

Researchers reveal multifaceted regulation of crassulacean acid metabolism in epiphytic orchid

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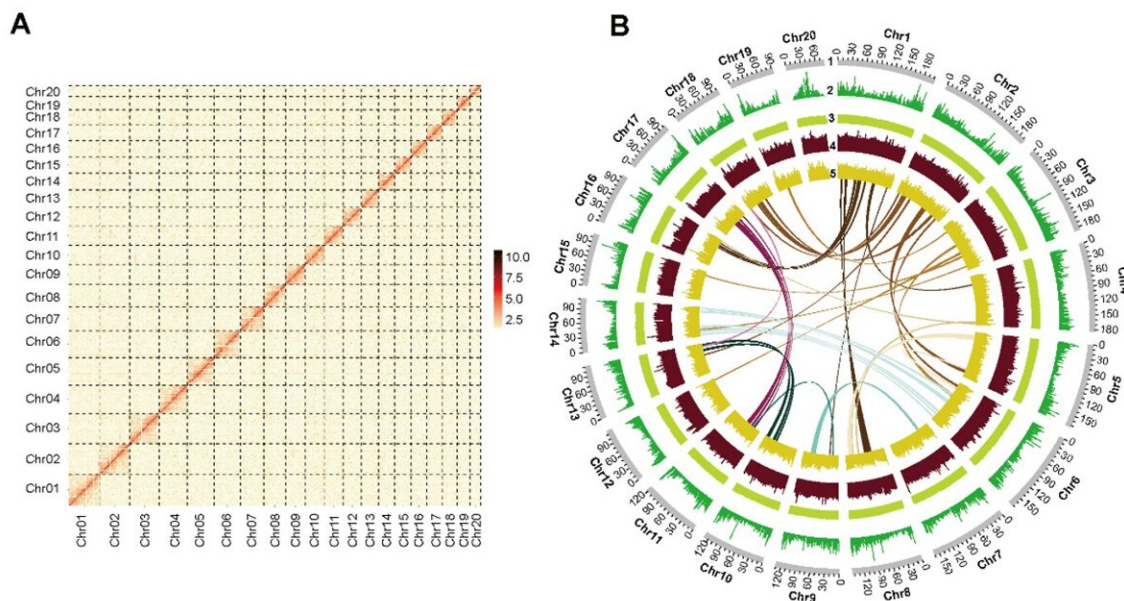


Figure 1. Chromosomal-level genomic features of *C. mannii*. Credit: KIB

Epiphytes are a distinct group in the Earth's carbon cycling ecosystems. Most vascular epiphytes are from the particularly species-rich orchid family (Orchidaceae), with about 70% of Orchidaceae species being epiphytes. Crassulacean Acid Metabolism (CAM) is a water-conserving carbon dioxide (CO₂) fixation pathway, and Epiphytes with CAM

photosynthesis are widespread in vascular plants.

By using a temporally separated carbon-concentrating mechanism, a CAM plant is able to photosynthesize during the day and exchange gases at night to minimize water loss. However, the understanding of the molecular regulation of CAM photosynthesis in epiphytes remains elusive.

Researchers from the Kunming Institute of Botany (KIB) of the Chinese Academy of Sciences (CAS) have assembled a high-quality genome of the epiphytic CAM orchid, *Cymbidium mannii*, integrating transcriptome, proteome and metabolome analysis to reveal the multifaceted regulation mechanism in CAM epiphytes.

Results have been published in *Plant Communications* entitled "High-quality *Cymbidium mannii* genome and multifaceted regulation of crassulacean acid metabolism in epiphytes."

