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Insights into Genetic Factors involved in the Control of Shoot Branching in Rice (*Oryza sativa* L.) under Low Nitrogen Cultivation and Abiotic Stress

Nkulu Rolly Kabange^{1†}, Youngho Kwon^{1†}, Ji-Yoon Lee¹, So-Myeong Lee¹, Jin-Kyung Cha¹, Dongjin Shin¹, Jun-Hyeon Cho¹, Jong-Hee Lee^{1*}

¹⁾ Dep. of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Korea

[Introduction]

As part of the efforts to reducing the emissions of greenhouse gases (GHG), countries have proposed ambitious actions in their nationally determined contributions (NDCs) and mitigation strategies to achieve zero GHG emissions for sustainable development. In plant crops such as rice, nitrogen (N) is required at all development stages, including tillering stage. Despite its preponderant roles, excessive application of nitrogen in rice cultivation has been shown to contribute to the emission of greenhouse gases (GHG), such as methane (CH₄) and nitrous oxide (N₂O), especially in flooded-prone cultivation areas (i.e. paddy fields). In rice, shoot branching is controlled by environmental factors, agricultural practices (i.e. nitrogen fertilization), or genetic factors. In recent years, we observed a growing interest in developing rice varieties having a high nitrogen use efficiency (NUE) and an enhanced tolerance to abiotic stress, which may help to reduce the over use of nitrogen, while maintaining a balanced plant growth and productivity.

[Materials and Methods]

Quantitative trait loci (QTLs) controlling shoot branching and panicle number in rice were investigated, using Kompetitive Allele-Specific PCR (KASP) and Fluidigm markers on a doubled haploid (DH) population (n=117, a cross between 93-11 (P1) and Milyang352 (P2), *indica* and *japonica*, respectively). One set of the mapping population was grown under normal nitrogen conditions (90 kg ha⁻¹ N, 45 kg ha⁻¹ P₂O₅, and 57 kg ha⁻¹ K₂O), and the other set under low nitrogen conditions (45 kg ha⁻¹ N, 22.5 kg ha⁻¹ P₂O₅ and 28.5 kg ha⁻¹ K₂O) until maturity.

[Results and Discussion]

Two QTLs *qTNL-2* (134 cM, LOD: 6.1, PVE: 20.5%) and *qPNL-4* (154 cM, LOD: 2.95, PVE: 11.9%) associated with the control of shoot branching and panicle number, respectively, in response to low nitrogen cultivation, were identified, and mapped on chromosome 2 and chromosome 4. The additive effects (1.81 for *qTNL-2* and 1.18 for *qPNL-4*) indicate that alleles from 93-11 (*indica*) explained the observed phenotypic variance for both tiller number and panicle number. The breakthrough is that most of the genes harbored by *qTNL-2*, here associated with shoot branching, are also proposed to be involved in the adaptive response mechanisms towards stress tolerance in plants. Therefore, all data put together suggest the existence a possible crosstalk between plant growth and stress response in plants.

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[†]These authors contributed equally to this work as first authors.

*Corresponding author: E-mail, ccriljh@korea.kr Tel, +82-53-350-1168 Fax, +82-55-352-3059