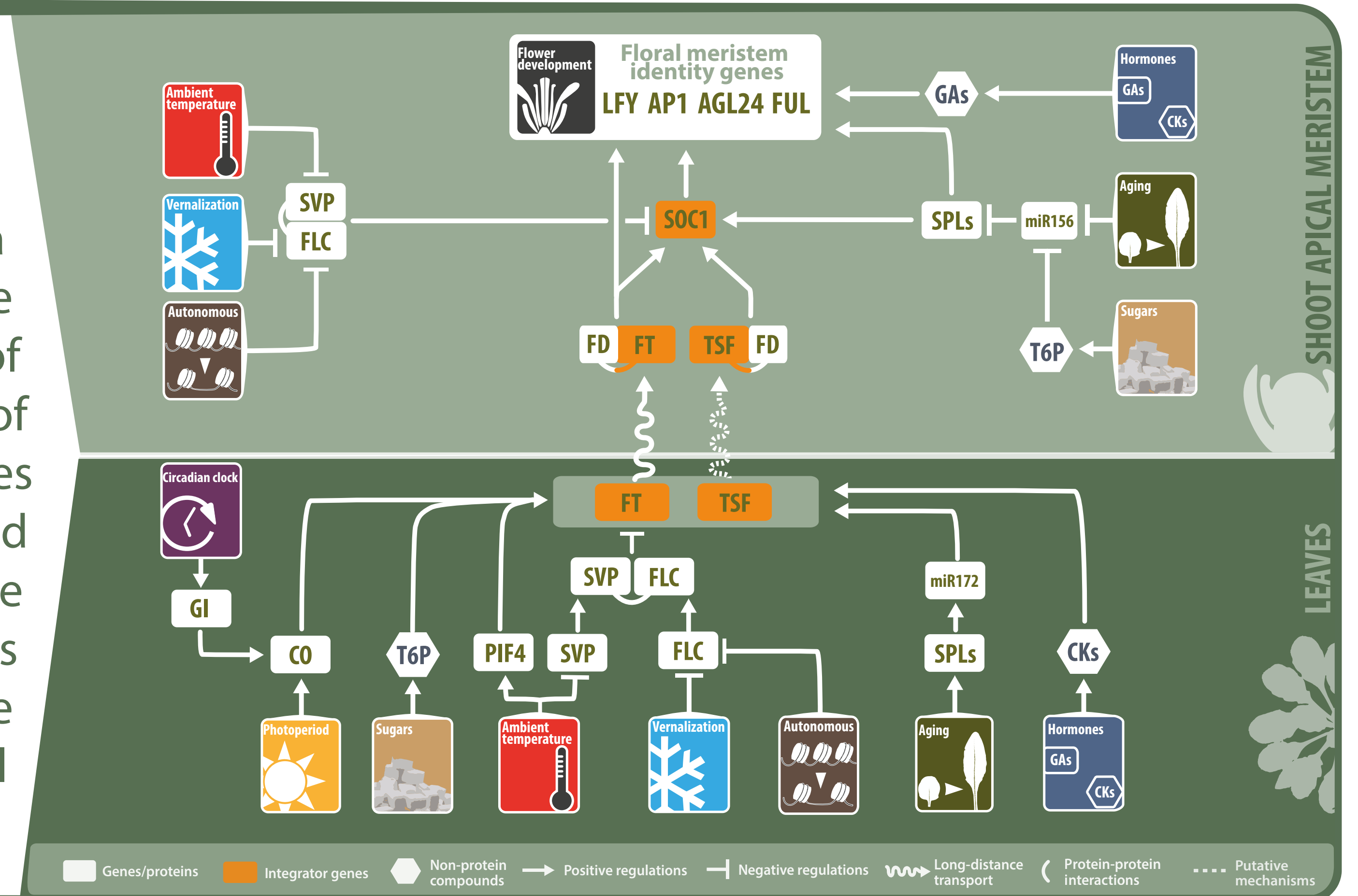# Perspectives for the update of the Flowering Interactive Database [www.FLOR-ID.org]

