学 位 論 文 内 容 の 要 旨

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学 位 論 文 題 名

Molecular-Genetic Study on Soybean Maturity Gene *E9* and its Role on Flowering
(ダイズの感光性遺伝子 *E9* とその開花に及ぼす役割に関する分子遺伝学的研究)

Knowledge of molecular mechanisms of flowering and maturity is important for understanding the phenology of seed crops and for maximizing yield in a given environment. Soybean is cultivated in wide regions of the world as an important crop to supply vegetable proteins and oil. This wide adaptability has been created by natural variations in major genes and quantitative trait loci to control flowering. However, the molecular basis of flowering and maturity still remains poorly understood. In this thesis, I studied molecular-genetic bases of flowering in soybean, in particular focusing on a maturity gene *E9*, which has been identified in the progeny of a cross between cultivated and wild soybeans.

I first analyzed genetic bases on flowering time segregated in the progeny of a cross between two early-maturing soybean cultivars, Toyomusume and Harosoy. The two cultivars flowered almost at the same time, but flowering times in the F_2 and F_3 populations varied widely. They differed in the genotypes at a maturity *E1* locus, a repressor for soybean orthologs of *FLOERING LOCUS T* (*FT*), which produces the most marked effect on flowering. Expectedly, the progeny exhibited segregation in flowering times closely associated with the *E1* genotypes. Further, I found by marker-assisted analysis that the progeny segregated for the *E9* locus, at which Toyomusume had the recessive *e9* allele for late flowering.

Then, I carried out fine-mapping of *E9* and delimited it to a 40.1-kb genomic region, which contained *FT2a*, an ortholog of *FT*. As a result of expression analyses in the progeny of 10 heterozygous F_2 plants, plants homozygous for *e9* exhibited reduced *FT2a* expressions, compared with those for *E9* in each family. Sequence analyses further revealed that the two cultivars had the identical sequence in the coding region,

but differed in a total of 30 DNA polymorphisms in the genomic sequence. From a comparison among different cultivars, I found the three DNA polymorphisms that differed consistently between the *E9* and *e9* alleles. Expression analysis for near-isogenic lines (NILs) and photoperiod-insensitive cultivars for different *FT2a* haplotypes demonstrated that low *FT2a* expression of *e9* was caused by the insertion of a *Ty1/copia*-like retrotransposon designated *SORE-1*.

Transposable elements in introns are well known to affect chromatin structure and modify RNA processing of the host gene and thereby influence its expression pattern. From the expression analysis for plants heterozygous for the *E9* locus, I found that the lower expression of *e9* was caused by allele-specific transcriptional repression. I further confirmed that *SORE-1* did not influence the RNA processing. Rather, lower mRNA level of *e9* was associated with *SORE-1* methylation, because the inserted *SORE-1* was highly methylated.

Based on the results obtained, I discussed on roles and functions of the *e9* allele in soybean flowering and adaptation. This allele is a leaky allele, because its regulation by other genes involved in photoperiod response was retained. The *FT2a* transcript abundance is directly associated with the variation in flowering time in soybean, and lower transcript abundance due to the insertion of *SORE-1* produce delayed flowering. It is considered that the *e9* allele had been selected for because of its action to maintain vegetative growth which enables higher yield in early-flowering genetic backgrounds. It may also be useful as a long-juvenile allele in cultivar development in low-latitude regions, where flowering is strongly promoted.