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主　論　文　の　要　旨

論文題目　Physiological and Genetic Mechanisms of Lateral Root Formation for the Improvement of Root System Architecture in Rice
（根系構造改良に向けたイネ側根形成の生理・遺伝機構の解析）

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論　文　内　容　の　要　旨

Lateral roots (LRs) determine the overall root system architecture, thus enabling plants to efficiently explore their underground environment for water and nutrients. In rice plants, the plasticity in LR development confers improved performance thereby maintaining productivity under rainfed ecosystems. However, although several genes controlling root development were identified by high-resolution QTL detection and availability of mutant lines with altered root phenotypes, the mechanisms regulating LR development remain unknown in rice plants. Our study aimed to determine the genetics and mechanisms of L-type LR formation through the utilization of rice mutants with high number and promoted L-type LRs and specifically focused on the characterization, expressions and functional analyses of the respective causative genes.

In the first study, we characterized a rice mutant, wavy root elongation growth 1 (*weg1*), that produced higher number of long and thick LRs (L-type LRs) formed from the curvatures of its wavy parental roots caused by asymmetric cell growth in the elongation zone. Consistent with this phenotype, the expression of the *WEG1* gene, which encodes a putative member of the hydroxyproline-rich glycoprotein family that regulates cell wall extensibility, was specifically localized in the root elongation zone. The asymmetric elongation growth in roots is well known to be regulated by auxin, but we found that the distribution of auxin at the apical region of the mutant and the wild-type roots was symmetric suggesting that the wavy root phenotype in rice is independent of auxin. However, the accumulation of auxin at the convex side of the curvatures, the site of L-type LR formation, suggested that auxin likely induced the formation of

L-type LRs. This was supported by the need of a high amount of exogenous auxin to induce the formation of L-type LRs. These results suggest that the MNU-induced *weg1* mutated gene regulates the auxin-independent parental root elongation that controls the number of likely auxin-induced L-type LRs, thus reflecting its importance in improving rice root architecture.

In the second study, we newly isolated a promoted lateral root rice mutant, *plr1*, that exhibited a higher density of thick and long LRs (L-type LRs) with longer parental roots than the wild-type. The mutant was also characterized to have a significantly lower starch level in the stem while the glucose and sucrose levels at the root zone for early stage of LR formation up to the root tip were significantly higher as compared to the wild-type, pointing us to the involvement of carbohydrates in the regulation of LRs. This was supported by the exogenous sugar treatments wherein *plr1* mutant seedlings increased L-type LR density, which may suggest that transported sugars are important for L-type LR formation. Interestingly, wild-type seedlings also increased L-type LR density. When wild-type seedlings were grown under N conditions, the seedlings reduced stem starch levels resulting to increased L-type LR development via increased amount of glucose in the roots, confirming that less stem starch accumulation regulates L-type LRs. At higher plant stage under N conditions, we further showed a strongly negative relationship of stem starch accumulation to L-type LRs only among the root traits examined. Taken together, we reveal a mechanism to induce L-type LRs regulated by the involvement of less stem starch accumulation via increased root sugars both at seedling and higher plant stages of rice.

In the third study, we present the molecular mechanisms involved in the regulation of L-type LRs in *plr1* mutant apart from the mechanisms of less stem starch accumulation via increased root sugars. In this study, we present the mutation gene of the *plr1* mutant, found at the ACID protein domain regulating transcription factor (TF) of the OsMED25, which encodes a member of the Mediator complex. The OsMED25 was revealed to interact with the MYB TF identified from yeast-two hybrid system. However, in conditions where L-type LR formation are known to be enhanced, we found that that the expression of MYB gene under different stressful conditions (i.e. drought, low phosphate) was downregulated but not under N condition, suggesting that MYB is may be associated with the regulation of LRs under stressful environments but not under N condition. Additionally, overexpression of MYB TF led to the greater expression of MYB gene and rendered the transgenic rice with significantly thinner diameter LRs, suggesting that MYB negatively regulates L-type LRs.

Collectively, our findings demonstrate the participation of MYB TF interacting with the OsMED25 in the suppression of L-type LR formation in rice.

Overall, we demonstrated newly identified mechanisms regulating LR development in rice. The rice mutant lines promoting LR formation were presented for the first time and, therefore, their root characteristics, might open a new breeding strategy to develop rice crops with improved root system architecture.