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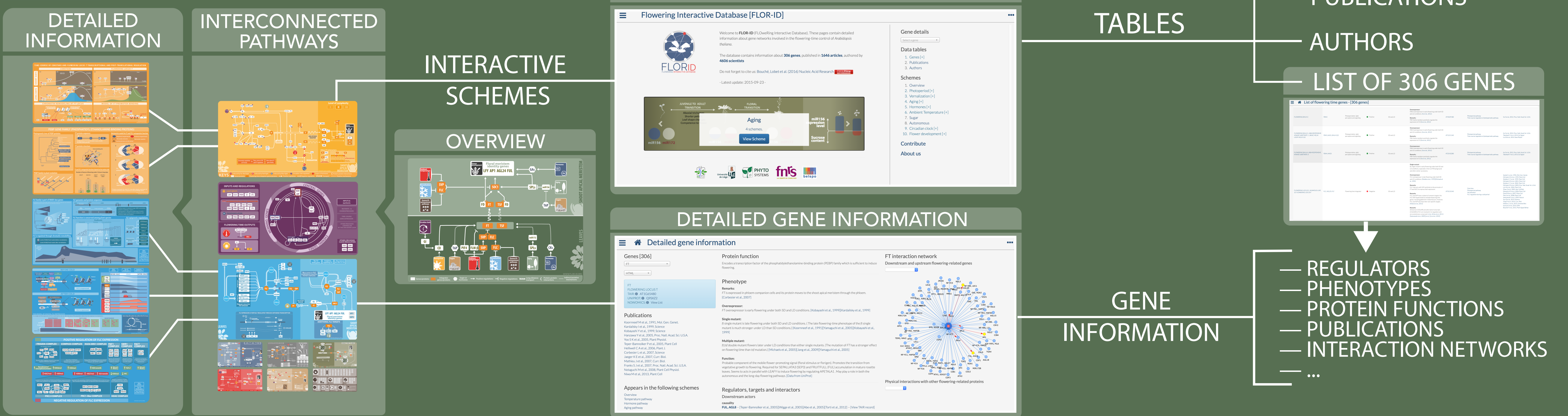
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THE FLOR-ID WEBSITE

The mechanisms controlling the onset of flowering are particularly well documented in *Arabidopsis thaliana*: hundreds of genes involved in interconnected regulatory networks converge toward the regulation of a few "integrator genes" that ultimately initiate the transition to reproductive development. In 2016, we published a hand-curated interactive database of flowering-time genes (www.flor-id.org) that summarizes the knowledge of >1500 articles on this topic. The website includes a set of interactive schemes relying on a list of 306 flowering genes, each of which has a specific detailed webpage describing its function and interactome. Our knowledge of the mechanisms fine-tuning the timing of flowering in Arabidopsis evolves quickly as new articles are published weekly on this topic. Therefore, we think that an update of the FLOR-ID database is timely and would be helpful to the research community.

STRUCTURE OF THE DATABASE

DETAILED INFORMATION — INTERCONNECTED PATHWAYS — INTERACTIVE SCHEMES — OVERVIEW — HOMEPAGE

TABLES
— PUBLICATIONS
— AUTHORS
— LIST OF 306 GENES

DETAILED GENE INFORMATION

GENE INFORMATION
— REGULATORS
— PHENOTYPES
— PROTEIN FUNCTIONS
— PUBLICATIONS
— INTERACTION NETWORKS
— ...

PERSPECTIVES FOR THE UPDATE

LITERATURE

The FLOR-ID database was released in January 2016. Since then, more than 400 hundred articles related to the control of flowering in Arabidopsis were published. The first step of the update will be to **implement this new knowledge in the FLOR-ID database**, including new flowering genes, new interactions, phenotypes, etc. We will also **update the interactive schemes** and associate the database with **versioning numbers** to facilitate the citation of the list of flowering genes when using it to perform genomic and transcriptomic studies.

ADDITIONAL DATA

We intend to implement **additional data resources** in the FLOR-ID database (*e.g.*, closest orthologs of flowering genes in other model species, additional information relative to the interaction between genes, conserved protein domains, etc.). A «**latest flowering research**» section will list recent publications. We will also improve the way data tables can be downloaded and test the **mapping of RNA-sequencing** data to flowering pathways.

COLLABORATIONS

The regulation of flowering is a very complex topic. Labs' research interests are more and more focused on specific aspects of flowering. **We are thus looking for collaborators** that are specialized in specific flowering pathways and/or flower development to help us curate and validate the FLOR-ID schemes as well as interaction data. We firmly believe that such inputs will **benefit the entire research community**.

USER CONTRIBUTIONS

The FLOR-ID database is widely used in the research community. We think that **user inputs are essential** to keep the database up-to-date. We intend to allow scientists to add **newly published articles**, suggest **novel flowering genes**, add data about their **interaction networks**, and leave **comments** that will be visible and useful to other users. These data will be validated by curators before being added to the online database. Gene interactions will be automatically used to create **interactive maps** of flowering pathways.

ANY IDEA TO FURTHER IMPROVE THE DATABASE? WANT TO CONTRIBUTE? ANY COMMENT? LET US KNOW!

We designed FLOR-ID as a tool for the research community. Your input is thus extremely useful for us to match future developments of FLOR-ID with the expectations of the flowering research community.

CONTRIBUTE HERE!
[Do not hesitate to include your email address if you want to contribute]