

Title:

Comparative Transcriptome Analysis Reveals Candidate Genes For Cold Stress Response and Early Flowering in Pineapple

Abstract:

Pineapple originates from tropical regions in South America and is therefore significantly impacted by cold stress. Periodic cold events in the equatorial regions where pineapple is grown may induce early flowering, also known as precocious flowering, resulting in monetary losses due to small fruit size and the need to make multiple passes for harvesting a single field. Currently, pineapple is one of the most important tropical fruits in the world in terms of consumption, and production losses caused by weather can have major impacts on worldwide exportation potential and economics.

To further our understanding of and identify mechanisms for low-temperature tolerance in pineapple, and to identify the relationship between low-temperature stress and flowering time, we report here a transcriptomic analysis of two pineapple genotypes in response to low-temperature stress. Using meristem tissue collected from precocious flowering-susceptible MD2 and precocious flowering-tolerant Dole-17, we performed pairwise comparisons and weighted gene co-expression network analysis to identify cold stress, genotype, and floral organ development-specific modules.

Dole-17 had a greater increase in expression of genes that confer cold tolerance. The results suggested that low temperature stress in Dole-17 plants induces transcriptional changes to adapt and maintain homeostasis. Comparative transcriptomic analysis revealed differences in cuticular wax biosynthesis, carbohydrate accumulation, and vernalization-related gene expression between genotypes. Cold stress induced changes in ethylene and abscisic acid-mediated pathways in both genotypes, however, these pathways showed greater changes in expression in MD2 than in Dole-17, suggesting that MD2 may be more susceptible to ethylene-mediated early flowering. The differentially expressed genes and module hub genes identified in this study are potential candidates for engineering cold tolerance in pineapple to develop new varieties capable of maintaining normal reproduction cycles under cold stress. In addition, a total of 461 core genes involved in development of reproductive tissues in pineapple were also identified in this study.

This research provides an important genomic resource for understanding molecular networks underlying cold stress response and how cold stress affects flowering time in pineapple.