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RNA-Seq analysis of aluminum stress response in sugarcane roots

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Sugarcane (*Saccharum* spp.) is an important source of sugar and ethanol and it is known that the global sugarcane production will increase by 21% by 2024. With increasing demand for energy, the sugarcane crop expansion is evident in Brazil. It is predicted that due to high demand for sugarcane and ethanol, the acreage under sugarcane will increase from 9.0 million ha to 64 million ha by the years 2018/2019. As a result, more unconventional soils rich in minerals will be brought under cultivation. Aluminum ions (Al^{+3}) together with silicon and iron are the three most abundant mineral elements in soil. Although silicon and iron are required for plant growth, Al is toxic, and its bioavailability is highest on acidic soils, resulting in inhibition of root growth and architecture leading to disruption of root elongation. Our goal is to understand the molecular mechanisms of abiotic stress tolerance in sugarcane and the role of miRNA's in transcriptional regulation. Towards this goal, a relatively tolerant sugarcane cultivar CTC-2 and the susceptible RB855453 cultivar was subjected to Aluminum stress at 221 µMol. RNA-Seq was performed on 12 root tissue samples using 108 bp paired end sequencing on an Illumina HiSeq2500 sequencer. Pairwise comparisons between different treatments in tolerant cultivar identified 16,340 non-redundant differentially expressed transcripts (DETs). Functional annotation of DETs revealed that AL^{+3} tolerance was controlled by several interacting pathways like calcium and G-protein coupled receptor mediated signaling, and regulation by WRKY and R2R3-MYB transcription factors. Some of these genes could be utilized by sugarcane breeders to improve Al^{+3} stress tolerance in field conditions.

Biography

Kameswara Rao Kottapalli has completed his PhD in Biotechnology and currently, he is a Research Associate Professor in Center for Biotechnology and Genomics. He has more than 10 years of experience in functional genomics with expertise in bioinformatics analysis of genotypic data, microarray data, large protein mass data, and next-generation DNA sequence data. He has successfully obtained federal grants like USDA-AFRI, NSF, Borlaug-USDA International award, USDA Ogallala Aquifer Initiative with major focus on bioinformatics and functional genomics. He has more than 25 publications in peer-reviewed journals and was awarded International Generation Challenge Program Postdoctoral Fellow in 2005-06. He currently teaches two graduate courses on gene expression profiling by nextgen sequencing (BTEC 5312) and bioinformatics (BTEC 5001-04). He is currently supervising several MS and PhD students with research focus on functional genomics and bioinformatics.

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