

Abstract of Thesis/Dissertation

Applicant

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Title : Analyzing quantitative trait loci of agronomic traits for plant architecture and yield in adzuki bean (*Vigna angularis*)

(アズキ (*Vigna angularis*) の草型および収量性に関する農業形質の量的形質遺伝子座の解析)

Abstract

The Tokachi region of Hokkaido is the primary adzuki bean (*Vigna angularis*) producer in Japan. However, sustainable production is affected by limitations in genetic knowledge related to plant architecture and yield, and machine harvesting efficiency. This study aimed to gain insights into the genetic mechanisms underlying key traits for enhanced adzuki bean production. The primary objectives encompassed: (i) elucidating genetic control of epicotyl length to improve mechanization efficiency; (ii) identifying genetic loci associated with plant height traits for ideal plant architecture; and (iii) clarifying genetic mechanisms underlying maturity and yield-related traits in adzuki bean. Mapping populations were generated using the breeding line 'Toiku161' and the cultivar 'Chihayahime' for subsequent quantitative trait loci (QTL) analyses.

Chapter 2 focused on the genetic control of epicotyl length (ECL) by analyzing recombinant inbred lines using QTL-seq. Four significant QTLs on chromosomes 2, 7, 10, and 11 were identified

that contribute to increased ECL. Two of these QTLs, *qECL7.1* and *qECL10.1*, were validated using insertion/deletion (InDel) markers. The chromosomal location of *qECL7.1* was fine-mapped to a 418 kb region using a substitution mapping method with InDel, cleaved amplified polymorphic sequence (CAPS), derived cleaved amplified polymorphic sequence (dCAPS), and single nucleotide polymorphism (SNP) molecular markers. This region harbors 35 candidate genes possibly influencing ECL. The identified genetic loci offer valuable insights for breeding adzuki bean genotypes with enhanced epicotyl length, a critical trait for mechanical weed control and harvesting efficiency.

Chapter 3 mapped the genetic loci affecting plant height (PH) and its related traits, including ECL, stem internode length below node 7 (STIL7), stem internode length above node 8 (STIL8), and the total number of nodes (NN). A total of 39 QTLs were related to these traits. Some QTLs showed stability by being detected consistently across the three years, including *qPH2* and *qSTIL8.2* on chromosome 2, *qPH4* and *qSTIL8.4* on chromosome 4, and *qSTIL7.7* and *qECL7.1* on chromosome 7. Remarkably, on chromosomes 2 and 4, a QTL affecting STIL8, an upper stem trait, co-localized with a QTL influencing PH. Likewise, on chromosome 7, a QTL affecting STIL7, a lower stem trait, co-localized with a QTL influencing ECL. This suggests the prospect of controlling the upper and lower stem parts independently to achieve enhanced plant height without compromising overall plant architectural integrity.

Chapter 4, analyzed genetic mechanisms for maturity and yield traits, including flowering (FLD), maturity (MAD), reproductive period (MADFLD), total pod number (PDTN), Grain weight (GWg), and number of grains per pod (NGP). A total of 30 QTLs were detected and a stable QTL for flowering *qFLD2* was found on chromosome 2 across the three-year study period. Flowering and maturity traits were generally located on either different chromosome or chromosomal positions.

This suggests independent genetic regulation of flowering and maturity times, presenting prospects for developing early-maturity varieties to minimize yield losses by frost. The study findings showed co-localization between plant architecture (PH, STIL, FLD, MAD) and yield (PDTN, GWg) traits, especially on chromosomes 2 and 4. The QTL network further evaluated causal relationships between plant height and yield traits, revealing 16 QTLs with direct and indirect effects on 11 traits. These QTL-to-trait interactions were distinctively grouped into 3: stem length and yield; seed weight, and seed quantity. Two important QTL hubs were identified within chromosomes 4 and 7. The identified pleiotropic and polygenic effects in the QTL-to-trait interactions provide useful insights into the understanding of regulatory mechanisms governing plant height and yield traits.

In conclusion, the quantitative trait loci, candidate genes, co-dominant markers, QTL-to-trait interactions, and QTL hubs identified in this study are invaluable aspects in the molecular-assisted breeding for ideal key traits including plant height, epicotyl length, maturity, and yield. This understanding is crucial to the development of genotypes with improved mechanized compatibility and increased yields thereby contributing to sustainable production of adzuki bean in Tokachi. Further studies are, however, recommended particularly on fine-mapping of remaining key traits and candidate gene identification for more impactful application in adzuki bean breeding programs.

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