Comparative Genomics Analysis Provides New Insight into Molecular Basis of Stomatal Movement in *Kalanchoë fedtschenkoi*

The Science

Crassulacean acid metabolism (CAM) plants prevent excessive evaporation of water by closing their stomata during daylight hours and opening them at night for gas exchange for photosynthesis. In this study, researchers use knowledge of genes associated with stomata in well-characterized non-CAM species combined with time-based differential expression analysis from both CAM and non-CAM species to gain insight into stomatal movement in CAM plants.

The Impact

CAM allows plants to survive in hot, arid climates by preventing water loss. Insights into the mechanisms underlying the process would provide great value for ameliorating the effects of drought on agriculture.

Summary

Many plant genomes are poorly annotated, so orthologous genes may be identified without a determined function. The researchers began by using a text-mining tool to identify additional proteins associated with stomata.

Then, using time-interval expression data from previous studies for *K. fedtschenko*, *Arabidoposis thaliana,* and *Solanum lycopersicum,* the authors processed the sequencing reads in KBase using FastQC and Trimmomatic, mapped the reads to reference genomes using TopHat, and then calculated fragments per kilobase of transcript using Cufflink.

Comparative analysis of the expression data for the time periods around dusk and dawn, when stomatal movement would be most active for *K. fedtschenkoi*, were performed by measuring gene expression enrichment. Finally, expression profiles of stomata-related ortholog groups were searched for genes that showed inverted expression in *K. fedtschenkoi* compared to *A. thaliana*. They identified 16 genes that matched these criteria, and created phylogenetics trees to measure the evolutionary dynamics that may have led to the development of CAM plants.

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