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Tissue-specific Enhancement of OsRNS1 with Root-dominant Expression is Required for the Increase of Crop Production

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[Introduction]
Root development is a fundamental process that supports plant survival and crop productivity. One of the essential factors to consider when developing biotechnology crops is the selection of a promoter that can optimize the spatial–temporal expression of introduced genes. However, there are insufficient cases of suitable promoters in crop plants, including rice.

[Materials and Methods]
osrns1 mutants had defects in root development based on T-DNA insertional mutant screening and *CRISPR* technology. To optimize the function of *OsRNS1*, we generated *OsRNS1*-overexpression plants under two different promoters: a whole-plant expression promoter and a novel root-preferred expression promoter. Root growth, yield-related agronomic traits, RNA-seq, and reactive oxygen species (ROS) accumulation were analyzed for comparison.

[Results and Discussion]
OsRNS1 was found to be involved in root development through T-DNA insertional mutant analysis and gene editing mutant analysis. To understand the gain of function of *OsRNS1, pUbi1::OsRNS1* was generated for the whole-plant expression, and both root growth defects and overall growth defects were found. To overcome this problem, a root-preferential overexpression line using *Os1-CysPrxB* promoter (*Per*) was generated and showed an increase in root length, plant height, and grain yield compared to wild-type (WT). RNA-seq analysis revealed that the response to oxidative stress-related genes was significantly up-regulated in both overexpression lines but was more obvious in *pPer::OsRNS1*. Furthermore, ROS levels in the roots were drastically decreased in *pPer::OsRNS1* but were increased in the *osrns1* mutants compared to WT. The results demonstrated that using a root-preferred promoter effectively optimizes the function of OsRNS1 and is a useful strategy for improving root-related agronomic traits and ROS regulation.

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