



University of Tsukuba

Plant Transgenic Design Initiative

75th PTraD Research Seminar

T-PIRC Research Seminar

日付: 2024年1月19日 (金) 14:00~15:00

場所: 総合 A 棟 205

Metabolite profiling of Arabidopsis epiRILs for the identification of epialleles

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Mutation in DNA sequence is not the only cause of different phenotypes. Loci with differential metastable DNA methylation (epialleles) can also cause phenotypic differences. Most of the epialleles reported so far had easily observable phenotypes such as pigment accumulation, suggesting the existence of more epialleles hidden to be discovered. However, screening for epialleles is not simple in commonly used recombinant inbred lines and natural accessions due to the co-existence of variations in DNA sequence and epigenetic states. Epigenetic recombinant lines (epiRILs), RILs that were designed to have near isogenic DNA sequences but different patterns of DNA methylation, allow the decoupling of these two variations making them optimal for the detection of epialleles. Previously, epigenetic QTLs (epiQTLs) associated with metabolite levels were detected using a subset (122 lines) of epiRILs. Recently, a different larger subset (169 lines) of epiRILs was epigenotyped opening the possibility of detecting still unidentified epiQTLs. In my presentation, I will present my project in which I performed metabolite profiling of both subsets of Arabidopsis epiRILs followed by epiQTL mapping. This led to the detection of novel epiQTLs associated with various metabolites including glucosinolates. In addition, an outlier that was not used for epiQTL mapping was found to flower earlier than the wild type and accumulate a kaempferol derivative. Intriguingly, this flavonoid was previously reported to not accumulate in Col-0 due to a point mutation in the responsible enzyme. Since epiRILs were created by crossing Col-0 background plants, this was an unexpected phenotype. I currently seek to clarify the cause of this phenotype. I will share the results that I recently obtained.

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