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The path to understanding salt tolerance in plants: Transcriptome assembly, profiling and analysis of the halophyte, *Suaeda fruticosa*

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Improvement of crop production will be required in order to feed the growing world population as the amount and quality of agricultural land decreases and salinity in soil increases. This has stimulated research to understand mechanisms of salt tolerance in plants. We have characterized the transcriptome of *Suaeda fruticosa*, an annual shrub in the family Chenopodiaceae that has the ability to sequester salts in its leaves. Twelve sequencing libraries prepared from control (0 mM NaCl treated) and optimum (300 mM NaCl treated) plants were sequenced using Illumina Hiseq 3000 to investigate differential gene expression between shoots and roots of *Suaeda fruticosa*. The reads were quality assessed, filtered and assembled *de novo* using Velvet and Oases k-45. We have clustered the transcripts using CDHIT-ESTand these generate 65,069 transcripts. There are 475 down regulated transcripts and 44 up regulated transcripts when comparing the plants grown under optimal salt to those grown with no salt. BLAST analysis identified the differentially expressed genes and annotated with a cutoff E-value of 10-10. This work has identified those involved in mechanisms of salt tolerance in *Suaeda fruticosa* and has provided an outline of tools to use for *de novo* analysis of transcriptomes. The assembly has covered a considerable proportion of the transcriptome to analyze differential gene expression and identify specific genes that may be involved in salt tolerance in this plant. These data provide a genetic resource for discovery of potential genes for salt tolerance in this species and may serve as a reference sequence for study of other succulent halophytes.

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