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Assessing the flowering genetic regulatory network in neotropical orchids

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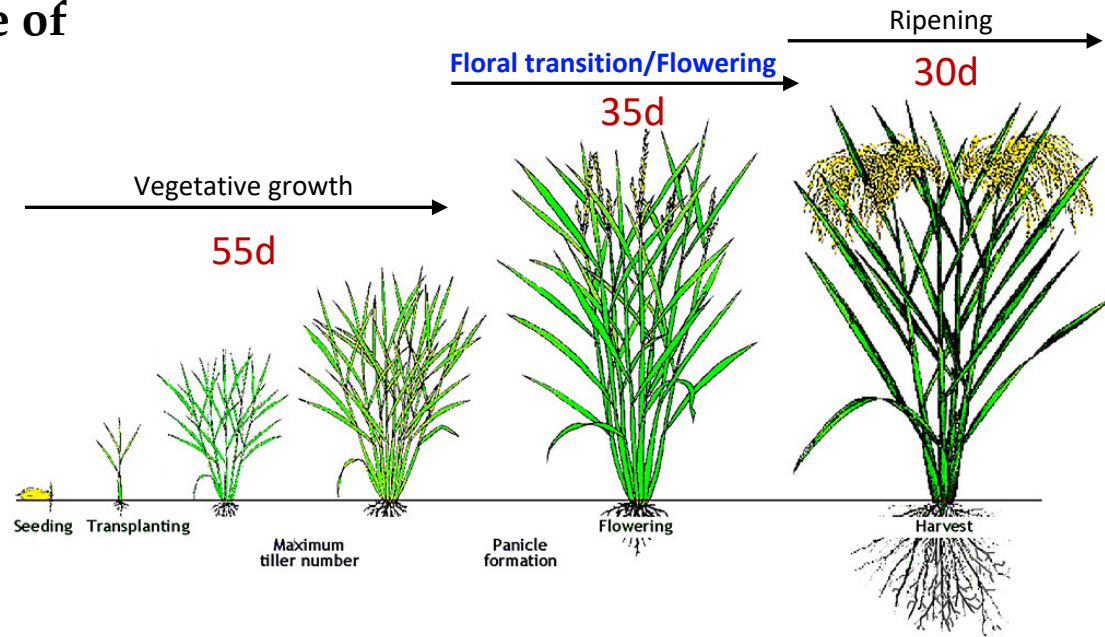
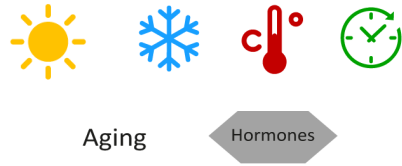
Abstract:

During the reproductive transition in flowering plants a vegetative apical meristem (SAM) transforms into an inflorescence meristem (IM) that forms bracts and flowers. In grasses, like rice, a Genetic Regulatory Network (GRN) involved in reproductive transitions has been identified. It includes the integration of promoters and repressors from different gene lineages, which have undergone different duplication events at different timepoints in angiosperm diversification. With the objective to understand the evolution and expression of flowering GRN in Orchidaceae, we performed comprehensive phylogenetic analyses of all genes from the flowering GRN and analyzed by RT-PCR the expression of targeted homologs in key developmental stages. Our ML results indicate that *FT/TFL1*, *FD*, *FLC/FUL*, *SOC1* and *AGL24/SVP* gene lineages have been subject to multiple duplications in monocots as well as in Orchidaceae as a result of recorded whole genome duplication events. Conversely, *FLC* genes are lost in Orchidaceae, suggesting major changes in the repression of flowering. Our studies also show active expression of many target genes in *Elleanthus aurantiacus* (Orchidoideae) in the SAM and in IM indicating important functions in the reproductive transition. We describe how the flowering GRN in orchids has significant variations in copy number and expression patterns when compared to the canonical rice flowering GRN

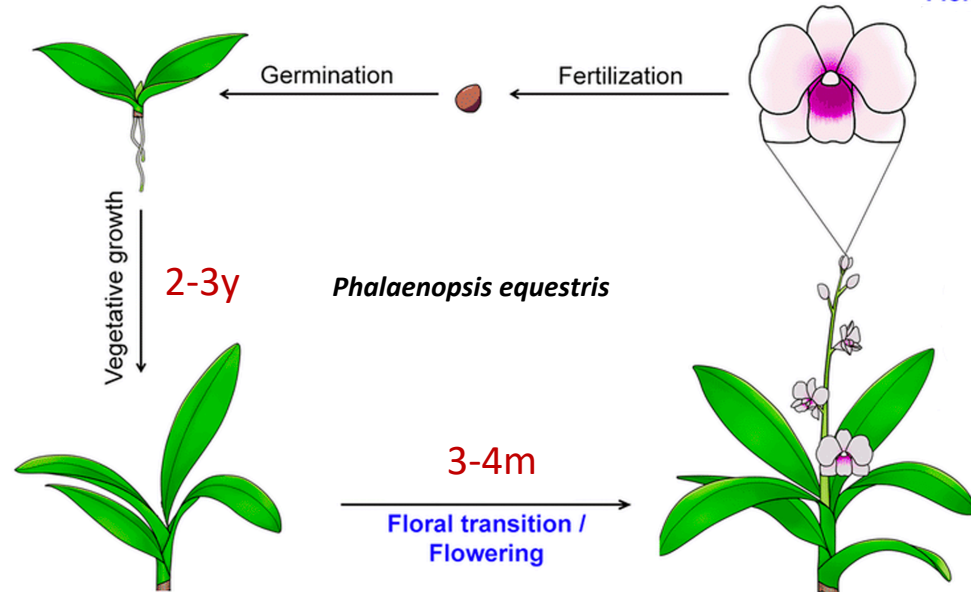
Keywords: AGAMOUS LIKE 24; Flowering; FLOWERING LOCUS T; FLOWERING LOCUS C; FLOWERING LOCUS D; Gene Evolution; Genetic Regulatory Network; Orchidaceae; SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1.

Flowering conditions in Angiosperms: a case of study in Orchids

Oryza sativa



Floral patterning



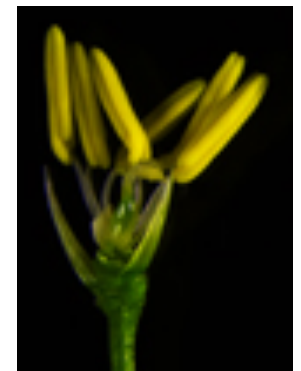
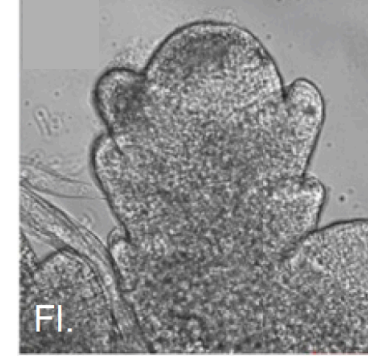
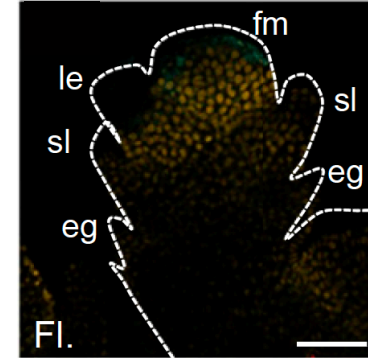
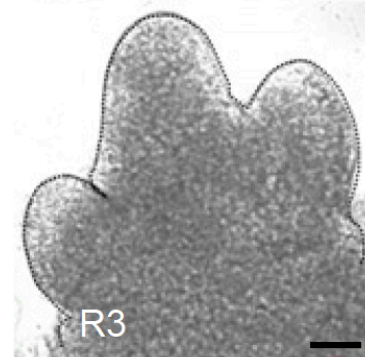
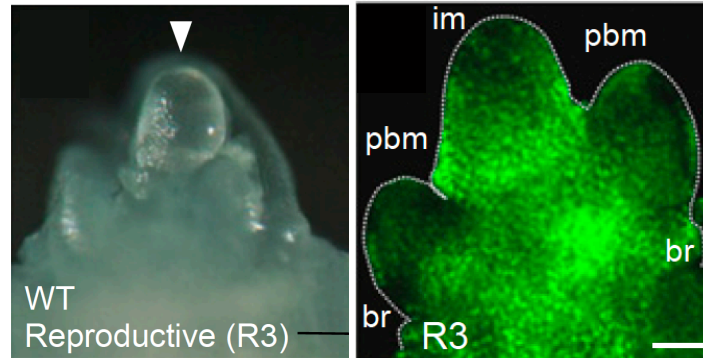
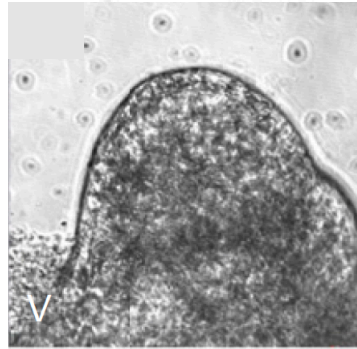
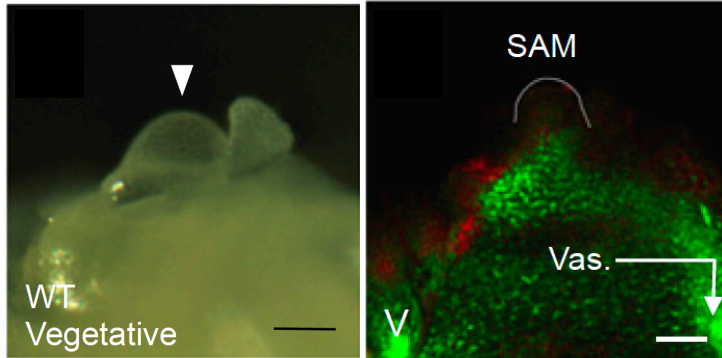
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The reproductive transition include changes between meristem identities

