DMP title

Project Name Identification and characterisation of lncRNAs regulating TAM phenotypic state. - DMP title

Project Identifier 1SC5122N

Principal Investigator / Researcher Yvessa Verheyden

Description Tumour-associated macrophages (TAMs) are a major component of the tumour microenvironment and can be classified according to their major histocompatibility complex class II (MHC-II) expression in MHC-II low and MHC-II high macrophages, having opposite effects on tumour growth. Since MHC-II low TAMs highly express proangiogenic factors and immune suppressive molecules which promote tumour progression and therapy resistance, specific targeting of MHC-II low TAMs or repolarization to MHC-II high TAMs are promising strategies to improve the response to cancer therapies and prevent relapse and therapy resistance. LncRNAs are transcripts longer than 200 nucleotides lacking coding potential. They have been implicated in many developmental pathways and because of their high tissue- and cell-specificity they are considered as excellent biomarkers and potential therapeutic targets. Recent studies have shown that several lncRNAs have a role in regulating cancer immunity. However, their role in tumour-associated macrophages remains unclear. The aim of my PhD project will be to identify and study lncRNAs regulating the phenotype of TAMs. The results of my study may bring to the identification of novel therapeutic opportunities.

Institution KU Leuven

1. General Information

Name applicant

Yvessa Verheyden

FWO Project Number & Title

1SC5122N - Identification and characterisation of lncRNAs regulating TAM phenotypic state.

Affiliation

- KU Leuven

2. Data description

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

- Generate new 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).

Type of data	Format	How created/source
Raw bulk RNA sequencing data	FASTQ	Next generation sequencing
Analyzed bulk RNA sequencing data	csv	Analyzed data of NGS generated in R
Analyzed single cell RNA sequencing data	xls	Analyzed data of single cell RNA sequencing data generated in R
Code of analysis single cell RNA sequencing data	R script	Written code of analysis single cell RNA sequencing
Cell lines	physical	
Protocols	docx	Protocol documented in docx file
qPCR results	xls	Quantstudio qPCR data exported as xls + figures generated in Prism
CRISPR/Cas guide sequences	xls	CRISPR/Cas guide sequences designed with online tools
Plasmids	physical	
Pictures fluorescent microscopy	tiff	Pictures taken with fluorescent microscope
FISH probe sequences	xls	FISH probe sequences generated with online tool
siRNA and/or ASO sequences	xls	siRNA and/or ASO sequences designed with online tools
Western blot images	tiff	Pictures taken from Western Blot + figures generated in Prism of quantification
ELISA results	xls	ELISA results generated by photospectrometer
Incucyte images	tiff	Pictures taken with Incucyte software + figures generated in Prism of quantification
Phagocytic capacity results	xls	Phocytic capacity results generated by photospectrometer
Metabolic assay results	xls	Results generated by Seahorse XF-analyser
Incucyte images	tiff	Pictures taken with Incucyte software + figures generated in Prism of quantification
Matrigel invasion assay/wound healing assay images	tiff	Pictures taken with Incucyte software + figures generated in Prism of quantification
Chorioallantoic membrane (CAM) assay images	tiff	Pictures taken with camera
Mass Spectometry	xls	Mass spectometry data generated by a mass spectrometer
FACS results	fcs	Results generated by FACS machine + analyzed data and figures in Prism
Measurements of toxicity: body weight, signs of distress, ALT levels,...	xls	Measurements collected in xls file
Measurements of therapeutic efficacy: tumour size, tumour weight	xls	Measurements collected in xls file

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

Privacy Registry Reference:
Short description of the kind of personal data that will be used:

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)

- Yes

In the second work package of the project, different mice models will be used. At the appropriate time, an ethical approval will be requested.

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?

- No

4. Documentation and metadata

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

Data will initially be collected in a variety of file formats and equipment specific software. These files will also be stored as standard/open formats. Digital images will be saved as TIFF files.

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

For microscopy images we use OME-XML or an equivalent alternative. For western blot images metadata is manually recorded in the laboratory notebook. Most machines record and store metadata in equipment specific file formats that we export as xls. For flow cytometry the Flow Cytometry Standard (FCS) will be used.

5. Data storage and backup during the FWO project

Where will the data be stored?

The raw data and the results of the downstream analysis will be stored in our laboratory drive on the KU Leuven server (1000GB) with automatic daily back-up procedures. Copies of the results will also be stored on the laboratory computers. Additionally, I will keep a laboratory notebook with details and dates on procedures. RNA and proteins will be stored at -80°C, gDNA at 4°C (short term) or at -20°C (long term). In addition, the lab uses routinely basecamp to exchange relevant results, updates on existing procedure and/or new protocols.

How is backup of the data provided?

All raw and processed data will be stored on the university's central servers with automatic daily back-up procedures. Copies of the results will also be stored on the laboratory computers and in personal lab books. In addition, the lab uses routinely basecamp to exchange relevant results, updates on existing procedure and/or new protocols.

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

Our lab drive is currently 1000GB of which 768.05 GiB is used. In case of need of additional space this will be purchased.

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

€51,9/100GB/year that will be covered by personal grants of the PI.

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

The data will be stored at the university's secure environment for private data.

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 raw and processed data will be stored for at least 5 years after the publication of the papers unless any of the samples (e.g. DNA and RNA preparations) will be exhausted.

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

The data will be stored on the university's central servers (with automatic back-up procedures) for at least 5 years, conform the KU Leuven RDM policy. Upon closure of the project (or intermediately if required), all data will be transferred to the archive on the K-drive for long term storage. Data placed on the K-drive is more strictly secured with only very specific members of the lab having the authority to place data on the K-drive and only the head of lab has the authority to have data removed by the IT department.

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

€51,9/100GB/year that will be covered by personal grants of the PI.

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?

All omics data and code & scripts will be made publicly available. Other data can be made available upon request through MTA exchange or collaboration agreement.

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

- In an Open Access repository

Sequencing data data sets will be made available on the NCBI Gene Expression Omnibus (GEO) or the EBI, ArrayExpress databases.

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?

The full dataset of sequencing experiment and the codes & scripts used for their analysis will be uploaded in their respective databases as an open access dataset under a CC-BY license. Therefore, it will be available to anyone for any purpose, provided that they give appropriate credit to the creators. All other data can be made available upon request by mail after signing an MTA. Access will be granted upon written request to the creators of the dataset. Commercial reuse is not allowed.

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

No costs

8. Responsibilities

Who will be responsible for data documentation & metadata?

The PhD student working on the project, Yvessa Verheyden.

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

The PhD is responsible of data storage, while KU Leuven IT department will be responsible for backing them up.

The PI is responsible for both.

Who will be responsible for ensuring data preservation and reuse ?

The PI

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

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