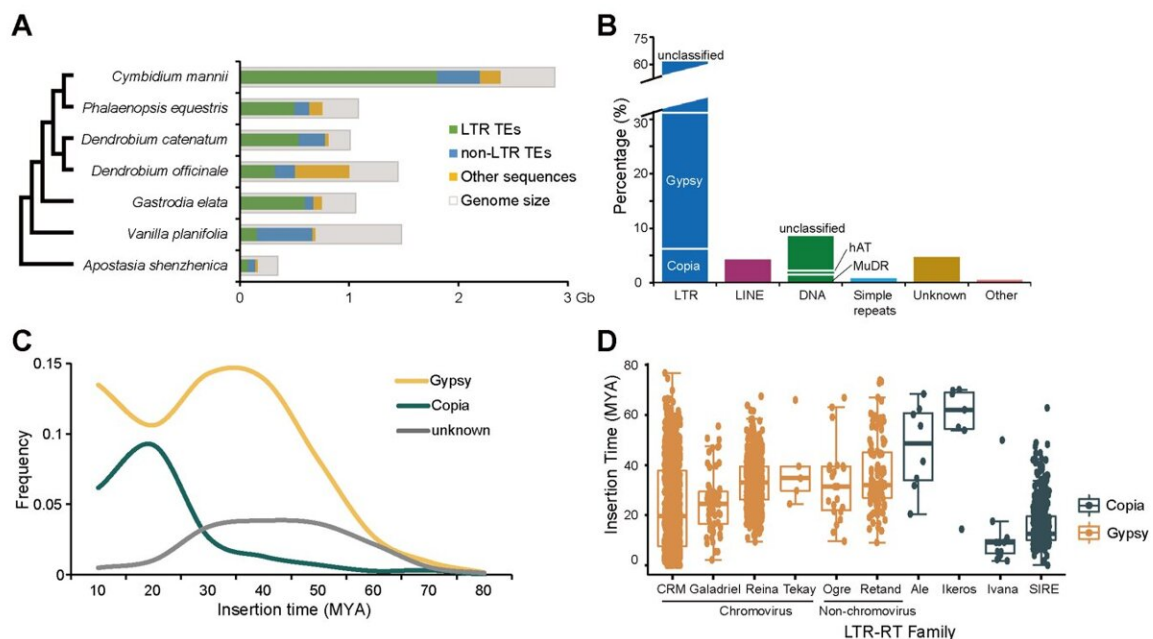


Figure 2. TE-mediated genome size expansion. Credit: KIB

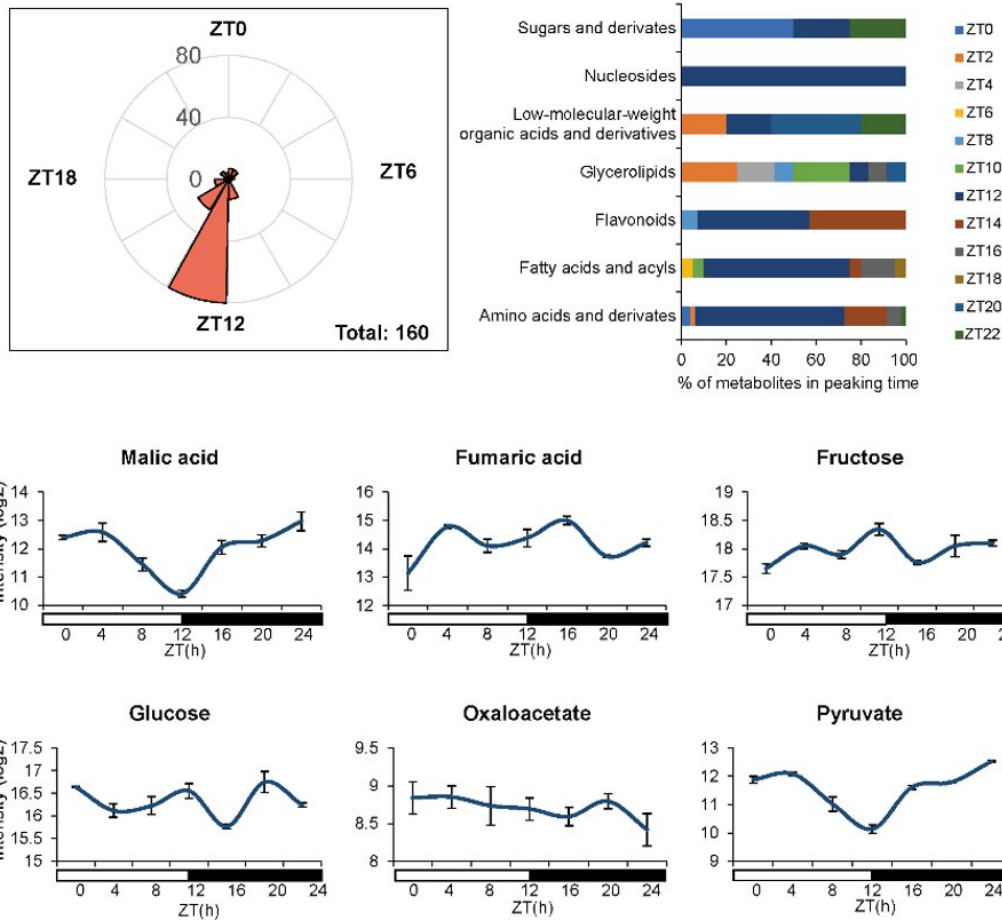


Figure 3. Rhythmic and selected CAM photosynthesis-related metabolites in *C. manni*. Credit: KIB

According to the researchers, the genome of *C. manni* is 2.88 Gb in length with a contig N50 of 22.7 Mb, of which 82.8% were repetitive elements. The genome size expansion in *Cymbidium* is mainly due to the

long terminal repeats insertions, and the insertion time is consistent with the time of the diversification of *Cymbidium* species.