Shoot Apical Meristem (SAM)

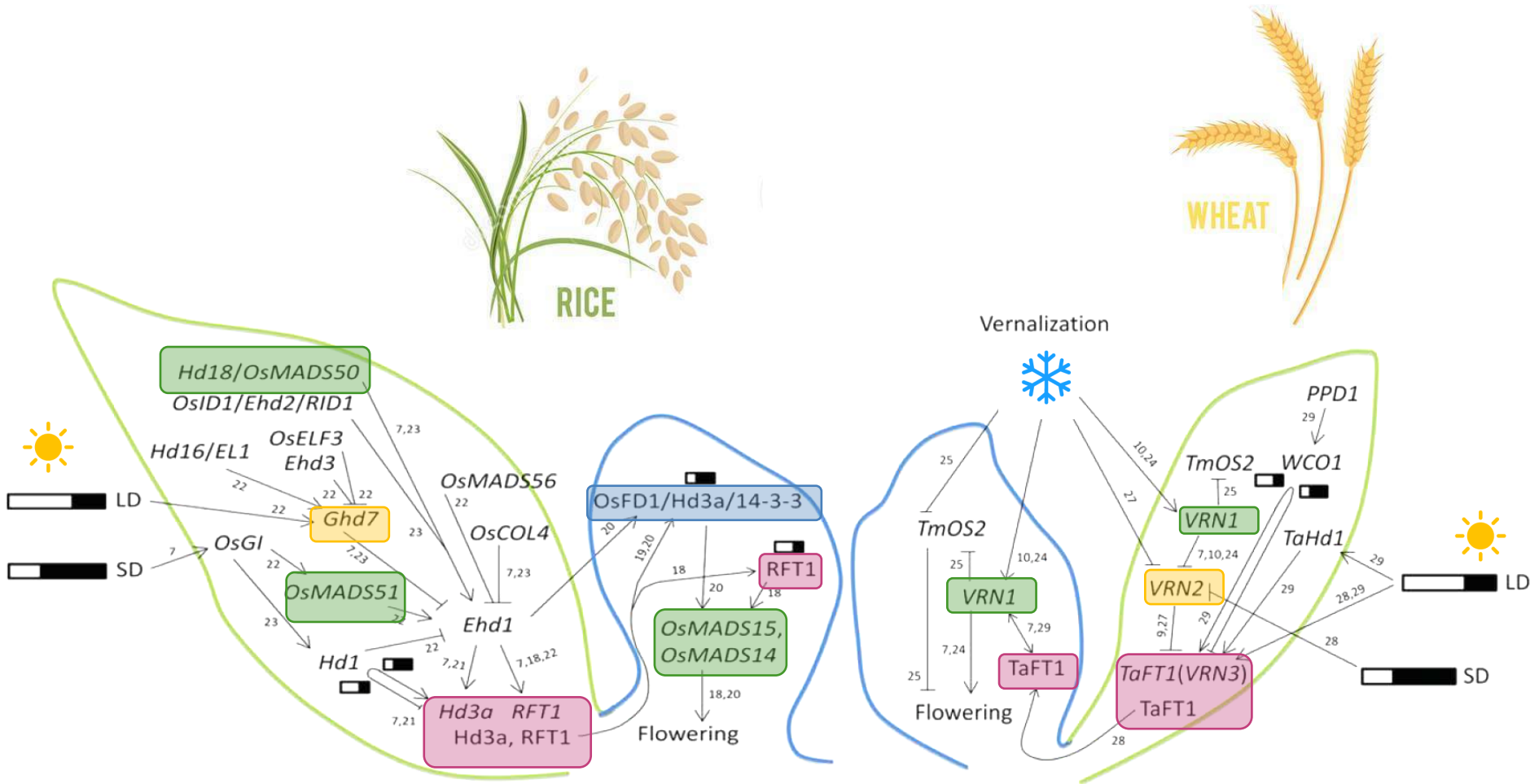
Inflorescence Meristem (IM)

Floral Meristem (FM)



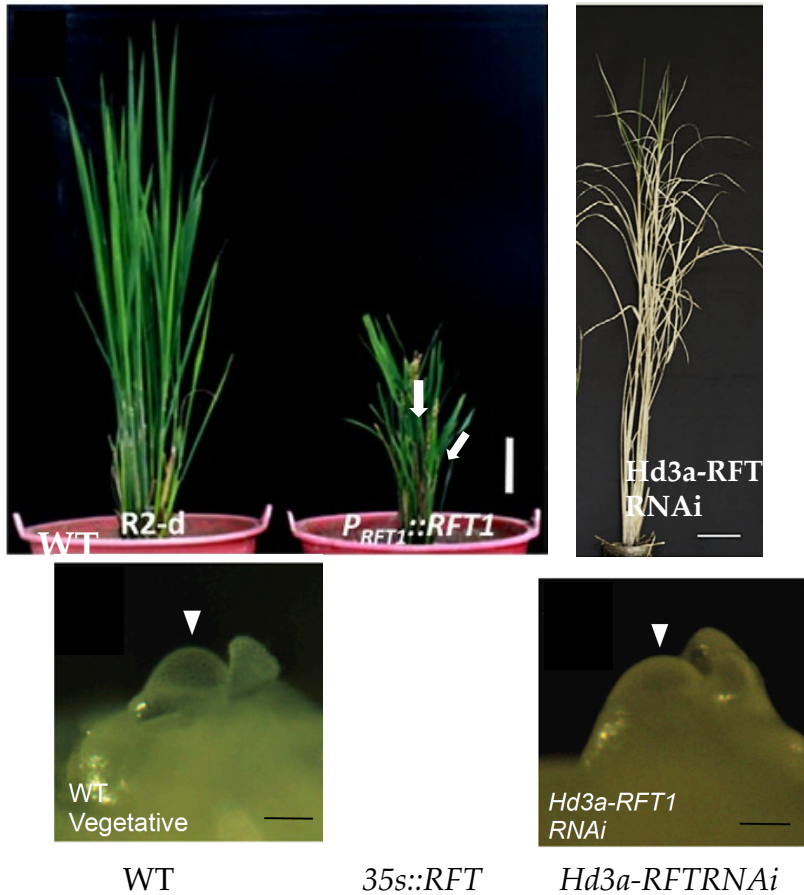
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Summarized Genetic Regulatory Network (GRN) that controls vegetative to reproductive transition in grasses

