectively. Their resistance alleles derived from the resistance parent 32R. Similarly, the QTLs of culm length and leaf angles also identified. The QTLs of plant height and Leaf angles can be utilize for the development of plant structure suitable for resistance of sheath blight. Additionally, the negative significant correlation between sheath blight disease and culm length suggest that plant height is unfavorable for sheath blight development. <i>qSBR1</i>, <i>qSBR7</i> and <i>qSBR9</i> shows characteristic of valuable QTLs that would enable to breed a resistance rice variety of sheath blight disease by the method of marker assisted selection (MAS).</p> <p>This study led to conclusion that the cross combination of 32R and Nipponbare can develop high yielding rice with sheath blight resistance capacity. The yield potential of the expected rice line might depend on source capacity and sink size. The rice line 32R containing valuable QTLs of sheath blight resistance and high yielding potential with cross combination of Nipponbare, could be a potential donor for the resistance to sheath blight disease in the field in future.</p>	