RNA-seq reveals the downregulated proteins related to photosynthesis in growth-inhibited rice seedlings induced by low-energy N\textsuperscript{+} beam implantation

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ABSTRACT. Transcriptomic research based on RNA sequencing (RNA-seq) technology is innovative and will provide new opportunities and biological perspectives for the use of ion-beam implantation in plants. Using RNA-seq, transcriptomes of whole rice seedlings generated from seeds implanted with a low-energy N\textsuperscript{+} beam were analyzed 96 h after planting. We identified 544 transcripts that were differentially expressed genes (DEGs) in the non-growth-inhibited sample implanted by an N\textsuperscript{+} beam, including 262 upregulated transcripts and 282 downregulated transcripts. Next, 776 transcripts were identified as DEGs in significantly damaged and growth-inhibited rice seedlings induced by N\textsuperscript{+} beam implantation, including 283 upregulated transcripts and 493 downregulated transcripts. The Gene Ontology (GO) analysis showed that 19 downregulated DEGs in the injured rice seedlings...
are enriched for the biological process GO term photosynthesis. The Kyoto Encyclopedia of Genes and Genomes pathway analysis also showed that 11 downregulated DEGs related to chlorophyll a/b-binding proteins are statistically significantly enriched in the photosynthesis-antenna protein pathway (Pathwayid: map00196). This result suggested that the downregulated and injured photosynthesis system contributed to the growth inhibition of rice seedlings induced by low-energy N⁺ beam implantation.

**Key words:** Growth inhibition; Low-energy ion-beam implantation; Transcriptome; RNA-seq; Photosynthesis