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# TOWARDS MAPPING KEY PROCESSES MODULATED BY T-DNA ORFS FROM RHIZOGENIC AGROBACTERIUM DURING HAIRY ROOT DEVELOPMENT IN ARABIDOPSIS THALIANA

*A Data Management Plan created using DMPonline.be*

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**Template:** FWO DMP (Flemish Standard DMP)

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**Project abstract:**

Rhizogenic agrobacteria cause hairy root disease (HRD) in several important hydroponically grown crops by transferring part of their DNA (T-DNA) into the plant's genome. In my previous research, using a composite plant assay, I analyzed the plant root response upon T-DNA transformation and identified several signaling peptides having a role in hairy root development. I also confirmed that most of the T-DNA encoded proteins contributed, to some extent, to the development of hairy roots. However, there is still a substantial knowledge gap on the molecular function of T-DNA encoded proteins. Building on the findings of my PhD and using novel and complementary approaches, this project aims at gaining a better understanding of the plant molecular pathways affected by the different T-DNA encoded proteins. To identify where and when in *Arabidopsis thaliana* roots the different T-DNA encoded proteins impact HRD we will first assess the spatiotemporal expression profile of the T-DNA genes. Next, using a cell-specific comparative transcriptomics upon inoculation of *Arabidopsis* roots with rhizogenic *Agrobacterium* T-DNA mutants, we will map how the different T-DNA encoded proteins trigger HRD. Finally, we will investigate the biological relevance of signaling peptides during HRD and analyze which T-DNA encoded proteins modulate their expression. In conclusion, we propose a powerful integrated approach combining various technologies and functional validation to map key processes in HRD.

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### **DPIA**

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#### **DPIA**

**Have you performed a DPIA for the personal data processing activities for this project?**

- Not applicable

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## Application DMP

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### Questionnaire

**Describe the datatypes (surveys, sequences, manuscripts, objects ... ) the research will collect and/or generate and /or (re)use. (use up to 700 characters)**

In this project, we will generate physical and digital datatypes including engineered rhizogenic Agrobacterium strains, novel plasmids with cloned genetic fragments, DNA and RNA samples, hairy root lines transcriptome sequencing data, histological cross-sections, microscopy images, etc..

Digital data generated within the project will be stored in standard formats (.xlsx, .docx, .pptx, .txt, .csv, .pdf, .r, .gb, .fasta, .fastq.gz, .seq, .ab1, .jpg, .png, .tiff). The estimated size of the digital datase will be ~5TB

Physical data include seeds, hairy root lines, plasmids, mutant strains of rhizogenic Agrobacterium, processed plant samples (RNA/DNA), histological cross-sections.

The research will reuse sequencing data and bacterial strains from our previous research. No personal data will be collected or used.

**Specify in which way the following provisions are in place in order to preserve the data during and at least 5 years after the end of the research? Motivate your answer. (use up to 700 characters)**

1. Designation of responsible person (If already designated, please fill in his/her name. Barbara De Coninck (Promoter) will be responsible for the preservation of the data at the end of the research
2. Storage capacity/repository
  - During the research, through KU Leuven ICTS service, our laboratory has access to 5TB of storage for digital datatypes. Additionally we also have 2TB of digital storage available through OneDrive. Physical datatypes will be stored at 4C, -20C or -80C for long term storage.
  - After the research, digital datatypes which have been published will be uploaded to public repositories (eg. ENA for sequencing data) and physical datatypes will be stored at 4C, -20C or -80C for long term storage.

**What's the reason why you wish to deviate from the principle of preservation of data and of the minimum preservation term of 5 years? (max. 700 characters)**

Not applicable

**Are there issues concerning research data indicated in the ethics questionnaire of this application form? Which specific security measures do those data require? (use up to 700 characters)**

Not applicable

**Which other issues related to the data management are relevant to mention? (use up to 700 characters)**

Not applicable.

# **TOWARDS MAPPING KEY PROCESSES MODULATED BY T-DNA ORFS FROM RHIZOGENIC AGROBACTERIUM DURING HAIRY ROOT DEVELOPMENT IN ARABIDOPSIS THALIANA**

## **FWO DMP (Flemish Standard DMP)**

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### **1. Research Data Summary**

List and describe all datasets or research materials that you plan to generate/collect or reuse during your research project. For each dataset or data type (observational, experimental etc.), provide a short name & description (sufficient for yourself to know what data it is about), indicate whether the data are newly generated/collected or reused, digital or physical, also indicate the type of the data (the kind of content), its technical format (file extension), and an estimate of the upper limit of the volume of the data.

