

Comparative Genomics Can Provide New Insights Into the Evolutionary Mechanisms and Gene Function in CAM Plants

Background

Crassulacean acid metabolism (CAM) is a CO₂-concentrating mechanism used by plants to adapt to hot and dry environments. CAM plants use a unique mechanism resulting in high water-use efficiency, which can be 3- to 20-fold and 2- to 10-fold that of C₃ and C₄ photosynthesis plants, respectively. Inspired by the potential for enhancing the sustainable production of food and biomass on semi-arid, abandoned, or marginal agricultural lands, rich genomics resources have been created for multiple CAM species.

Highlights

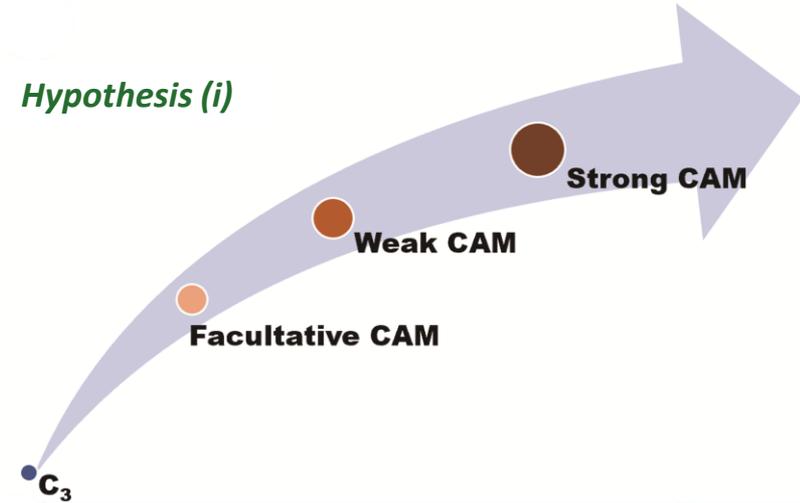
- Comparative analysis of DNA/protein sequences and diel (“daily”) gene expression patterns in various CAM species has identified candidate genes involved in CAM-related biological processes (e.g., CO₂ fixation, stomatal movement, circadian rhythm).
- Linking genes to the differences between C₃ and CAM physiology has provided new insights into the molecular mechanisms underlying the evolution of CAM from C₃ photosynthesis plants.
- Two testable hypotheses were developed based on new insights gained from linking genes to the differences between C₃ and CAM physiology: (i) CAM evolution followed a linear course leading from facultative CAM to strong constitutive CAM or (ii) facultative and constitutive CAM evolved independently

Significance

The comparative genomics framework and CAM evolution hypotheses presented in this article will inform future research to exploit the potential of engineering CAM into C₃ crops for genetic improvement of crop plants to enhance food and bioenergy production on semi-arid or marginal agricultural lands.

A conceptual framework of CAM evolution can be used to develop working hypotheses to incorporate CAM metabolism into other plants.

Hypothesis (i)



Hypothesis (ii)