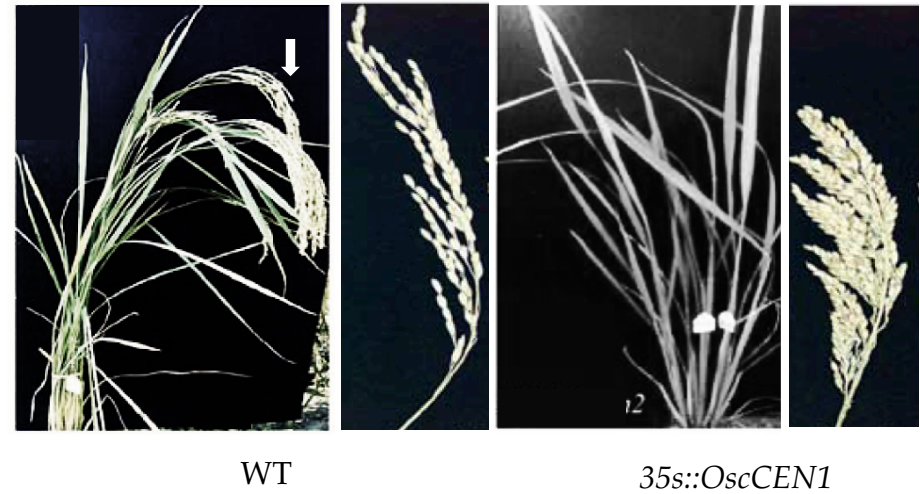


FT and *TFL1* are paralogous and mobile signals with opposite functions in the transition to flowering

FLOWERING LOCUS T (*FT*)



TERMINAL FLOWER 1 GENES (*TFL1*)



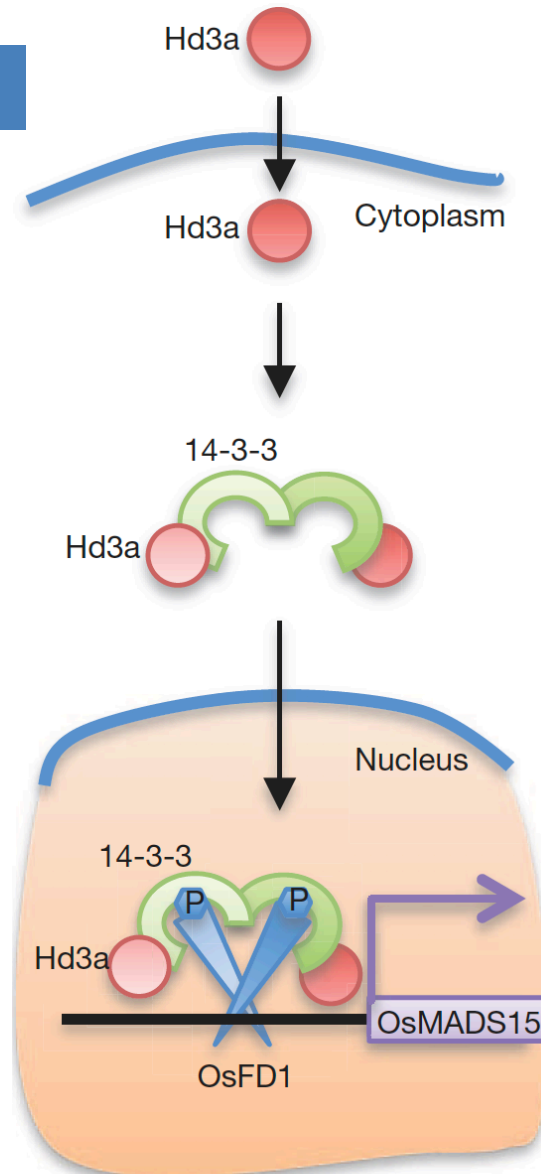
FT interact with FD to control flowering through a Florigen Activation Complex (FAC)

FLOWERING LOCUS D GENES (FD)



WT

Osf1



SOC1 together with *AGL24* directly activates Floral Meristem (FM) identity genes *AP1/FUL*

Suppressor Of Overexpression of *CONSTANS* genes (*SOC1*)

AGAMOUS-Like 24 genes (*AGL24*)

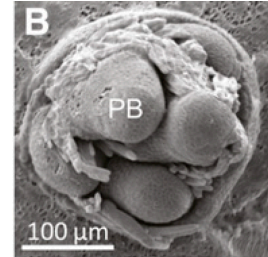


WT *Osmads50/51*



WT 35S::*OsMADS50*

APETALA1/FRUITFULL genes (*AP1/FUL*)



