

DMP title

Project Name FWO-DMP-G0B5322N - DMP title

Project Identifier DMP-G0B5322N

Grant Title G0B5322N

Principal Investigator / Researcher Isabel Beets

Description Animal brains are wired according to genetic programs that evolved over millions of years. Much of our behavior, however, is shaped by experiences during life that reprogram the brain by altering gene expression. Here we aim to deliver a much-needed understanding of how these lasting changes alter brain function. Many genes regulated by experience have been identified. Yet, how they sculpt neural circuits and behavior is poorly understood. To bridge this gap, we will use the mini-brain of *C. elegans* and its homeostatic circuit for gas sensing. We recently discovered that activity-dependent gene expression in this circuit modulates behavioral responses to sensory input. We will use recently developed tools to identify which genes are regulated by different experiences in the gas-sensing neurons. Pilot data suggests these include several genes conserved between *C. elegans* and humans. We will study how these genes contribute to experience-dependent changes in neural activity and behavior, and unravel the cellular pathways regulating their expression. This project will shed light on fundamental mechanisms that underpin experience-dependent gene expression and its role in neural plasticity. Because the molecular pathways and gene targets involved in activity-regulated transcription are evolutionarily ancient and well conserved, from worms to humans, we expect our findings will contribute to insights on how experience reprograms more complex brains.

Institution KU Leuven

1. General Information

Name applicant

Isabel Beets

FWO Project Number & Title

G0B5322N - Decoding experience-dependent transcription in the regulation of neural circuit and behavioral plasticity

Affiliation

- KU Leuven

2. Data description

Will you generate/collect new data and/or make use of existing data?

- Generate new data
- Reuse existing data

Describe in detail the origin, type and format of the data (per dataset) and its (estimated) volume. This may be easiest in a table (see example) or as a data flow and per WP or objective of the project. If you reuse existing data, specify the source of these data. Distinguish data types (the kind of content) from data formats (the technical format).

All objectives will generate:

- processed data files and data representations (up to 500 GB): figures in SVG and AI format; tabular data in MS Excel; statistical analysis in Graphpad, MATLAB, and R Studio
- DNA plasmids (± 100 plasmids): stored at -20°C and as glycerol stock at -80°C , overview kept in MS Excel and SnapGene.
- *C. elegans* mutant and transgenic strains (± 200 strains): stored at -80°C , overview kept in MS Excel.
- microscopy images ($\pm 6\text{TB}$): generated by (confocal) fluorescence microscopy in Ism, oib, stk and tiff format. Image analyses will be done in MATLAB and Image J.
- movies and tracking data of *C. elegans* behaviors ($\pm 12\text{TB}$): generating tabular data (in xls) and video data (in wmf, bmp and avi). Data analysis will be done in MATLAB, Graphpad and R Studio.
- documentation: lab notebooks (hard copy and/or electronic versions exportable as PDF or MS Word files) and protocols (in MS Word and PDF)

In addition, WP2 will generate RNA samples and sequencing data (\pm 1TB; in FASTQ format) for identifying activity-regulated gene candidates by RNA sequencing. Statistical analysis of differential gene expression will be done in DESeq (in txt format).

We will re-use *C. elegans* mutants and DNA plasmids from community stock centers, i.e. *Caenorhabditis* genetics center (<https://cgc.umn.edu/>), National BioResource Project (<https://shigen.nig.ac.jp/c.elegans/faq/index.xhtml>) and AddGene (<https://www.addgene.org/>). These reagents cannot be distributed outside of the recipient's organization, but can be obtained by other researchers directly from the stock centers.

We will also re-use published RNAseq resources of *C. elegans*, e.g. CeNGEN resource (<https://www.cengen.org/>). This data is openly available to the community under a CC-BY-NC-4.0 license.

3. Legal and ethical issues

Will you use personal data? If so, shortly describe the kind of personal data you will use. Add the reference to your file in KU Leuven's Register of Data Processing for Research and Public Service Purposes (PRET application). Be aware that registering the fact that you process personal data is a legal obligation.

- No

Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? If so, add the reference to the formal approval by the relevant ethical review committee(s)

- No

Does your work possibly result in research data with potential for tech transfer and valorisation? Will IP restrictions be claimed for the data you created? If so, for what data and which restrictions will be asserted?

- No

Do existing 3rd party agreements restrict dissemination or exploitation of the data you (re)use? If so, to what data do they relate and what restrictions are in place?

- Yes

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We will also re-use published RNAseq resources of *C. elegans*, e.g. CeNGEN resource (<https://www.cengen.org/>). This data is openly available to the community under a CC-BY-NC-4.0 license.

4. Documentation and metadata

What documentation will be provided to enable reuse of the data collected/generated in this project?

All digital data (raw and analyzed data files) will be stored on Desktop File Storage and Large Volume Storage. Digital files will be organized in folders per WP and experiment, including a txt file with a clear description of what the data represent and how they were generated. Within each folder, each dataset will be identified by key experimental factors including the date of the experiment, unique identifier(s) of samples/reagents used in the experiment, and treatment. Experimental procedures will be fully documented as word files and in hardcover notebooks. RNA-seq reads will be deposited in the NCBI Sequence read archive after publication. Details on samples, including plasmid maps and strain genotypes, will be archived in excel files with an overview of their location in frozen stock collections.

Will a metadata standard be used? If so, describe in detail which standard will be used. If no, state in detail which metadata will be created to make the data

easy/easier to find and reuse.

