

Genetic study on heading time of rice landraces (*Oryza sativa* L.) in Myanmar

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Title : Genetic study on heading time of rice landraces (*Oryza sativa* L.) in Myanmar
(ミャンマーにおけるイネ在来品種の出穂期に関する遺伝学的研究)

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Thesis Summary

Heading date is a key agronomic trait for the adaptation of rice varieties to different cultivation areas and crop seasons. Improving the trait for early heading and high yielding by using the genetic potentials of landraces is the main challenge in Myanmar and neighbor countries. The rice variety, Paw San Hmwe is famous in Myanmar for their eating quality and fragrant aroma and Inn Ma Yebaw is also famous for their eating quality. Understanding the genetic basis and genetic control of heading time is a key challenge for developing novel varieties in rice with enhanced regional and seasonal adaptability. The objectives of this study are to determine the genetic basis of heading characteristics observed in a core collection of rice varieties in Myanmar and to investigate the genetic factors controlling heading date in high yielding and early maturing promising lines derived from Paw San Hmwe and Inn Ma Yebaw.

In Chapter 1, the genetic mechanism of heading date was investigated using a genome-wide association study (GWAS) in 250 Myanmar *indica* diversity panels (MDPI) collected from different geographical regions. The days to heading (DTH) of 2018, 2019 and 2020 monsoon season sowing were analysed for GWAS using the genomic best linear unbiased prediction (gBLUP). The GWAS revealed one common genomic region on chromosome 3 highly associated with DTH namely MTA3. One of the phytochrome gene, *PHYC* was located at the LD region of MTA3 suggesting that the MTA3 is corresponded to the *PHYC* and major genetic factor controlling heading date in MDPI. The haplotypes of 2kb promoter region and coding region of *PHYC* exhibit the four different haplotypes, HapA, HapB, HapC and HapD. The HapA associated with late heading was predominant in the delta and coastal regions whereas the HapC associated with early heading was frequently observed in mountainous region.

In Chapter 2, the MTA3 was confirmed using F₂ populations by crossing two Myanmar accessions with a Vietnamese rice variety, Khang Dang 18 (KD18). QTL analysis was performed by the marker regression using R/qtl package based on the genome-wide SNPs obtained by genotyping-by-sequencing (GBS) markers. Four major QTL region were detected including the major heading date genes *PHYC*, *Hd6* on chromosome 3, *RFT1* and *Hd3a* on chromosome 6 and *DTH8/Ghd8/Hd5* on chromosome 8. The QTL detection in MTA3 region including *PHYC* and *Hd6* on chromosome 3 revealed the confirmation of genetic variation of DTH among Myanmar accession. Moreover, the QTL detection in *RFT1*, *Hd3a*, and *DTH8/Ghd8/Hd5* region explained genetic difference of KD18 and Myanmar accessions.

In Chapter 3, the genetic variation in critical day length and phenological parameters of Myanmar rice accessions on the developmental rate model were estimated. The DTH of eight varieties were investigated by periodical year-round sowing in 2019-2020 at Nay Pyi Taw, Myanmar. The DTH, daily temperature data and daily photoperiod data were used for the parameter estimation. The comparison of two models, the model developed in this study including critical day length (CDL) and previously developed by Nakagawa et al. 2005 (NK05), revealed that the CDL model was more accurate in prediction of heading date in photoperiod sensitive varieties.

In Chapter 4, to improve strong photoperiod sensitivity of elite rice varieties in Myanmar, Paw San Hmwe (PSH) and Inn Ma Yebaw (IMY), early heading date phenotype from photoperiod insensitive variety ST12 (the donor parent of *WFP*) and the NIL carrying *Gn1a* with the genetic background of KD18 were introduced to the PSH and IMY, respectively and the causative genes for early heading was investigated. In

BC₂F₃ generation, genetic analysis of QTL controlling heading date was performed using GBS. The traits for number of primary branches and grain number were investigated by marker-assisted selection and phenotypic selection until the BC₂F₇ generation. As a result, the promising lines showing higher yield and early growth duration approximately 20 ~ 30 days earlier than PSH and IMY were developed. The chromosome segments including *PHYC* and *Hd6*, or ones including *RFT1* and *Hd3a* derived from ST12 and KD18 were substituted in the resulting promising lines with the genetic background of PSH and IMY.

The present study clearly revealed the major genetic factors controlling heading date in Myanmar rice accessions. The natural variation of DTH in *PHYC* were useful for the breeding of early maturing rice among Myanmar landraces. Furthermore, *RFT1*, *Hd3a* and *DTH8/Ghd8/Hd5*, the heading date genes come from photoperiod insensitive varieties including KD18 were valuable gene resources for developing early maturing rice promising lines of strong photoperiod sensitive varieties such as Paw San Hmwe and Inn Ma Yebaw.