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# FLOWER-LAYER

Plan de gestion de données créé à l'aide de DMP OPIDoR

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**Affiliation du créateur principal :** ENS de Lyon

**Modèle du PGD :** INRAE - Trame générique projet

**Dernière modification du PGD :** 28/10/2020

**Financier :** Agence nationale de la recherche (ANR)

**Numéro de subvention :** ANR-19-CE13-0019

## Résumé du projet :

How cells coordinate their growth and division to generate organs with defined shapes is a long-standing question in biology. In plants, organs are formed by clonally-distinct cellular layers that remain independent throughout organ development. In the mean time, organ identity, shape and size are specified by master regulators. The main objective of the project is to understand how a master regulator can trigger organ development in all cellular layers in a coordinated manner, ensuring the robust acquisition of a proper identity, size and shape. We will tackle this question using *Petunia hybrida* flowers, whose petals are organized in a tube ending with colourful limbs. We obtained chimeric flowers in *Petunia hybrida*, originating from the layer-specific excision of a transposon inserted in the *PhDEF* gene, a MADS-box gene controlling petal development. These chimeras revealed that expression of *PhDEF* in the epidermis of the petal directs growth of the limbs, while its expression in the internal layers directs growth of the tube. This suggests that the tube and the limbs constitute two independent developmental modules, whose growth is controlled in a layer-specific fashion. Moreover, we obtained evidence for non-cell-autonomous effects between layers since *PhDEF* expression in the internal layers of the petal restores some petal epidermal features.

The objective of this project is to characterize the layer-specific PhDEF regulatory network in the *Petunia hybrida* petal, in order to understand how PhDEF can direct tube or limb growth independently from specific cellular layers. For this, after a detailed characterization of the chimeric flowers we obtained, we will recreate these chimeras as transgenic plants. This will allow us to identify PhDEF target genes and interactors specifically for each cellular-layer, by a combination of cell sorting, RNA-Seq, CHIP-Seq and co-IP. We will also identify the non-autonomous targets of PhDEF induced in one layer by expression of PhDEF in another layer. Finally we will functionally characterize some key target genes, aiming to understand how they can direct tube or limb growth in a layer-specific fashion. Altogether this project should advance the field of plant developmental biology by addressing how a master regulator directs organ growth and identity in all cellular layers in a coordinated manner.

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**Produits de recherche :**

1. Phenotypic data : Phenotypic data from star and wico flowers ( Jeu de données )
2. Transcriptomic data : Transcriptomic data from star and wico petals at 3 developmental stages ( Jeu de données )
3. Transgenic lines : Transgenic *Petunia hybrida* lines to control cell-layer specific gene expression ( Collection )

**Droits d'auteur**

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## Informations sur le plan de gestion

Question sans réponse.

Laboratoire de Reproduction et Développement des Plantes (RDP)  
ENS de Lyon  
46 allée d'Italie 69364 Lyon Cedex 07

22/10/2020

Question sans réponse.

Question sans réponse.

## Informations sur le projet

AAPG 2019

Agence Nationale de la Recherche (ANR)

ANR Jeune Chercheur/Jeune Chercheuse (JCJC)

ANR-19-CE13-0019

FLOWER-LAYER

Investigating the contribution of cell layers to petal development in Petunia flowers

Centre National de la Recherche Scientifique (CNRS), France

Question sans réponse.

01/04/2020 - 31/03/2024 (42 months)

## Présentation générale des données du projet

### Phenotypic data : Phenotypic data from star and wico flowers

Star and wico flowers, originating from the cell-layer-specific excision of a transposon inserted into the petal identity gene PhDEF, were measured for tube length and limb area. Pictures were taken from the side and from the top (compressing the flower against a glass slide to flatten the limbs) and measurements were done with ImageJ on at least 2 flowers from 4 independent revertant lines.

### Transcriptomic data : Transcriptomic data from star and wico petals at 3 developmental stages

Petals from wild-type, star and wico flowers (1 line) were collected at three developmental stages, and sepals from the phdef mutant were collected at the late stage only. For each stage, the petals from 2 flowers were collected, and 3 biological replicates were performed. Tissue was grinded and RNA was extracted on a fraction of the tissue. The total RNA, after rRNA depletion, was sequenced with Illumina Next Seq 500.

### Transgenic lines : Transgenic Petunia hybrida lines to control cell-layer specific gene expression

Transgenic Petunia hybrida lines were generated as an attempt to express PhDEF in one cell layer of the petal only in an inducible manner. Three constructs were generated and transformed in planta. Plants are now at the third generation after transformation.

## Droits de propriété intellectuelle

Data will remain the property of the RDP laboratory.

