報 告 番 号	※ 　 　 第 　 　 号

主 論 文 の 要 旨

論 文 題 目　Study on the genetic diversity of soybean roots under field conditions
（圃場におけるダイズの根の遺伝的多様性に関する研究）

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論 文 内 容 の 要 旨

Abstract

The study was conducted to evaluate the genetic diversity of soybean roots grown under field conditions in a diverse soybean germplasm consisting of 200 accessions, of which mainly were from the mini core-collections (the World mini core-collection and the Japan mini-core collection). Soybean was grown under field conditions in a sandy field in Tottori, Japan for three years under two irrigation treatments: irrigated and non-irrigated treatment. The study revealed a high diversity in root traits across the whole panel under both irrigated and non-irrigated conditions. And of note, higher genetic diversity in most root traits was seen among genotypes from the world mini-core collection, compared with accessions from Japan mini-core collections.

Soybean accessions which showed large root improvement with irrigation and those with the stable performance of root traits across environments were identified. These accessions can be used as promising materials for the genetic improvement of soybean root. In addition, a genome-wide association study (GWAS) was applied to dissect the genetic controls of root traits, and 7QTLs and candidate genes associated with root traits were identified. Among the candidate genes, *Glyma.07G084300,* associated with total root length under irrigated conditions, known as the *Arabidopsis CDK-activating kinase 1AT*, was reported for the roles in cell proliferation, cell expansion, and the regulation of root cell initiations. Finally, attempts have been made to predict the root traits of soybean using (i) genomic prediction approach, and (ii) prediction of root traits from available data in the shoot environment using machine learning methods (ML). The results from these two approaches proved that it's promising to predict the root traits in the field conditions using either genomic data or easily assessable data obtained in the field. The success of prediction models in our study was also improved when the interaction of genotype and environment was incorporated.