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Transcriptomic profiling reveals molecular aspects of nitrogen oxide-induced adventitious rooting in mung bean seedlings

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Recent studies showed that nitrogen oxide (NO) strongly promoted adventitious rooting in plants. To gain further insight into the molecular mechanisms underlying this process, the transcriptome analysis was performed using RNA-Seq and qRT-PCR technologies. The RNA-Seq data showed that NO donor sodium nitroprusside treatment significantly enhanced gene expression at the root induction stage but reduced gene expression at the root initiation stage compared with the water and IBA treatments. GO enrichment analysis indicated that oxidoreductase activity was the common GO subcategory that was significantly regulated in all the samples; and microtubule-based process, nitrogen compound response, cell cycle, and hydrolase activity were the most highly up-regulated GOs at the root induction stage while response to stress, response to chemical stimulus, nitrate and sulfur compound transmembrane transporter activity, and cell wall biogenesis were the most highly up-regulated GOs at the root initiation stage by NO. KEGG pathway enrichment showed that cell cycle, metabolism of terpenoids, lipid metabolism, protein processing, energy metabolism, phenylalanine metabolism, and xenobiotics biodegradation were the most highly up-regulated pathways at both the root induction and initiation stages by NO. The analysis of the most highly regulated genes (RPKM≥10 and fold change≥2) indicated that NO significantly regulated the genes associated with nitrogen compound response, stress response, oxidative stress response, cell wall modification, signal transduction, protein processing, secondary metabolism, metabolic processes, and transcription factors, as well as plant hormone signaling, including auxin, ethylene, cytokinin, gibberellin, and abscisic acid pathways. These results strengthen the current understanding of NO-induced adventitious rooting and the molecular traits of NO in plants.

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Chromosome-based survey sequencing of *Triticum dicoccoides*

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Wild emmer wheat, *Triticum turgidum* ssp. *dicoccoides* is the wild relative of *Triticum turgidum*, the progenitor of tetraploid durum and bread wheat. With its direct ancestry to modern wheat cultivars and its rich gene pool carrying favorable alleles for grain quality and stress tolerance, *T. dicoccoides* is a promising source for wheat improvement. Here, we report a chromosome-based insight into its entire genome, through the survey sequencing of all its 14 chromosomes. Genomic scaffolds constructed by aligning *de novo* assembled contigs to the recently assembled genome of Zavitan genotype and delivered important clues into the *T. dicoccoides* genome, unraveling coding regions including flanking regulatory sequences for a number of agronomically important genes. Repetitive element annotations revealed considerable differences in content and distribution in A- and B-genome chromosomes. Gene contents of the chromosomes varied widely, not necessarily correlating with chromosome sizes. Syntenic relationships and virtual gene orders indicated several small-scale rearrangements, in addition to, providing evidence to the 4AL-5AL-7BS translocation in wild emmer wheat at the sequence level. Chromosome-based sequence assemblies also revealed 7 novel miRNA families, of a total of 47 putatively encoded genes by the entire genome. The survey sequences from all 14 chromosomes of *T. dicoccoides* not only shed light into its genome, but also provided a large-scale, much needed additional resource for the discovery of potentially new alleles and design of novel molecular markers that should benefit fellow researchers and breeders.

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