Not applicable.

## Confidentialité

Not applicable.

Not applicable.

If necessary, a confidentiality agreement will be established.

## **Partage des données à l'issue du projet**

### **Phenotypic data : Phenotypic data from star and wico flowers**

The ANR encourages open science and open data access.

The phenotypic data will be integrated into a publication.

Question sans réponse.

No

The phenotypic data will be integrated in a publication, first on preprint on BioRxiv, then after acceptance by a journal the publication will be loaded on the open archive HAL depository.

No licence.

As soon as the publication is deposited on BioRxiv.

The publication will always be accessible on BioRxiv or HAL.

No.

Question sans réponse.

### **Transcriptomic data : Transcriptomic data from star and wico petals at 3**

## **developmental stages**

The ANR encourages open science and open data access.

The transcriptomic data will be shared with the scientific community as soon as it has been generated.

Collaborators working on petal development might be interested in looking at deregulation of their genes of interest in our transcriptomic dataset.

No.

Before publication of the transcriptome, it will be shared to collaborators by transferring an excel file with normalized read counts through a secure file transfer system (system for big file transfer from the ENS de Lyon). Just before publication, the transcriptome will be deposited on the Transcriptome Shotgun Assembly (TSA) from NCBI and will be accessible for any user.

No licence.

As soon as the transcriptome data has been generated.

Data will always be accessible through the TSA NCBI database.

Data will have a TSA master record.

Not applicable.

## **Transgenic lines : Transgenic *Petunia hybrida* lines to control cell-layer specific gene expression**

The ANR encourages open science and open data access.

Seeds from validated transgenic lines will be sent to collaborators upon request, only after publication of the data generated with them. A MTA will specify the obligation of the recipient.

Question sans réponse.

Not applicable.

Question sans réponse.

## **Description et organisation des données**

### **Phenotypic data : Phenotypic data from star and wico flowers**

Excel file with phenotypic measurements.

None.

None.

Not applicable.

Date of modification always added to the name of the file. Raw data on the first sheet of the excel file, never modified.

Question sans réponse.

### **Transcriptomic data : Transcriptomic data from star and wico petals at 3 developmental stages**

Raw read counts are normalized with DESeq2. This generates a large txt or csv file with gene identifiers and normalized read counts, which is further used for analysis.

Excel file with description of samples and methodology for tissue collection.

None.

Not applicable.

The raw read counts data are never modified. Normalized read counts have been generated with DESeq2 and transferred into an excel file used for analysis. The name of this excel file contains the date of modification and old versions are stored in the same folder.

Question sans réponse.

### **Transgenic lines : Transgenic Petunia hybrida lines to control cell-layer specific gene expression**

All transgenic lines are registered into a local excel file, then after validation they are registered into our data management software Labcollector, accessible for all members of the laboratory.

The plasmids used to generate the transgenic lines are registered into Labcollector. Each transgenic plant will get a unique identifier and details about the ascendancy are registered into an excel file stored on our local server Biodata. This file is regularly saved.

None.

Not applicable.

Question sans réponse.

Question sans réponse.

## **Stockage et sécurité des données**

All data is stored on the servers of the laboratory (Biodata servers from ENS de Lyon) which are saved daily. An automatic daily back-up of the datafolder is made on the server: "<http://sauvegardes.biologie.ens-lyon.fr>" (which is provided by IT support services of the home institution, ENS de Lyon).

The pieces of data to be shared will be occasionally shared with collaborators via the secure large file transfer system for ENS de Lyon. Occasional transfer to USB sticks for personal use on different computers.

Transcriptomic data: around 20 Gb.  
Other pieces of data: negligible.

All data is stored on the servers of the laboratory (Biodata servers from ENS de Lyon) which are saved daily.

The servers of the laboratory are located in the ENS de Lyon.

Yes.

Data will be shared to collaborators upon request.

All data will be shared freely upon request (open science access encouraged by the ANR).

Free access after discussion about the scientific use for the data.

Physical laboratory notebooks register the generation of biological data (sample collection for transcriptome, generation of transgenic lines). Informatic protocols, as well as all generated and analyzed data, are regularly updated and stored on local servers, and are accessible to all group members.

## **Archivage et conservation des données après la fin du projet**

All raw data and the final analyses files will be kept for long term. Intermediate analysis files will be trashed.

Phenotypic data will be stored on local servers. Transcriptomic data will be accessible for long term through the NCBI TSA database. Information about transgenic lines will be accessible by Labcollector.

Question sans réponse.

The director of the laboratory will be responsible for the long term data conservation.

Question sans réponse.

The RDP laboratory pays for space on the local servers.