WT



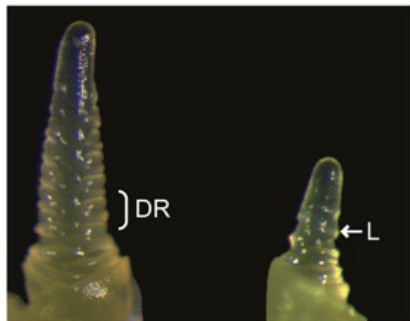
Osmads14/15/18/pap

Vernalized grasses respond to cold exposure to activate flowering

FLC-like genes

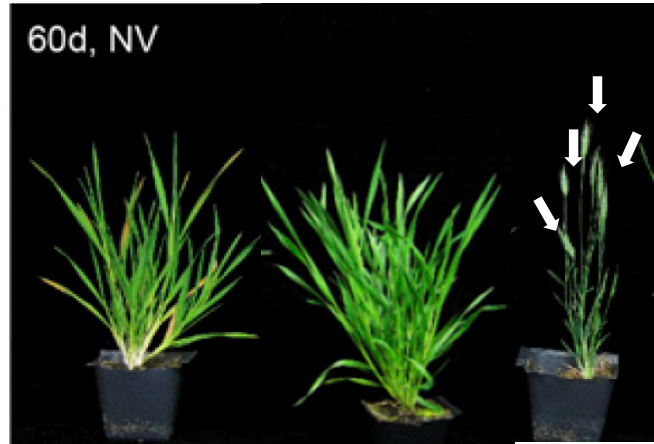


WT OxHvOS2-20



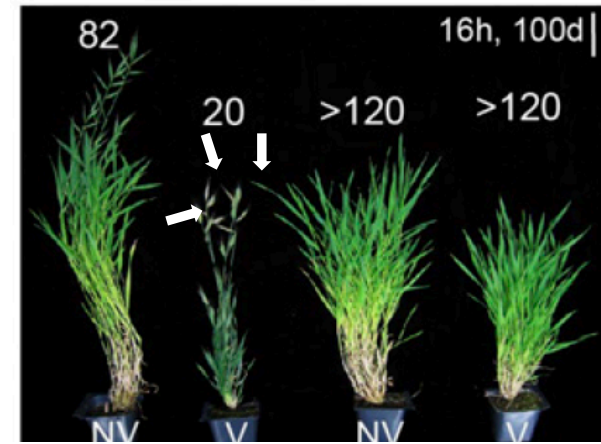
WT OxHvOS2-20

VRN2 genes

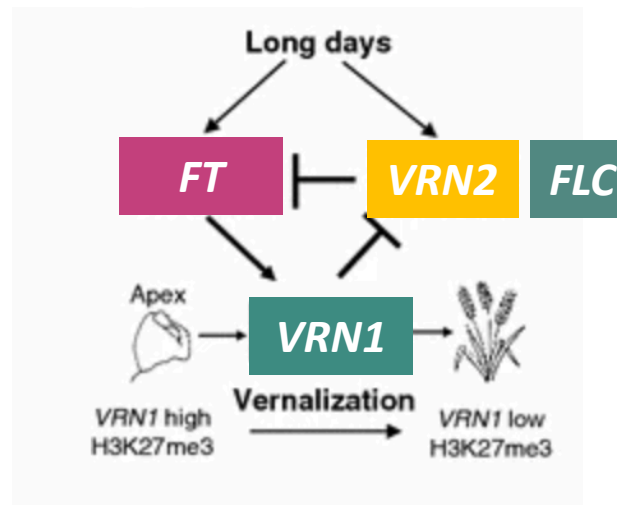


WT UBI:VRN2 Bdvrn2

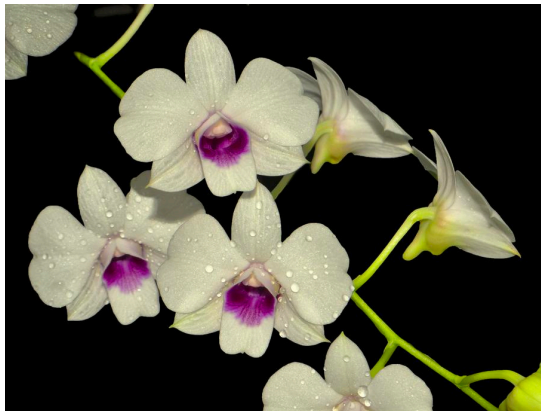
VRN1 genes



WT Bdvrn1



There are only some reports on the expression of *FT/TFL1* and *MADS-box* genes in orchids



