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Reducing Greenhouse Gases (GHGs) Emissions from Rice (*Oryza sativa* L.) Cultivation: Exploring the Role of Radial Oxygen Loss and Nitrogen use Efficiency

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[Introduction]

Agriculture serves as both sinks and sources of greenhouse gases (GHGs), and is the second most important GHGs emitting sector after the industry. Reducing GHGs emissions from agriculture is gaining momentum in agricultural research communities, which aim at minimizing application of synthetic fertilizers, particularly in flood-prone crops cultivation, including rice paddy fields. Methane (CH₄) and nitrous oxide (N₂O) are the major GHGs emitted from agriculture, having a global warming potential (GWP) higher than that of carbon dioxide (CO₂), resulting from abundance of application of nitrogen (N)-rich fertilization and the nitrification and denitrification processes, as well as the decomposition of organic matter. A panel of strategies to reduce GHGs emissions from agriculture have been proposed, among which breeding for high radial oxygen loss (ROL) and improved nitrogen use efficiency (NUE) in rice are favored. Although there are controversial reports in the literature on the net impacts of N-rich fertilizers rates on CH₄ and N₂O emissions, a strong consensus exists on the fact that various rates of N applications differentially influence the activity of methanogens and methanotrophs. In the same way, oxygen level in the rhizosphere is proposed to influence the activity of methanogens and methanotrophs. Therefore, exploring the genetic basis associated with ROL and their possible interplay with N fertilization regimes on GHGs emissions might provide insights to tackle this important issue.

[Materials and Methods]

(1) Quantitative trait loci (QTLs) associated with radial oxygen loss (ROL) and root area (RA) in rice were investigated employing 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). The mapping population was grown on iron (II) sulfide (FeS)-modified agar medium for two weeks. (2) To exploring the NUE, an initial experiment was conducted on a set of six potassium chlorate (KClO₃) sensitive rice lines carrying either the indica alleles of nitrate reductase (OsNR2) or nitrate transporter (OsNRT10) and their parents were evaluated under gradient nitrogen levels (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).

[Results and Discussion]

QTLs *qROL-2-1* (127 cM, LOD: 3.04, PVE: 11.61%) and *qRA-8-1* (97 cM, LOD: 4.394, PVE: 15.95%) associated with the control of ROL and RA, respectively. The qPCR validation of a set of genes found within the *qROL-2-1* region suggested that *OsTCP7*, *OsMYB21*, and *OsARF8* encoding transcription factors (TFs), coupled with *OsTRX*, *OsWBC8*, and *OsLRR2* would act as positive regulators of ROL in rice. However, the differentially regulated genes *OsDEF7* and *OsEXPA*, and the significant reduction in the transcript accumulation of *OsNIP2*, *Oscb5*, and *OsPLIM2a* suggest that they might be involved in the control of oxygen flux level in rice roots.

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