They found that the patterns of rhythmically oscillating metabolites, especially CAM-related products, reflect the circadian rhythmicity of metabolite accumulation in epiphytes.

Genome-wide analysis of transcript and protein level regulation revealed phase shifts in the multifaceted regulation of circadian metabolism. The researchers show the diurnal expression of several core CAM genes (in particular β CA and PPC), which could temporally fix carbon sources.

The gene expression levels of NADP-ME and PPDK in *C. manii* were highly consistent with those in *Kalanchoe fedtschenkoi* and *Sedum album*, showing that they all prefer to use the nicotinamide adenine dinucleotide phosphate malic enzyme (NADP-ME) and pyruvate orthophosphate dikinase (PPDK) pathways for decarboxylation.

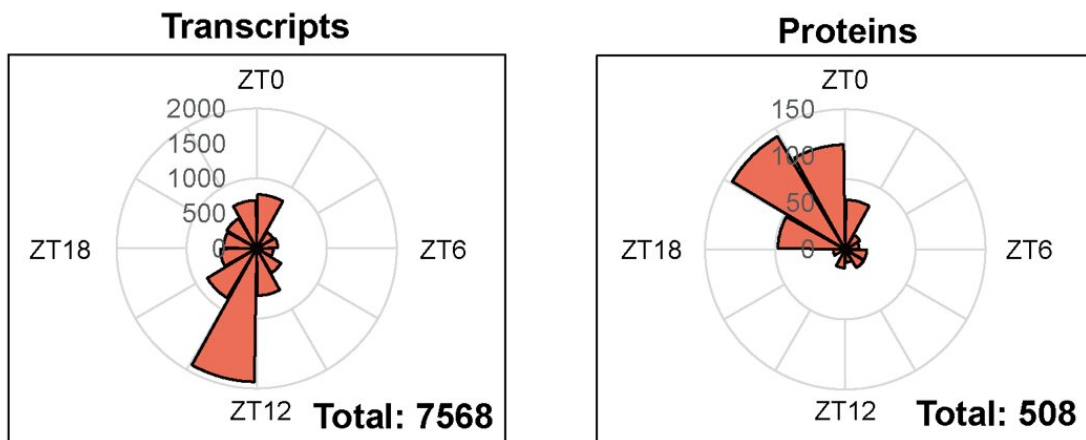


Figure 4. Phase shift between proteomic and expression profiles. Credit: KIB

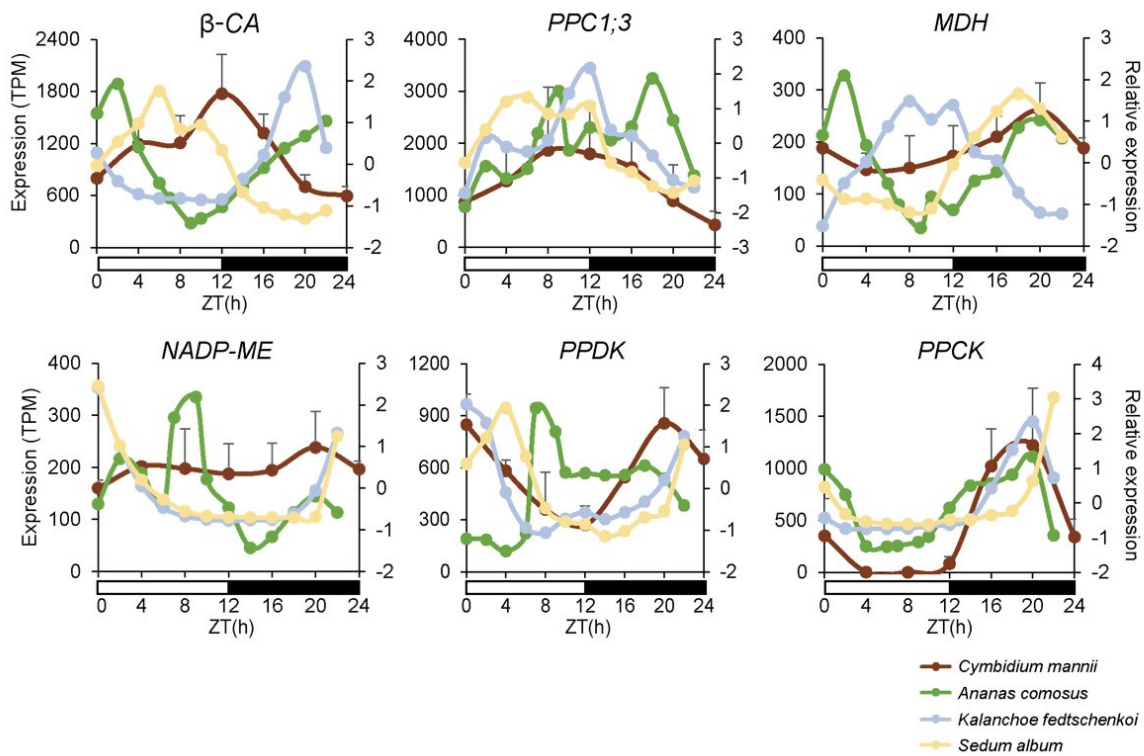


Figure 5. Selected cycling core CAM gene expression in *C. mannii* and compared with terrestrial CAM plants. Credit: KIB