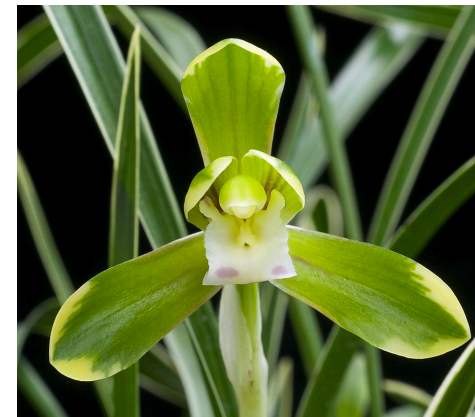
Dendrobium Chao Praya Smile



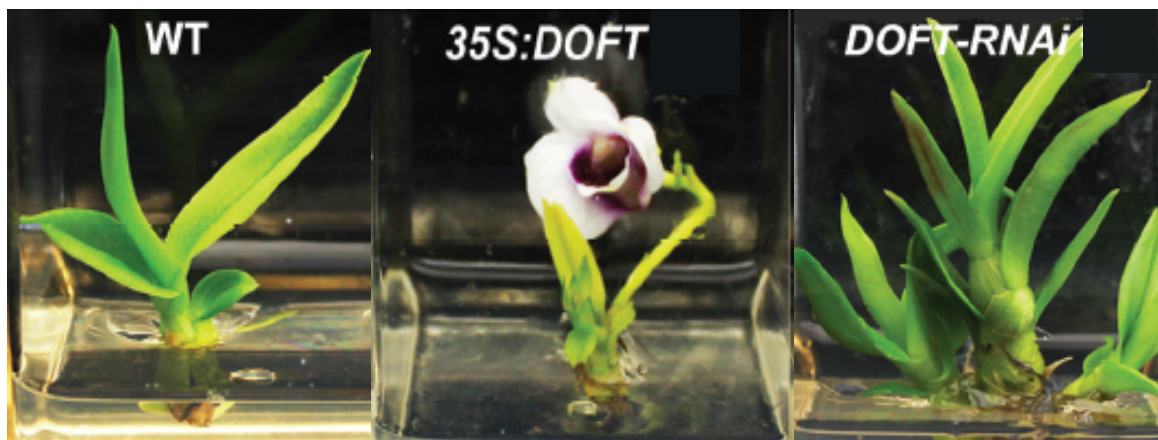
Phalaenopsis equestris



Oncidium Gower Ramsey

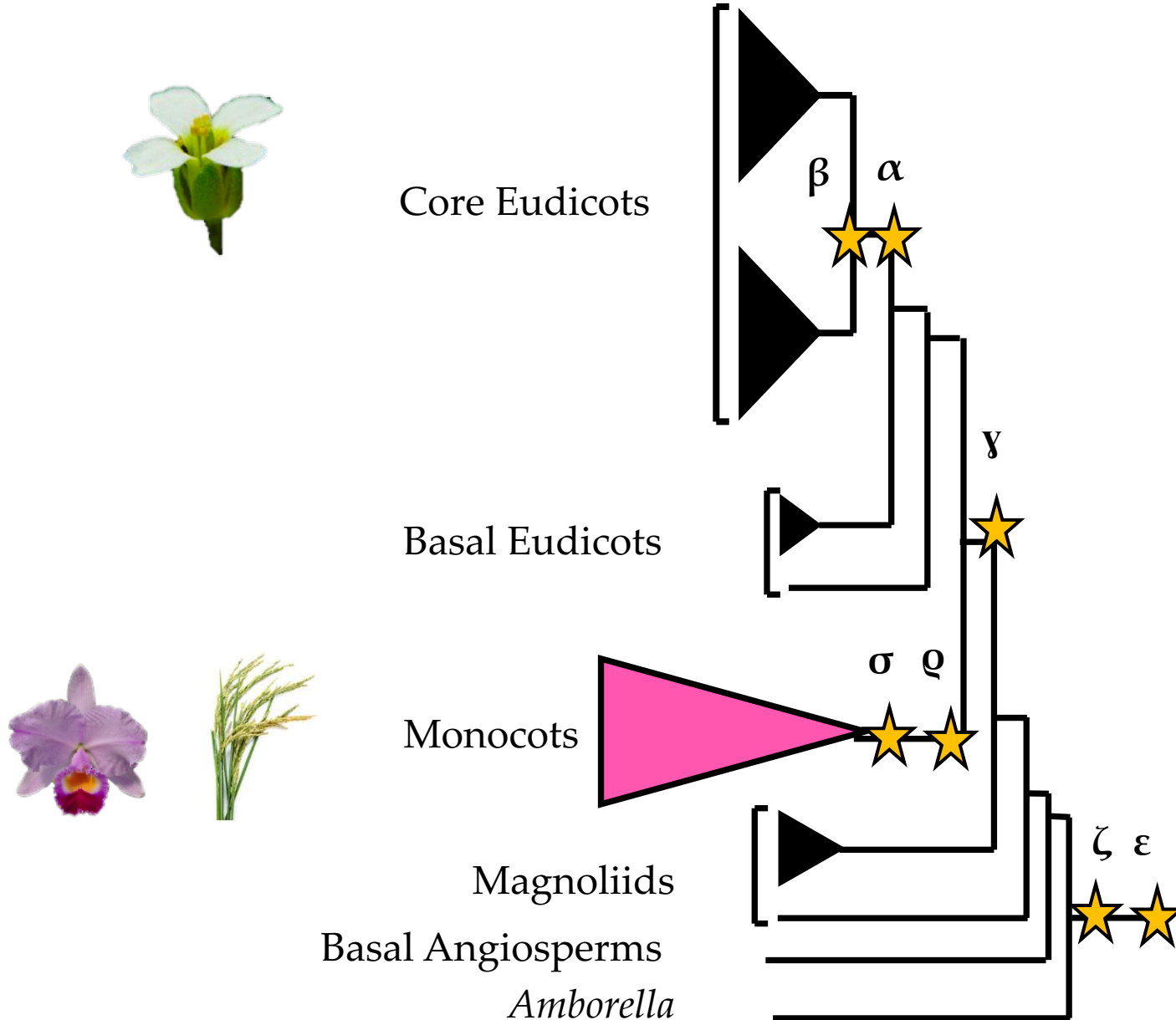


Cymbidium goeringii



FT genes in *Dendrobium* that are involved in the promotion of flowering

Orchid genetic complement is not the same than model species



Results: We have sequenced 13 neotropical orchid mixed transcriptomes



Vanilla aphylla



Gomphichis scaposa



Tolumnia Cherry red x Ralph yagi



Oncidium Grower Ramsey



Oncidium Twinkle



Masdevallia coccinea



Masdevallia wendlandiana



