

Pan-Transcriptomes & Gene Regulation Network in Response to Drought & Salt Stresses in Alfalfa

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Autotetraploid alfalfa (*Medicago sativa* L.) is an important legume forage grown worldwide and its productivity is affected by drought and salt stresses. In this work, three alfalfa populations: Wilson (drought tolerant), Saranac (susceptible to drought and salt), and PI467895 (salt tolerant) were used for unraveling the alfalfa response to drought and salt stresses through full-length transcriptome analysis. Twenty-one different RNA samples were extracted from three tissue sources (leaf, stem and root) of plants subjected to salt, drought and control non-stress treatments. These samples were sequenced using the PacBio SMRT and the Illumina HiSeq platforms to obtain comparative transcriptomic profiles in response to drought and salt stresses. PacBio reads were corrected using a hybrid approach with Illumina reads to improve the quality of transcriptomes, resulting in 91,378 unique transcripts with 1,124,275 unique isoforms among all treatments (Figure 1). Transcriptomic analysis identified the transcriptional and post-transcriptional differences among populations, tissue sources, and stress conditions including alternative splicing events (ASE), long non-coding RNAs (lncRNAs), transcription factors, fusion genes, and nonsense-mediated mRNA decay (NMD) events. Finally, a weighted gene co-expression network allowed us to identify hub genes that may play important roles in regulation of drought and salt stress tolerance in alfalfa (Figure 2).