- Yes

Data produced and/or used in the project will be linked to metadata:

1. Metadata about *C. elegans* strains and DNA/RNA samples will be created and curated manually (in MS Excel) following the community guidelines as published on the Nomenclature section of the community resource (www.wormbase.org).
2. Metadata to microscopy images acquired by confocal microscopy and calcium imaging is embedded automatically within the lsm, oib and tiff multidimensional image formats that these platforms generate. This proprietary microscopy image data and metadata can be read using the Bio-Formats/Open Microscopy Environment (OME) standard, for which plugins for most commonly used image analysis software packages exists, including ImageJ/Fiji and MATLAB.
3. For the video recording of *C. elegans* locomotion parameters, the camera's acquisition settings will be specified either in an XML file using StreamPix (Norpix Inc) or within the DC20.ini configuration settings file for the DinoCapture 2.0 (Dino-Lite, Dunwell Tech, Inc) acquisition software. Both metadata files can be read by standard text editors such as MS Notepad.
4. For RNA sequencing reads, the metadata guidelines from the NCBI Sequence Read archive will be followed.
5. Digital data are organized in folders per research objective and experiment, including a 'readme' text file with a clear description of how, when and by whom the data was generated. Metadata records will be kept for each experimental folder in text/MS Word format, documenting following specifications: date, time, unique identifier and version of the protocol used to generate the data, deviations from the protocol, unique identifier(s) of physical reagents, and treatment(s). In addition, individual file headers will refer to the key experimental factors (e.g. reagent and treatment).
6. For published manuscripts, a folder containing all relevant data files is generated upon acceptance of the publication, which serves archiving purposes.

5. Data storage and backup during the FWO project

Where will the data be stored?

All digital data will be stored centrally on storage facilities of the university via KU Leuven Large-Volume Network Storage, and on university-based and external cloud services (e.g. KU Leuven OneDrive for Business, Dropbox).

Physical samples will be stored centrally in storage facilities of the research group.

Hardcover and electronic notebooks will be kept personally by all researchers involved during the project, and by the PI after the end of their affiliation with KU Leuven.

How is backup of the data provided?

We will use the central server storage of KU Leuven, hosted in the KU Leuven ICTS data center, which provides incremental backups on at least a daily basis. All data is mirrored to a second ICTS data center.

Physical samples are stored at least in duplicate at two different storage facilities (freezers) in the research group, equipped with emergency power.

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

Network storages for digital data hosted by the KU Leuven ICTS data center can provide sufficient storage and back-up capacity (fee-based).

What are the expected costs for data storage and back up during the project? How will these costs be covered?

Digital data will be preserved on (fee-based) university network storages for at least 10 years, in accordance with KU Leuven RDM policy. Cloud-based storages offered by the university are free in use and provide a storage capacity up to 2.5 TB per staff member. As this storage capacity will not suffice for video and imaging datasets, KU Leuven Large Volume Network storage services

will be used to store large-volume datasets, which costs 565 EUR per 5 TB per year. We expect no major changes in pricing of data storage and back-up during the project. Thanks to a mix of accessible and large volume (less accessible) data storage, the total estimated cost would be 1000-2000 EUR per year, and these costs will be covered by the project's budget as well as other research grants (after the end of the project in particular).

Data security: how will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?

We will not be working with personal, confidential or sensitive data but will ensure data security by storing data at secured KU Leuven Network storages and buildings.

6. Data preservation after the FWO project

Which data will be retained for the expected 5 year period after the end of the project? In case only a selection of the data can/will be preserved, clearly state the reasons for this (legal or contractual restrictions, physical preservation issues, ...).

All data, including digital files and samples, will be stored at least 5 years after the end of the project.

All published data, including digital files and samples, will continue to be stored for at least ten years, conform the KU Leuven RDM policy. Old (>10 years) unpublished data will be triaged yearly by researchers in agreement with the PI, to avoid excessive costs for unnecessary data storage.

Where will the data be archived (= stored for the longer term)?

Digital data will be archived on Large Volume Storage hosted in the KU Leuven ICTS data center with automatic back-up procedures. Physical samples will be kept for long-term storage in facilities (-80 freezer or liquid nitrogen) at the research unit.

What are the expected costs for data preservation during the retention period of 5 years? How will the costs be covered?

Expected costs for data storage and back-up after the project are estimated at 1000 EUR yearly, which will be covered by research grant budgets.

7. Data sharing and reuse

Are there any factors restricting or preventing the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)?

- No

Which data will be made available after the end of the project?

Digital data and samples resulting from this project will be made available after publication of results.

Where/how will the data be made available for reuse?

- In an Open Access repository
- In a restricted access repository
- Upon request by mail

Publications resulting from this project will be archived in the KU Leuven Lirias 2.0 repository. RNA-seq reads will be deposited in the NCBI Sequence read archive after publication. Samples can be requested from the principal investigator by mail.

When will the data be made available?

- Upon publication of the research results

Who will be able to access the data and under what conditions?

Data will be available to anyone after publication of the research results.

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

Expected costs for data sharing encompass publication fees, which will be covered by the allocated FWO budget.

8. Responsibilities

Who will be responsible for data documentation & metadata?

The principal investigator and all research staff involved in the project will be responsible for data documentation.

Who will be responsible for data storage & back up during the project?

The principal investigator and all research staff involved in the project will be responsible for data storage and back-up.

Who will be responsible for ensuring data preservation and reuse ?

The principal investigator and all research staff involved in the project will be responsible for ensuring data preservation and reuse.

Who bears the end responsibility for updating & implementing this DMP?

The PI bears the end responsibility of updating & implementing this DMP.