Genome-wide transcriptomic analysis reveals the gene regulatory network that controlled by SRL1 in regulating rice leaf rolling

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Xizhi Li
GuangXi University

Min Li
Guangxi University

Beibei Zhou
Guangxi University

Jinlin Bao
Guangxi University

Liang Zhu
GuangXi University

Pengbo Xue
Guangxi University

Jun Wang
Guangxi University

Jian Jin
Guangxi University

✉ jinjian@gxu.edu.cn *Corresponding Author*
ORCID: <https://orcid.org/0000-0002-1978-500X>

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Abstract

Background

SRL1 (SEMI-ROLLED LEAF 1) also named as CLD1 (CURLED LEAF AND DWARF 1), encoding a putative glyphospholipidininol-anchored membrane protein, has been characterized as a gene involved in the regulation of leaf morphology in rice. Mutants of srl1-1 (point mutation) and srl1-2 (transferred DNA insertion) exhibit defects in leaf development resulting in a phenotype with adaxially rolled leaves.

Results

To explore the gene regulatory network of leaf development that controlled by SRL1 in rice, we created a homozygous SRL1 knock out (KO) line by CRISPR/Cas9, which showed defects in leaf development with adaxially rolling. By comparing the leaf transcriptome of a homozygous SRL1 KO line (srl1-KO) with the control, a total number of 3,178 genes were identified as differentially expressed genes, of which 1,216 genes were significantly up regulated, while 1,962 genes were down regulated. Further analyses indicated that, a group of known leaf rolling related genes, which involved in bulliform cells and cuticle development such as OsZHD1, OsLBD3-7, RFS, ACL1, CFL1, SND1, OsCESA5 and OsCESA6 were up or down regulated in the srl1-KO.

Conclusions

SRL1 might control leaf rolling by regulating a couple of genes that affecting cytological architecture of leaf cells such as bulliforms and cuticle of leaves.

Full Text

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However, the manuscript can be downloaded and accessed as a PDF.

Figures

Figure 1

The CRISPR/Cas9 target site of *SRL1* and phenotype of the KO plants. (a) Schematic of *SRL1* gene structure and the CRISPR/Cas9 target site. The exon was indicated by gray rectangles,

the untranslated region was indicated by white rectangles. The translation initiation codon (ATG) and termination codon (TGA) are shown. The target site nucleotides are shown in capital letters, and the protospacer adjacent motif (PAM) site is underlined. (b) Genomic structures at the SRL1 locus in KO and non-KO line. (c) The original sequencing chromatograms of the target site for SRL1 in non-KO and homozygous KO line. The protospacer adjacent motif (PAM) site is underlined, the “T” marked with an asterisk was the inserted in the srl1-KO. (d) Whole plant of non-KO and srl1-KO (e, f) Leaf blade phenotype of non-KO and srl1-KO.

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Figure 2

Overview of the DEGs. (a) Correlation between any two replicates was calculated by Pearson's Correlation Coefficient value. (b) Numbers of up-regulated and down-regulated DEGs. (c) KEGG pathway assignment of the assembled unigenes (top 50 pathways according to enrichment factor). The vertical axis represents the enriched KEGG pathways and the horizontal axis represents the number of unigenes in each pathway. (d) The expression profiles of twelve leaf rolling related genes were validated by qPCR. Values are shown as means $\pm$ s.d. (n = 3)

Supplementary Files

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