Maxillaria aurea



Stelis pusilla



Epidendrum fimbriatum

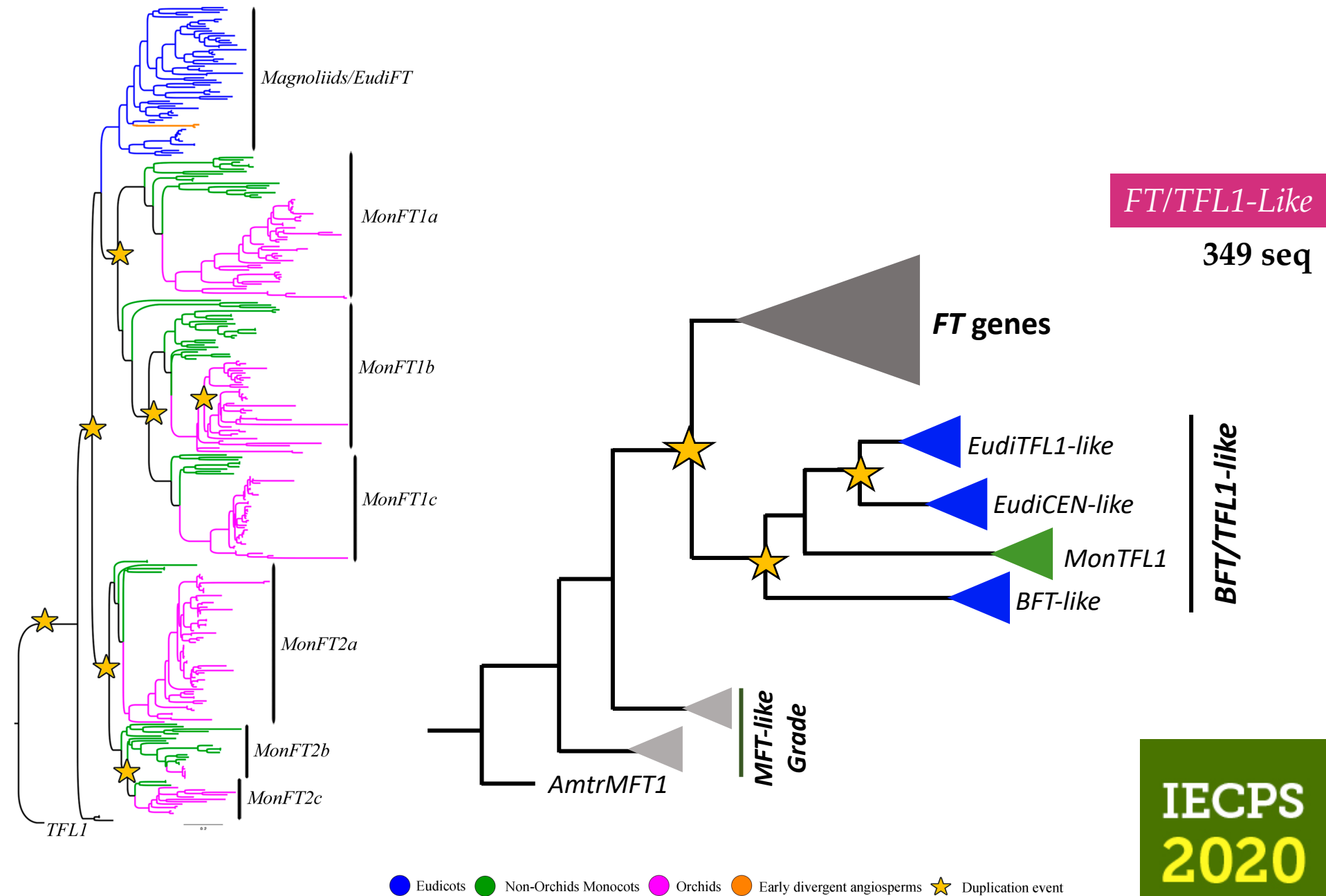


Miltoniopsis roezlii

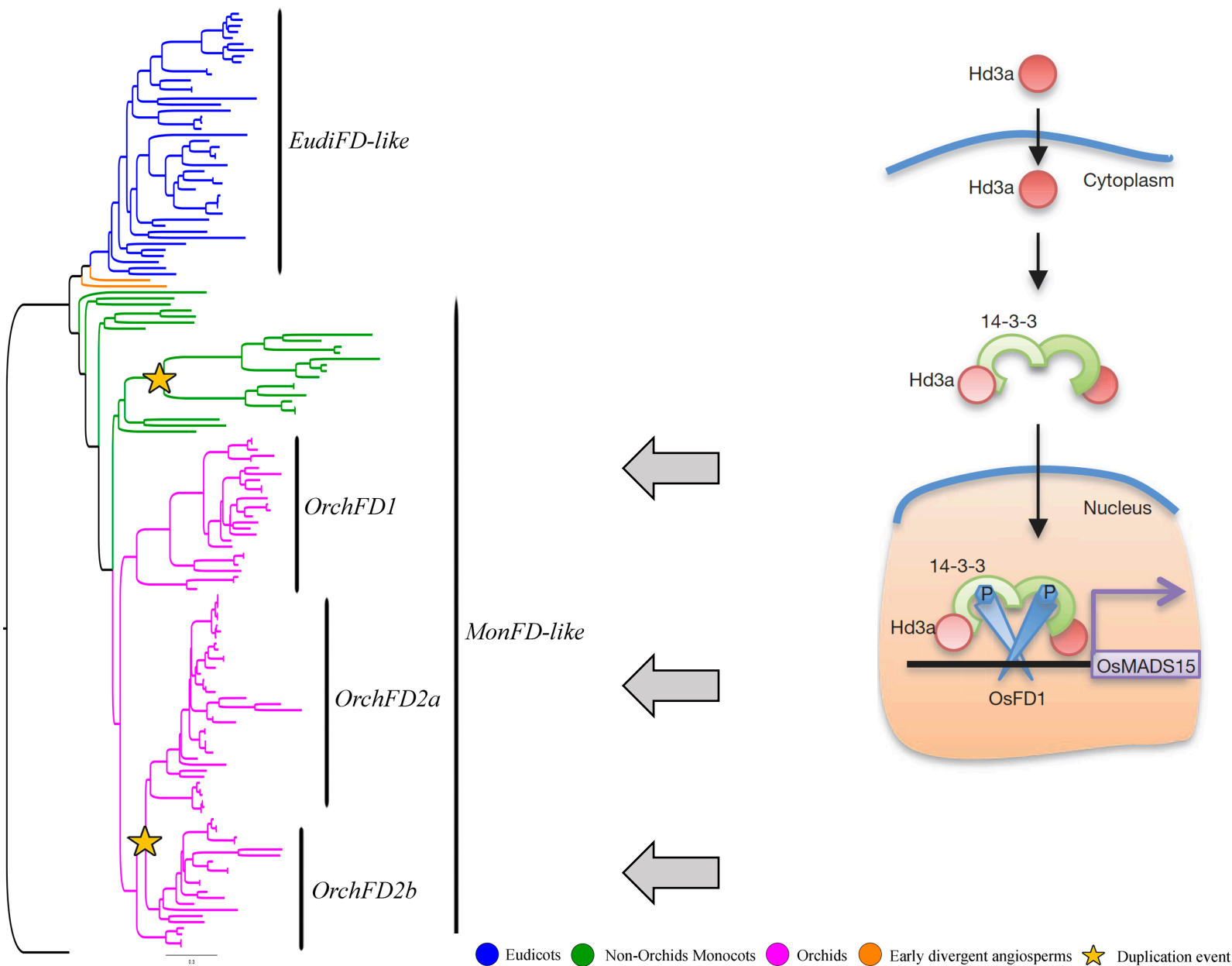


Elleanthus aurantiacus

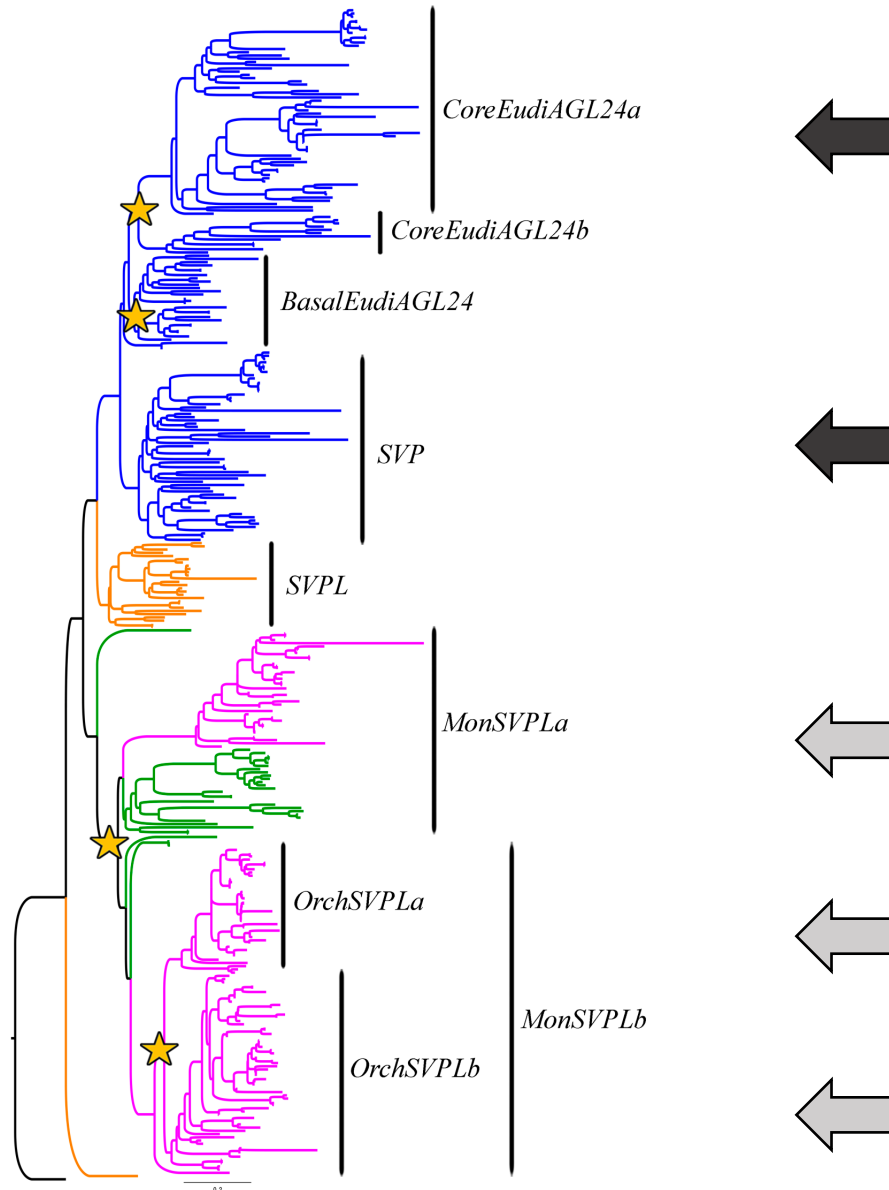
FT genes have undergone a lot of duplications in Angiosperms



FD genes have undergone at least three duplication events prior to the diversification of the Orchidaceae

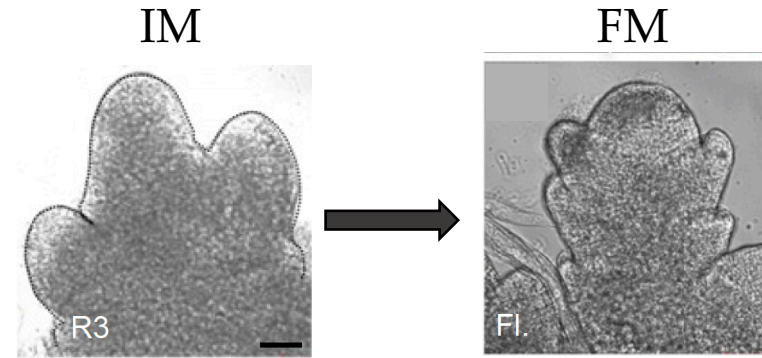


Orchidaceae have at least three copies of *AGL24/SVP* genes



AGL24/SVP-like

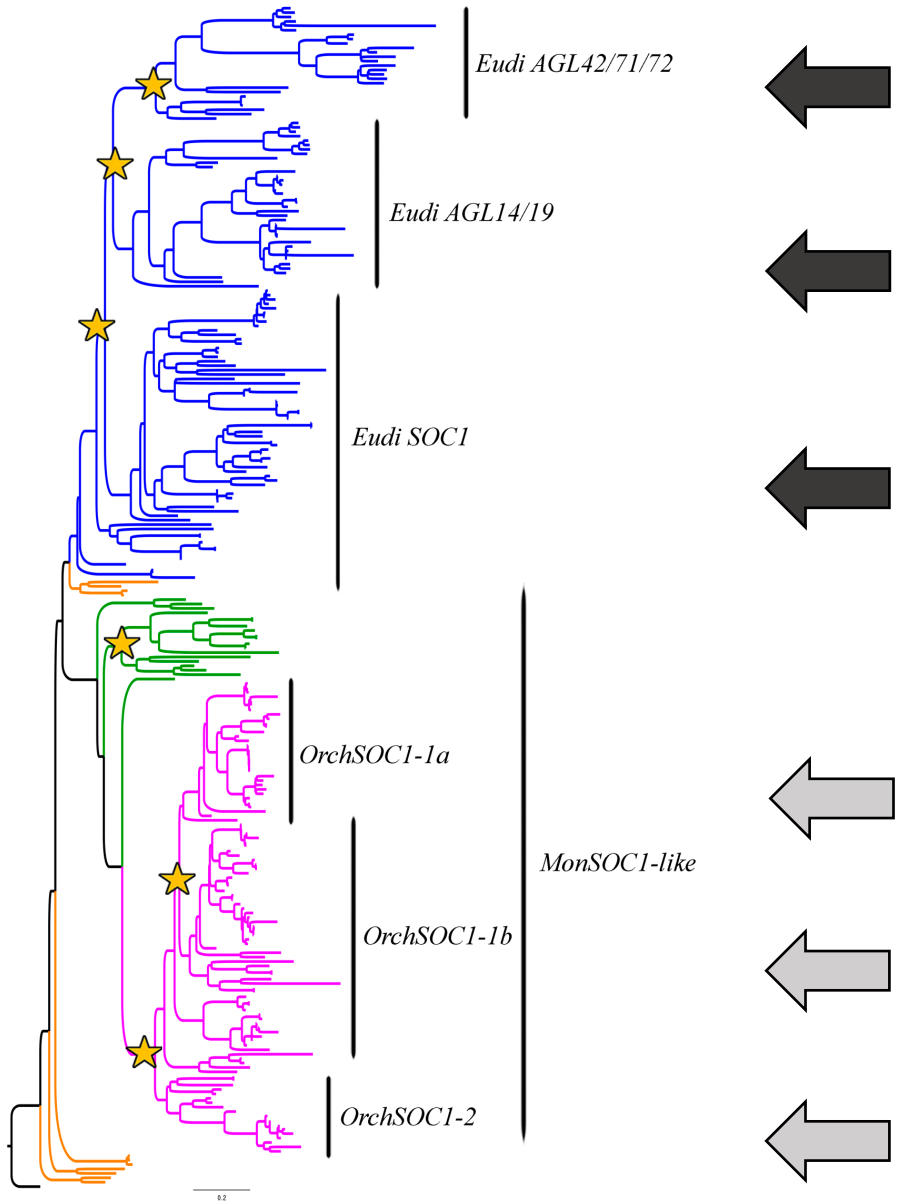
363 seq



The *AGL24* and *SVP* clades are eudicot specific.