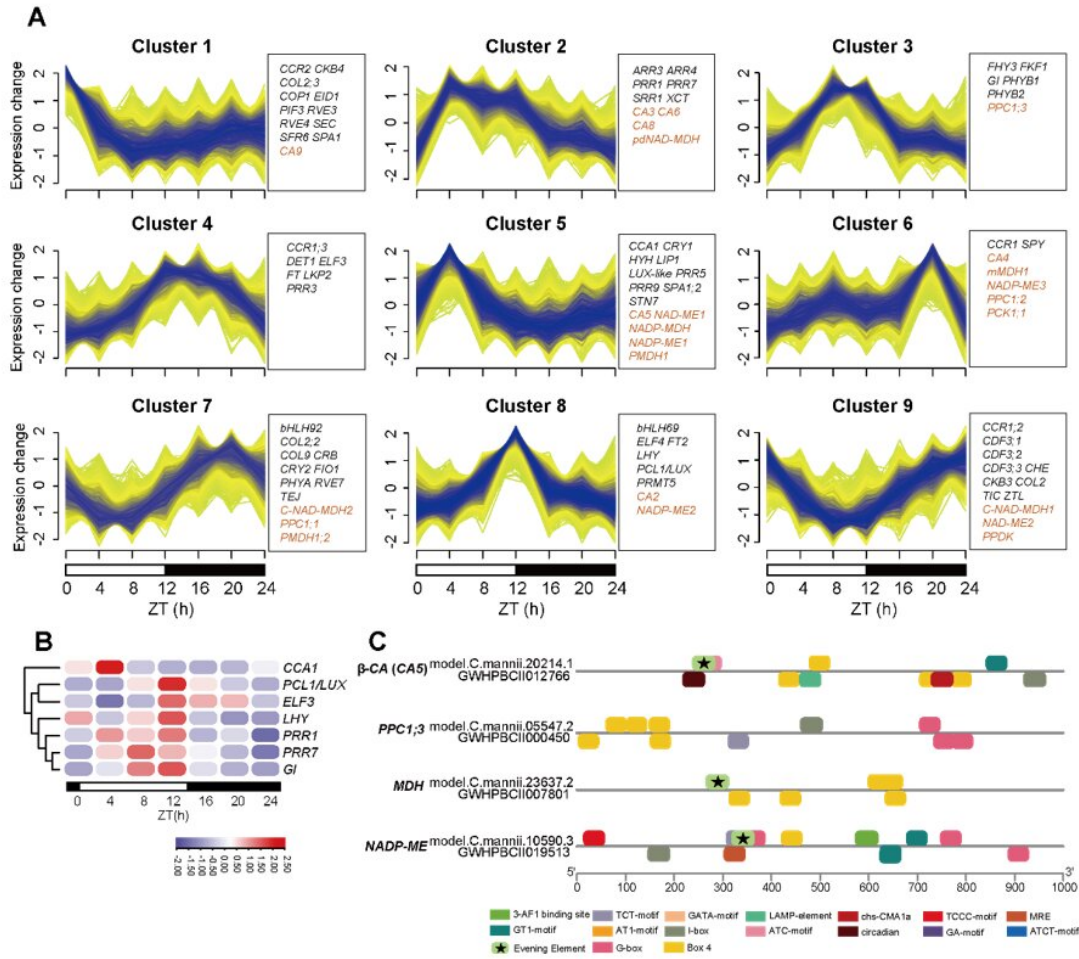


Figure 6. Core circadian clock gene expression level and CREs in selected CAM genes. Credit: KIB

Since the circadian clock-associated genes and cis-regulatory elements (CREs) play a crucial role in regulating the CAM pathway, the researchers examined the expression pattern of the [circadian](#) clock and CAM genes during the diel cycle and found the light-responsive CREs in promoter regions that may be involved in photoperiodism.

More information: Weishu Fan et al, High-quality *Cymbidium mannii* genome and multifaceted regulation of crassulacean acid metabolism in

epiphytes, *Plant Communications* (2023). DOI: [10.1016/j.xplc.2023.100564](https://doi.org/10.1016/j.xplc.2023.100564)

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