				Only for digital data	Only for digital data	Only for digital data	Only for physical data
Dataset Name	Description	New or reused	Digital or Physical	Digital Data Type	Digital Data format	Digital data volume (MB/GB/TB)	Physical volume
		<i>Please choose from the following options:</i> <ul style="list-style-type: none"> <li>• Generate new data</li> <li>• Reuse existing data</li> </ul>	<i>Please choose from the following options:</i> <ul style="list-style-type: none"> <li>• Digital</li> <li>• Physical</li> </ul>	<i>Please choose from the following options:</i> <ul style="list-style-type: none"> <li>• Observational</li> <li>• Experimental</li> <li>• Compiled/aggregated data</li> <li>• Simulation data</li> <li>• Software</li> <li>• Other</li> <li>• NA</li> </ul>	<i>Please choose from the following options:</i> <ul style="list-style-type: none"> <li>• .por, .xml, .tab, .csv, .pdf, .txt, .rtf, .dwg, .gml, ...</li> <li>• NA</li> </ul>	<i>Please choose from the following options:</i> <ul style="list-style-type: none"> <li>• &lt;100MB</li> <li>• &lt;1GB</li> <li>• &lt;100GB</li> <li>• &lt;1TB</li> <li>• &lt;5TB</li> <li>• &lt;10TB</li> <li>• &lt;50TB</li> <li>• &gt;50TB</li> <li>• NA</li> </ul>	
Plasmids	Genome engineering plasmids	Generate new data	Physical				60 samples
Agrobacterium strains	Mutant strains	Generate new data	Physical				60 samples
E. coli strains	E. coli strains with plasmids	Generate new data	Physical				60 samples
Cross-sections	Histological root cross-sections	Generate new data	Physical				~100 glass slides
Microscopy	Microscopy of root cross-sections	Generate new data	Digital	Observational	.png, .tiff, .jpg	<100GB	
Processed DNA samples	Genomic DNA from plants and bacteria	Generate new data	Physical				
Processed RNA samples	Total RNA from plants	Generate new data	Physical				50-100 samples
DNA sequencing data	Sanger sequencing/ Illumina Sequencing/ Nanopore Sequencing	Generate new data	Digital	Experimental	.gb, .ab1, .fasta	<1GB	
RNA sequencing data	Illumina sequencing	Generate new data	Digital	Experimental	..fastq, .fasta, .gff, .gtf, .bam	<5TB	
Hairy root lines	Propagated lians from hairy roots	Generate new data	Physical				~ 60 lines

If you reuse existing data, please specify the source, preferably by using a persistent identifier (e.g. DOI, Handle, URL etc.) per dataset or data type:

Not applicable

Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? Describe these issues in the comment section. Please refer to specific datasets or data types when appropriate.

- No

Will you process personal data? If so, briefly describe the kind of personal data you will use in the comment section. Please refer to specific datasets or data types when appropriate.

- No

Does your work have potential for commercial valorization (e.g. tech transfer, for example spin-offs, commercial exploitation, ...)? If so, please comment per dataset or data type where appropriate.

- Yes

Mutant rhizogenic Agrobacterium strains for Ri lines of plants

Do existing 3rd party agreements restrict exploitation or dissemination of the data you (re)use (e.g. Material/Data transfer agreements/ research collaboration agreements)? If so, please explain in the comment section to what data they relate and what restrictions are in place.

- No

Are there any other legal issues, such as intellectual property rights and ownership, to be managed related to the data you (re)use? If so, please explain in the comment section to what data they relate and which restrictions will be asserted.

- No

## 2. Documentation and Metadata

Clearly describe what approach will be followed to capture the accompanying information necessary to keep data understandable and usable, for yourself and others, now and in the future (e.g., in terms of documentation levels and types required, procedures used, Electronic Lab Notebooks, README.txt files, Codebook.tsv etc. where this information is recorded).

A lab notebook with day-to-day activities including aim, materials and methods used, results and conclusions is recorded daily. Final protocols are added to a digital .docx file shared with the lab.

