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Title paper: Key players in the reproductive transition in neotropical orchids: a departure from model monocots

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During the reproductive transition in angiosperms, flowering integrators set the timing of meristem fate shifts, when a vegetative apical meristem (SAM) forming leaves, becomes an inflorescence meristem (IM) that forms bracts and flowers. This process has been well studied in model grasses, like *Oryza sativa* and includes flowering promoters like Heading date 3a (*Hd3a*) (*FLOWERING LOCUS T-FT*), Heading date 1 (*Hd1*) (*CONSTANS-CO*), *FLOWERING LOCUS D* (*OsFD1*) and 14–3–3 proteins that activate floral meristem identity genes. Repressors involved in the maintenance of the vegetative phases include *TERMINAL FLOWER LOCUS 1 (TFL1)* and *OsMADS55* (*AGL24/SVP*). Additional repressors have been identified in vernalization responsive grasses like wheat, specifically *FLOWERING LOCUS C (FLC*) and *VERNALIZATION 2 (VRN2)*. Here we studied the morpho-anatomical and molecular basis of the flowering transition in the Orchidaceae, one of the most diverse angiosperm lineage (ca. 29,000 species) with outstanding habit variations and niche adaptations. We combine RNA-seq analyses targeting differentially expressed genes (DEGs) between SAM and IM with targeted evaluation of spatio-temporal expression patterns of major regulators in *Epidendrum fimbriatum,* a miniature terrestrial orchid with nearly constant flowering in the field. We found 40 DEGs between SAM and IM involved in reproductive transition that let us to re-evaluate the Flowering Genetic Regulatory Network (FGRN) in orchids when compared to the model species *O. sativa*. We found that: 1) flowering integrators are present in multiple copies in orchids but only few of them are transcriptionally active and 2) the canonical flowering integrators are maintained, but due to copy number variation functional changes seem plausible. For instance, *PEBP* gene expression patterns suggest sub-functionalization with *TFL1* expressed in the SAM, *FT1C* in leaves, and *FT2A* in the IM. Similarly, *SVP* genes, have also specialized, as *SVP2A* is expressed in both the SAM and IM, but *SVP2B* is restricted to the IM and *SVP1* restricted to the SAM. Conversely, *FD*, *LFY* and *SOC1* genes show broad expression during vegetative and reproductive stages, suggesting they may act redundantly. Our comprehensive analysis of the orchid FGRN point to a modified set of flowering integrators in the reproductive transition, with FT2 and FUL-like genes as major promoters and SVP1 and SVP2A homologs as key repressors in the absence of FLC, deviating from model monocot FGRNs.

Keywords:
flowering, Orchidaceae, Evo-Devo, Gene evolution, gene expression,
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