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学位論文審査の要旨

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学位論文題名

The genome constitution of rice resources in the Mekong Delta and their association with salinity stress

（メコンデルタにおけるイネ栽培系統集団のゲノム構成と塩ストレスとの関連性）

The dissertation consists of four chapters, which include 23 figures and 14 tables in a total of 89 pages.

Rice (*Oryza sativa* L.) farming is the principal agricultural activity in many countries, particularly, South and Southeast Asia countries. Rice is a staple food because of directly feeding more people than any other cereals. Nearly half of the world's population and 90% of Asian people rely on rice every day. In Vietnam, rice produced in the Mekong Delta contributes to 54% of the total rice productivity and 90% of the total export volume of Vietnam. Currently, about 2,000 samples of local and improved rice varieties in the Mekong Delta have been collected and conserved at Mekong Delta Development Research Institute (MDI) - Can Tho University (Viet Nam) as the genetic material for salinity tolerance rice breeding.

In this study, Mr. Tam used 99 *indica* rice accessions collected from 10 provinces in the coastal region of Mekong Delta in Vietnam to evaluate the genomic structure and screen salinity tolerance at seedling stage. Moreover, he identified the relationship between genotype and phenotype on salt-traits by using SNPs from RAD-seq and whole genome sequence.

1. Comparative study on SNP composition and simple profiling using low π-value genomic regions

After double digest restriction-site associated DNA sequencing of the 99 rice accessions and subsequent filtering; 2,301 SNPs were generated and used in subsequent analyses. Within the 3K dataset, MDI landraces fell into an

Ind3 cluster consisting of accessions from Southeast Asian countries, while MDI improved varieties were grouped in cluster Ind1B. A principal component analysis suggested that geographical location strongly affects phylogenetic relationships of Southeast Asian rice accessions, and the MDI landraces were placed into a Vietnam+Cambodia group. The genomic distribution of π-values representing the nucleotide diversity of each population also reflected these phylogenetic relationships and suggested a genetic adaptation to Southeast Asian locations. To display the characteristics of local populations, he constructed a genomic map as a simple profile representing low π-value regions. His simple profiling using low π-value genomic regions was able to reveal regional characteristics of rice genomes and should be useful for identifying local rice populations.

2. The genome-wide association study of salinity responses

A total of 99 accessions were phenotyped and genotyped against salinity tolerance at seedling stage in 100 mM sodium chloride (NaCl) under hydroponic conditions. After growing the accessions for 20 days under NaCl stress, he found 5 highly tolerant, 47 moderately tolerant, 17 sensitive and 28 highly sensitive accessions. The standard evaluation system (SES) was applied to evaluate the salinity tolerance/sensitivity for the examined accession. The strong correlations were observed between the SESs and relative elongation values of the shoot height, root length, shoot and root dry weights under NaCl treatment at 20 days after treatment (DAT). Based on genome wide association study (GWAS), he found three genomic regions in chr01, chr04, and chr10, which located QTLs related to salinity traits. Particularly, chr01 and chr10 were highly associated with SES score at all 4 treatment periods; 5 DAT, 10 DAT, 15 DAT and 20 DAT. He also found Doc Phung cultivar that was extremely tolerant to salt stress at 20 DAT. This cultivar is useful for salinity tolerance breeding programs.

Therefore, we acknowledge that the author is qualified to be granted the Degree of Doctor of Philosophy in Agriculture from Hokkaido University.