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学位論文の要旨 Abstract of Thesis	
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学位論文題目 Title of Thesis (学位論文題目が英語の場合は和訳を付記)	
Studies on Salinity Tolerance Relating Grain Productivity using Chromosome Segment Substitution Lines in Ric  (イネの染色体断片置換系統を用いた子実生産性に関わる耐塩性の研究)	
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<p>Rice, a major staple food for the ever-increasing world population, is one of the most salinity-sensitive crops. However, genetic and physiological knowledge related to long-term salinity stress is still limited. The aims of this study were to evaluate the mechanisms of long-term salinity tolerance in a salinity-tolerant variety of rice, Nona Bokra, and to detect the quantitative trait loci (QTLs) responsible for the salinity tolerance by using chromosome segment substitution lines (CSSLs) carrying segments from Nona Bokra in the genetic background of a salinity-sensitive variety, Koshihikari. In the research consisting of four experiments, the first two experiments were to identify and characterise the chromosome regions of Nona Bokra related to long-term salinity tolerance, and the following two experiments were to detect the QTLs using SL506 and SL535 populations. Plants were grown under saline and/or control conditions for phenotyping and genotyping evaluations.</p> <p>In experiment 1, the plant dry weight and grain yield of 44 CSSLs under saline and non-saline conditions were measured and compared with Koshihikari to evaluate the salinity tolerance. Among the CSSLs, the plant dry weight of 10 lines was higher than that of Koshihikari while the grain yield of 4 lines was higher than that of Koshihikari under saline conditions. The result suggests that those CSSLs carry the salinity-tolerance QTLs in the chromosome segments of Nona Bokra.</p> <p>In experiment 2, six CSSLs that showed high dry weight and grain yield in experiment 1, and Koshihikari were used. The plant dry weight, grain yield, yield components and ion content in plant at 29 days after salt treatment, full heading and maturity stages under saline and control conditions were measured to clarify the salinity tolerant traits of Nona Bokra. Comparison of plant growth and grain yield of CSSLs grown under long-term saline conditions suggests that the salinity tolerance of Nona Bokra associated with the improvement of plant dry matter, panicle number, and grain productivity. Furthermore, Nona Bokra has the chromosome regions for the improvement of the grain yield on chromosome 2 and on chromosome 6 or 10 under salinity conditions. Low Na<sup>+</sup> and Cl<sup>-</sup> contents in whole plant at full heading stage would be vital for improving the yield under long-term saline conditions. It was suggested that these chromosomal regions were related to Na<sup>+</sup> and Cl<sup>-</sup> exclusion.</p>	

In experiment 3, in order to identify the QTLs related to salinity tolerance underlying the chromosome segment of Nona Bokra in SL506, the F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> progeny populations were developed from SL506 crossed with Koshihikari. The 80 F<sub>2</sub> plant-population was exposed to saline conditions from seedling stage to maturity stage. Phenotypic and genotypic data from 16 SSR markers were used for QTL analysis. Five putative salinity-tolerance QTLs for grain yield, plant dry weight, panicle number and weight of thousand grains were detected with LOD ranging from 2.4 to 3.8. In the next year, the QTL analysis with similar method was conducted using 67 F<sub>4</sub> plant-population with 11 SSR markers. Three salinity-tolerance QTLs located on chromosome 2 related to plant dry weight, grain yield, and panicle number were re-detected with LOD values ranging from 3.2 to 3.4 that explained from 14.7 to 19.7% of the phenotypic variance.

In experiment 4, the F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> populations were developed from SL535 crossed with Koshihikari for QTL analysis in chromosome 6 and chromosome 10. In the first-year, two putative salinity-tolerance QTLs related to dry weight and panicle number were detected on chromosome 6 with LOD at 5.1 and 4.2 explained for 22.6% and 18.0% of phenotypic variance, respectively. In the second year, 111 F<sub>3</sub> and 70 F<sub>4</sub> populations with 14 SSR markers were used. Two salinity-tolerance QTLs for plant dry weight and panicle number were re-detected accounting for 45.5% and 37.5% of the total phenotypic variance with LOD scores at 22.1 and 16.7, respectively.

From these four experiments, it was concluded that the different chromosome segments of Nona Bokra which control high plant dry weight, panicle number and grain yield under long-term saline conditions are related to low Na<sup>+</sup> and Cl<sup>-</sup> contents in plant at full heading stage. Five novel QTLs for salinity tolerance could potentially be useful for developing rice varieties with high yield under long-term salinity stress. The findings also are expected to provide important considerations for better rice breeding program.