Transcript, protein and metabolite temporal dynamics in the CAM plant *Agave*

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Background:

Crassulacean acid metabolism (CAM) is a specialized type of photosynthesis that has much higher water-use efficiency than C_3 and C_4 photosynthesis.

Objective:

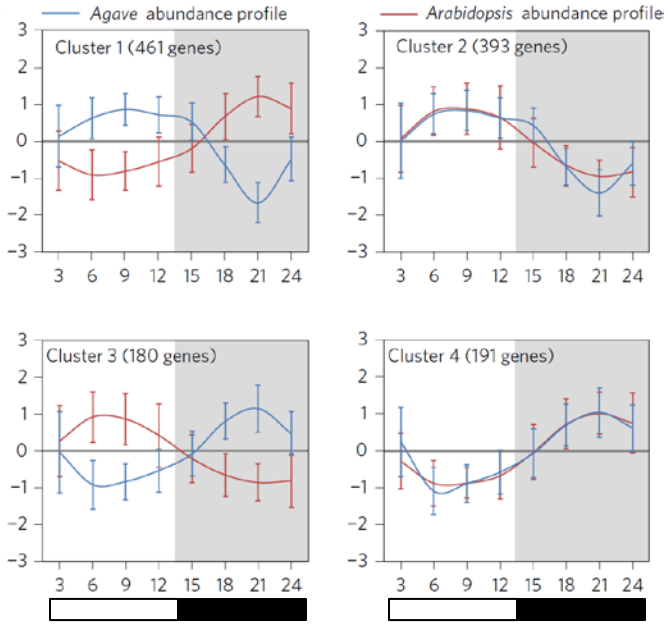
Understand post-transcriptional and -translational hierarchies that govern CAM in *Agave*.

New science:

- We report high-resolution temporal behaviors of transcript, protein and metabolite abundances across a CAM diel cycle and, where applicable, compare those observations to a non-CAM model plant, Arabidopsis.
- We identify rescheduled expression of genes associated with signal transduction mechanisms that regulate stomatal opening/closing.

Significance:

- Provide new insights into the molecular basis of CAM pathway in *Agave*.
- Provide a resource to inform efforts to engineer more water-use efficient CAM pathway traits into economically valuable C_3 crops.



Gene clusters with the diel transcript abundance profiles of *Agave* genes being different than (left panel) or similar (right panel) to those of their *Arabidopsis* counterparts, highlighting prominent anti-correlative and correlative relationships. White and black bars indicate daytime and nighttime, respectively.

Citation: Abraham PE, Yin H, Borland AM, Weighill D, Lim SD, De Paoli HC, Engle N, Jones PC, Agh R, Weston DJ et al. 2016. Transcript, protein and metabolite temporal dynamics in the CAM plant *Agave*. Nature Plants 2: 16178. doi: 10.1038/nplants.2016.178

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