

High utilization efficiency of Nitrogen and phosphorus nutrient in crops

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Nitrogen, a critical macronutrient for plant growth and development, is a major limiting factor in most agricultural systems. RNA sequencing analysis can more precisely measure transcript levels and allow the absolute quantification of gene expression. cDNA libraries from leaf sheaths and roots of rice plants grown under N-deficient or -sufficient conditions for 12 h were constructed. Sequencing the libraries resulted in identification of 33,782 annotated genes including 2,986 novel transcripts. A comparison of abundances revealed 1,650 transcripts that were differentially expressed (fold-change ≥ 2) due to an N-deficiency including 86 transcription factors and were confirmed by RT-PCR and GUS assays. RNA-Seq data identified 8,509 multi-exonic genes with 19,628 alternative splicing events. The results provide valuable information about N-starvation-responsive genes and will be useful when investigating the signal transduction pathway of N-utilization. Furthermore, the numerous EMS mutant lines of maize were generated by our group. The screening of high utilization efficiency of nitrogen and phosphorus nutrient was performed using these lines in low nutrient stress field. The lines showing significant phenotype were used to identify the mutant genes to elucidate its biological function under abiotic stress.

Biography

Yang wenzhu obtained PhD degree from Kyung Hee University this summer. She engaged in the metabolism regulation of nitrogen and phosphorus.

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