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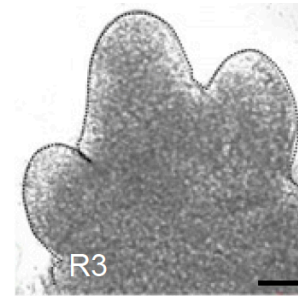
SOC1 genes have three independent duplications prior to the diversification of the Orchidaceae.



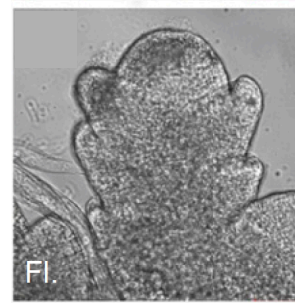
SOC1-like

268 seq

IM



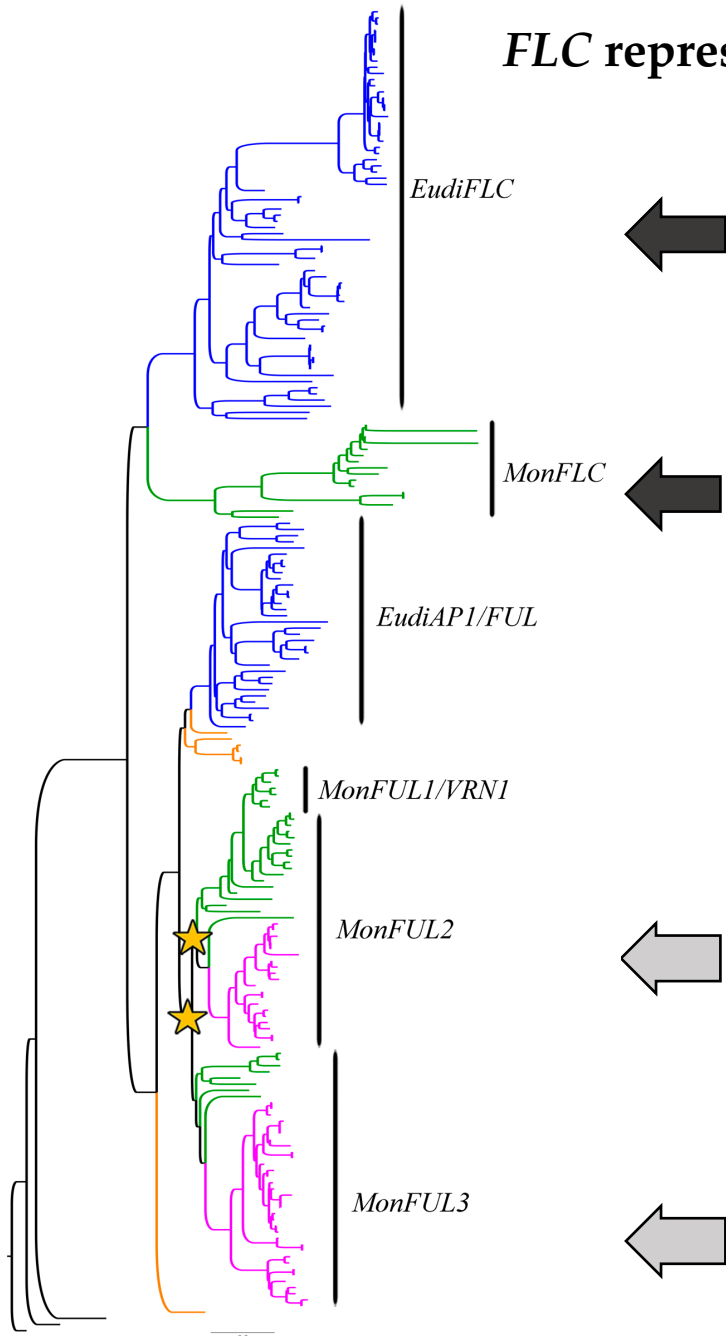
FM



SOC1 genes have at least three duplications prior to the diversification of eudicots.

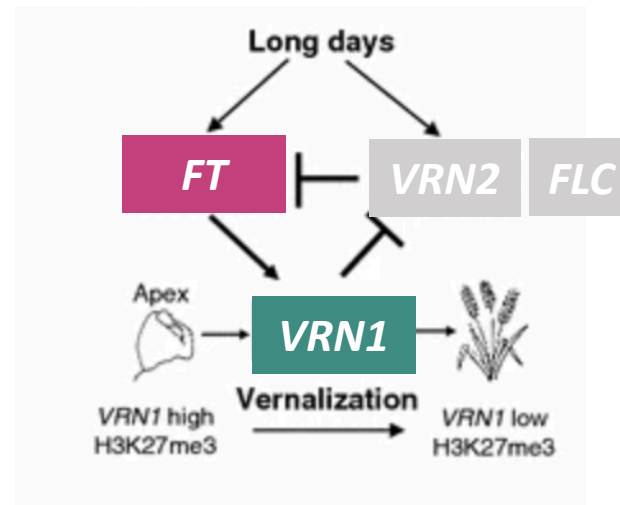
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FLC repressor and VRN1 promoter genes are lacking in orchids



FLC/FUL

215 seq



FUL homologs are duplicated in both eudicots and monocots

Developmental stages in flowering transition in *Elleanthus aurantiacus*

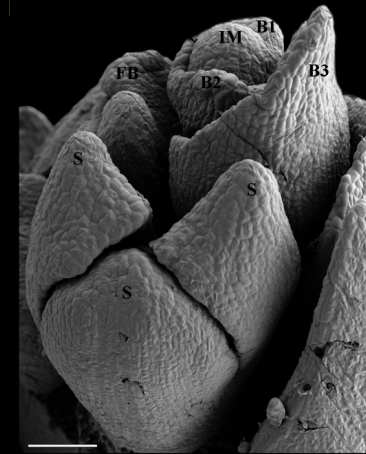
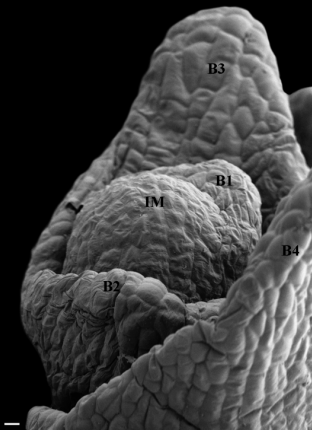
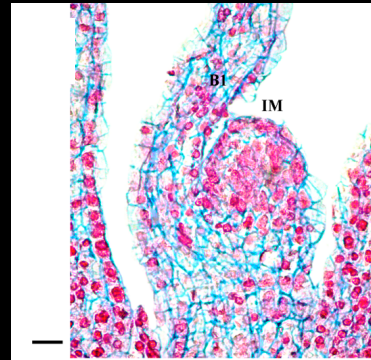
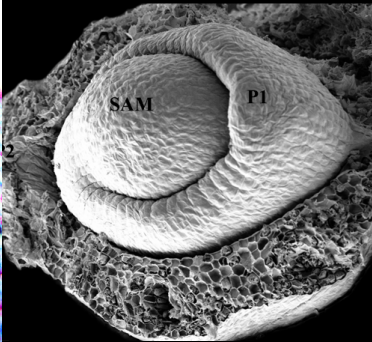
Shoot Apical Meristem (SAM)



Inflorescence Meristem (IM)

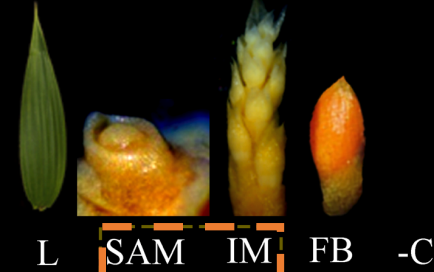


Floral Meristem (FM)