Additionally information recorded for the different datatypes information is shown below

- Plasmids - .xlsx file detailing relevant characteristics and location
- Agrobacterium strains- .xlsx file detailing relevant characteristics and location
- E. coli strains- .xlsx file detailing relevant characteristics and location
- Cross-sections - .xlsx file detailing relevant characteristics and location
- Microscopy - .xlsx and .pptx files detailing relevant characteristics
- Processed DNA samples - .xlsx file detailing characteristics and location
- Processed RNA samples - .xlsx file detailing characteristics and location
- DNA sequencing data - Digital folders detailing types of samples and relevant data
- RNA sequencing data - Digital folders detailing types of samples
- Hairy root lines - .xlsx file detailing characteristics and location

Will a metadata standard be used to make it easier to find and reuse the data? If so, please specify (where appropriate per dataset or data type) which metadata standard will be used. If not, please specify (where appropriate per dataset or data type) which metadata will be created to make the data easier to find and reuse.

- Yes

A standard metadata will be used in compliance with the FAIR principles. The RDM guide will be used for this.

### 3. Data storage & back-up during the research project

**Where will the data be stored?**

1. Digital data will be stored on the Shared Drive system provided by KU Leuven with a backup on external harddrive and OneDrive
2. Physical data such as cross-sections will be stored at room temperature, seeds will be stored at 4C, DNA samples including plasmids at -20C and RNA and bacterial stocks at -80C

**How will the data be backed up?**

All digital data is also stored on OneDrive and external harddrives.

**Is there currently sufficient storage & backup capacity during the project? If yes, specify concisely.  
If no or insufficient storage or backup capacities are available, then explain how this will be taken care of.**

- Yes

A shared drive with 5TB of space is available for deposition of data. Additionally an external harddrive and OneDrive each with 2TB is available for Backup.

**How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?**

Our shared drive restricts access to different shared folders such that only the researcher can access/edit their own folder while all other members can only view the contents of the shared drive.

**What are the expected costs for data storage and backup during the research project? How will these costs be covered?**

For digital storage on the drive, a price of 105 EUR / TB / Year is estimated. These costs will be covered with funding from FWO/research group.

### 4. Data preservation after the end of the research project

**Which data will be retained for at least five years (or longer, in agreement with other retention policies that are applicable) after the end of the project? In case some data cannot be preserved, clearly state the reasons for this (e.g. legal or contractual restrictions, storage/budget issues, institutional policies...).**

Plasmids, Agrobacterium and E. coli strains and Histological cross-sections will be stored indefinitely.  
Processed RNA/DNA samples will be stored till publication.  
DNA/RNA sequencing results will be stored for five years at least.

**Where will these data be archived (stored and curated for the long-term)?**

Data will be archived on the KU Leuven Archive Drive for long term storage.

**What are the expected costs for data preservation during the expected retention period? How will these costs be covered?**

For digital storage on the drive, a price of 105 EUR / TB / Year is estimated. These costs will be covered with funding from research group.

## 5. Data sharing and reuse

**Will the data (or part of the data) be made available for reuse after/during the project? In the comment section please explain per dataset or data type which data will be made available.**

- Yes, in a restricted access repository (after approval, institutional access only, ...)
- No (closed access)
- Plasmids - After approval
- Agrobacterium strains- After approval
- E. coli strains- After approval
- Cross-sections - After approval
- Microscopy - After approval
- Processed DNA samples - After approval
- Processed RNA samples - After approval
- DNA sequencing data - After approval
- RNA sequencing data - No
- Hairy root lines - After approval

**If access is restricted, please specify who will be able to access the data and under what conditions.**

Access to the restricted datatypes will be provided by Barbara De Coninck (promoter) after approval.

**Are there any factors that restrict or prevent the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)? Please explain in the comment section per dataset or data type where appropriate.**

- Yes, Intellectual Property Rights

Agrobacterium strains- IPR

**Where will the data be made available? If already known, please provide a repository per dataset or data type.**

DNA sequencing data - ENA  
RNA sequencing data - ENA



**When will the data be made available?**

Upon publication of the research results

**Which data usage licenses are you going to provide? If none, please explain why.**

Creative Commons Attribution Noncommercial NoDerivatives 4.0 International

**Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, you have the option to provide it in the comment section.**

- Yes

**What are the expected costs for data sharing? How will these costs be covered?**

None

## **6. Responsibilities**

**Who will manage data documentation and metadata during the research project?**

Savio Rodrigues

**Who will manage data storage and backup during the research project?**

Savio Rodrigues

**Who will manage data preservation and sharing?**

Barbara De Coninck

**Who will update and implement this DMP?**

Savio Rodrigues/ Barbara De Coninck