学位論文の要旨

Abstract of Thesis

研究科 School	Graduate School of Environmental and Life Science
専　攻 Division	Agricultural and Life Science
学生番号 Student No.	77430856
氏　名 Name	NGUYEN SAO MAI

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）

Identification and validation of salt-tolerant QTLs relating to grain yield and yield components using IR64 CSSLs in the genetic background of Koshihikari and their backcross progenies

（コシヒカリを遺伝背景としたIR64染色体断片置換系統とその戻し交配後代を用いた収量および収量構成要素に関わる耐塩性QTLの同定と検証）

学位論文の要旨 Abstract of Thesis

Salt stress is one of the major abiotic stresses limiting rice production worldwide. Since the expansion of the saline soil continues, there is a need to develop salt-tolerant rice varieties with high yields to ensure food security. Detecting quantitative trait loci (QTLs) for salt tolerance contributes greatly to breeding; however, limited studies have reported on the reproductive stage due to time-consuming and laborious processes. Moderately tolerant variety IR64 might possess characteristics independent from tolerant varieties, and very little is known about salt tolerance at the reproductive stage. This study aimed (1) to screen salt tolerance of 42 IR64 chromosome segment substitution lines (CSSLs) in the genetic background of Koshihikari under the long-term salt stress condition; (2) to examine physiological characteristics associated with salt tolerance of selected CSSLs showing superior tolerance than Koshihikri; (3) to map QTLs for grain yield and yield components under salt stress conditions by using backcross progeny populations from SL2007 and Koshihikari; and (4) to validate and fine-map detected QTLs associated with grain filling and panicle number by comparing near-isogenic lines (NILs) and QTL analysis approaches.

In the first chapter, the plant dry weight and panicle weight of 42 CSSLs under non-stress and salt stress (NaCl; EC = 7 dSm^{-1}) were measured and compared with Koshihikari to evaluate the salt tolerance. Four CSSLs (SL2007, SL2008, SL2027, and SL2038) that showed better performance than Koshihikari under the salt stress condition were selected further to evaluate ion contents and yield components. Since SL2007 and SL2038 consistently produced higher panicle weight under salt stress than did Koshihikari, IR64 chromosome segments of chromosomes 2, 3, 10, and 11 harbored in these CSSLs might be responsible for maintaining panicle weight under salt stress. Later investigation found that these two CSSLs produced higher grain yield and yield components and also accumulated significantly lower Na^+ and Cl^- contents in the whole plant at the full heading stage than Koshihikari. Therefore, maintaining grain yield and yield components in these salt-tolerant CSSLs could be attributed to low Na^+ and Cl^- accumulations in the whole plant at the full heading stage.

In the second chapter, to understand the genetic control of its grain yield and yield components under salt stress, an SL2007/Koshihikari F_2 population was generated for QTL analysis. A linkage map was constructed using 19 polymorphic SSR and Indel markers on 70 F_2 plants by MAPMAKER/EXP 3.0b. Composite interval mapping detected two QTLs for grain yield and panicle weight (*qSTGY2.1* and *qSTPW2.1*)

Name	NGUYEN SAO MAI

on the short arm of chromosome 2 and four QTLs for plant dry weight, panicle number, panicle weight, and grain yield (*qSTDW2*, *qSTPN2*, *qSTPW2.2*, and *qSTGY2.2*) on the long arm of chromosome 2. The QTLs detected in this study explain 9.91–31.84% of the phenotypic variance with LOD values ranging from 2.71 to 4.70. Since the QTLs on the short arm of chromosome 2 had already been reported, the QTLs on the long arm of chromosome 2 were focused. Comparing NILs selected from a SL2007/Koshihikari F_5 population, the region of two co-localized QTLs, *qSTGY2.2* and *qSTPW2.2,* was delimited to a 2.5 MB region and novel *qSTPN2* to a 0.6 Mb region. Moreover, a newly-detected QTL (*qSTGF2*) for grain filling, an important contributor for grain yield of SL2007, was confirmed to a 2.3 Mb region.

In the third chapter, we narrowed down *qSTGF2* and investigated its regulatory mechanism contributing to grain yield as little is known about grain filling maintenance under salt stress. Regarding the region of *qSTGF2*, two NILs were selected for analyzing pollen characteristics and measuring panicle weight under salt stress in 2020. NIL1 showed higher pollen germination percentage on media but no difference in grain weight as compared with NIL2 under salt stress which might be due to the adverse effect of high temperature during the flowering period. Therefore, the *qSTGF2* region was still confined to the 2.3 Mb region, and the QTL was considered to be associated with high pollen germination under salt stress.

In the fourth chapter, the *qSTPN2* region was fine mapped and validated using a QTL analysis approach. Single-marker analysis on a SL2007/Koshihikari F_7 population suggested the QTL was significantly associated with 12 markers. In other words, *qSTPN2* was confined to a region between RM1367 and RM13893. In combination with the validation outcome, this result suggested the constant presence of the QTL in a 0.18 Mb region. *OsDhn1,* which is involved in stress tolerance via scavenging reactive oxygen species, was considered a responsible candidate in this QTL region.

Taken together, our results suggested that accumulation of low Na^+ and Cl^- content in the whole plant at the full heading stage could play an important role in maintaining grain yield and yield components in salt tolerance of SL2007 and SL2038. Moreover, novel QTLs for grain filling (*qSTGF2*) and panicle number (*qSTPN2*) provide valuable materials for breeding salt-tolerance rice varieties with high grain yield and further studies on the genetic and regulatory mechanisms underlying salt tolerance.