E. aurantiacus plants grow on 1400-2700m altitude and form racemose inflorescences on rainy season two times per year

Qualitative expression analysis of GNR in *Elleanthus aurantiacus*



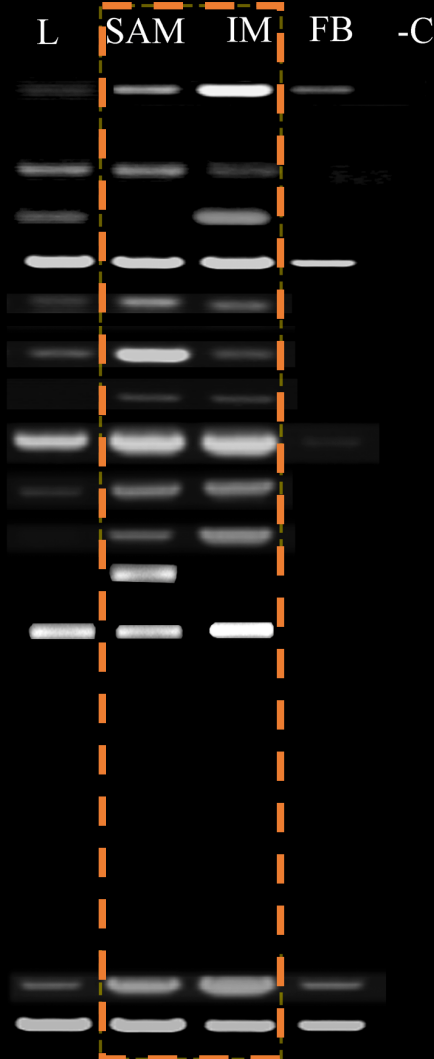
GRN genes are expressed in the SAM and in IM, suggesting important functions in the reproductive transition

PEBP

bZip

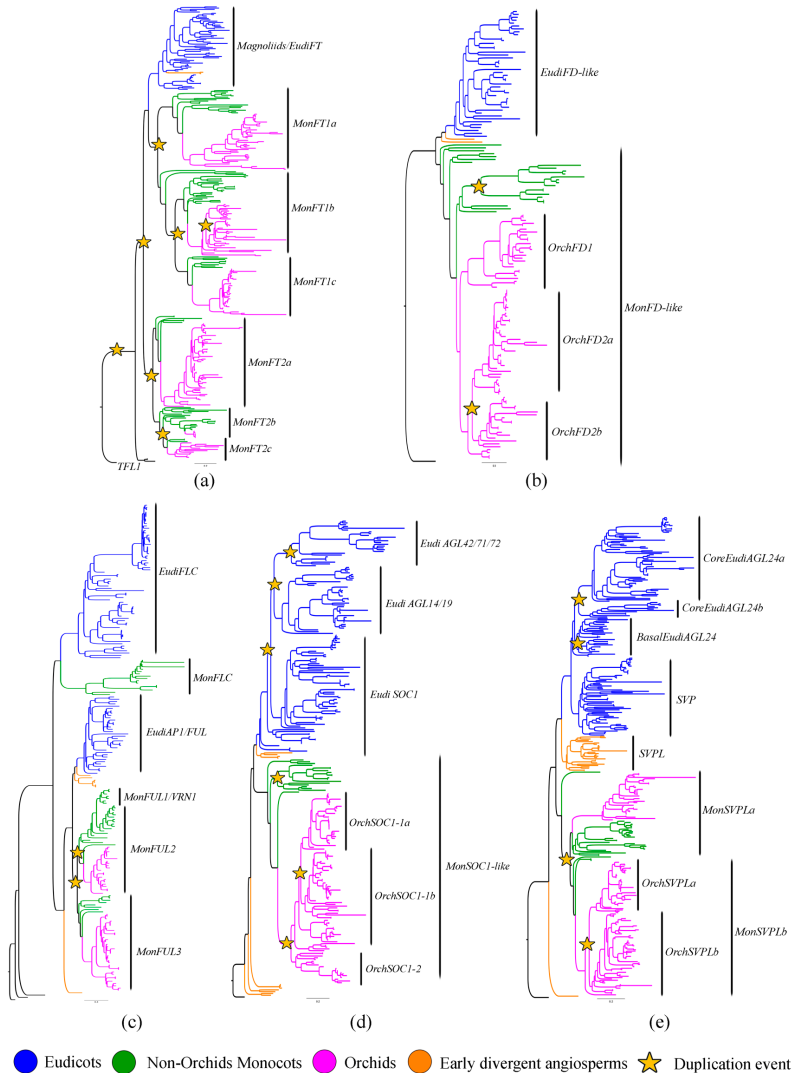
MADS-box

ElauFT1A
ElauFT1C_1
ElauFT1C_2
ElauFT2A_1
ElauFT2A_2
ElauMFT
ElauFD1
ElauFD2
ElauSOC1-1
ElauSOC1-2
ElauSOC1-3
ElauSVP1
ElauSVP2
ElauSVP3
ElauSVP4
ElauSVP5
ElauSVP6
ElauSVP7
ElauGADPH
ElauActin

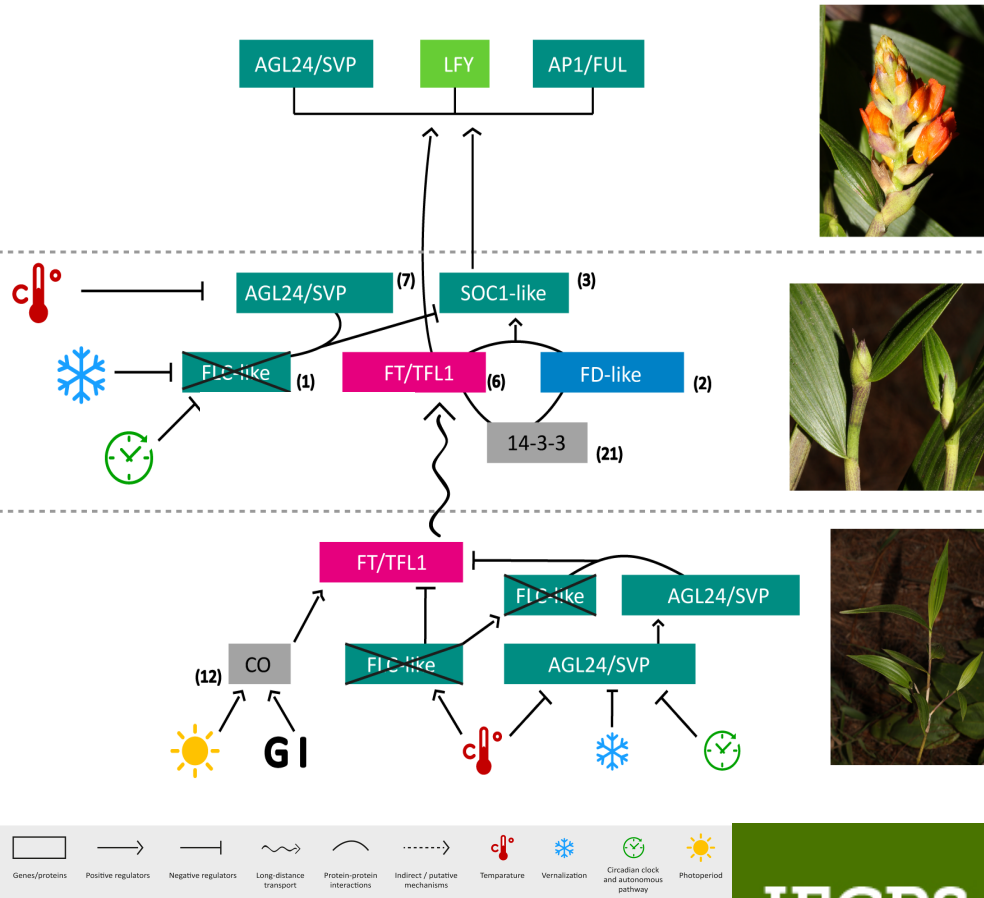


Conclusions

1: GRN in orchids have undergone different evolution pathways in comparison with grass model species, due to independent duplication events



2: GRN has remarkable changes in the increase of gene copy number in orchids with unknown functions



Acknowledgments



CODI Regionalización 2017
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COLCIENCIAS

Convocatoria 808



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Student Research Award**



Dr. Natalia Pabon-Mora



Diego Ospina-Zapata



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¿Questions?

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Thank you..

