Plan Overview

A Data Management Plan created using DMPonline

Title: Engineering evolutionary trajectories in Bdellovibrio to develop sustainable crop protection

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Funder: Biotechnology and Biological Sciences Research Council (BBSRC)

Template: University of Manchester Generic Template

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Project abstract:

Bacterial plant diseases cause major yield losses in globally important crops, yet current control relies heavily on antibiotics and pesticides that damage ecosystems and contribute to resistance. There is an urgent need for sustainable alternatives that remain effective as pathogens evolve. *Bdellovibrio bacteriovorus* (Bd) is a naturally occurring predatory bacterium that attacks a wide range of Gram-negative species. Its distinct mode of action—surface recognition, invasion and lysis—offers a route to suppress plant pathogens without relying on agrochemicals. Unlike conventional treatments, Bd can itself adapt as prey evolve, raising the prospect of deliberately shaping its evolutionary trajectory to develop more robust biocontrol strains.

This project will investigate whether this approach can deliver a sustainable, evolution-resilient method for controlling bacterial diseases in crops. Specifically, we will investigate Bd as a nature-based solution for controlling bacterial speck of tomatoes, which can reduce tomato yield by 20–75%. In preliminary work, we have demonstrated the feasibility of this approach. Bd improves tomato seedling health during infection with *Pseudomonas syringae* pv. tomato (Pst), the agent of bacterial speck, without harming uninfected plants. A pilot coevolution assay further shows that Bd and Pst undergo rapid reciprocal genetic change, with prey mutations affecting surface and biofilm traits and predator mutations in sensory and regulatory pathways. These findings indicate that Bd can counter prey escape strategies and could be engineered by evolution to enhance performance.

The project has three main objectives. In **Objective 1**, we will run controlled evolution experiments between predator and prey in the laboratory. These experiments will track how both species change over hundreds of generations, identifying genetic and behavioural changes that help the predator kill more effectively, or help the pathogen avoid predation. This will provide Bdellovibrio strains engineered by evolution to be better predators against

plant pathogens.

In **Objective 2**, we will assess predator performance in the context of the natural microbial community associated with growing tomato seedlings. This will determine whether evolutionary changes influence infection, disease severity, plant growth and the composition of plant-associated microbial communities. This will show whether training the predator improves disease control in realistic plant environments and whether pathogen resistance carries any cost to the plant.

In **Objective 3**, we will carry out greenhouse trials to assess Bd performance under greenhouse conditions, mimicking tomato crop production. These trials will determine how long the predator survives on plants and in soil, how it interacts with beneficial microbes, and which application methods (for example, soil drench or leaf spray) are most effective. Both natural and trained predators will be assessed to understand their potential use in agriculture. These trials will provide the first quantitative evaluation of Bd-based pathogen control.

By integrating evolution experiments, molecular analysis and realistic plant trials, this project will determine whether Bd can be developed as a sustainable biocontrol agent and whether evolutionary training offers a practical route to maintain efficacy as pathogens adapt. The proposed work aligns closely with BBSRC priorities in sustainable agriculture, resilient production systems and frontier bioscience to address food and environmental security. The outcomes will inform deployment strategies, guide engagement with growers and establish a foundation for evolution-guided biocontrol technologies.

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Copyright information:

Engineering evolutionary trajectories in Bdellovibrio to develop sustainable crop protection

Manchester Data Management Outline

1. Will this project be reviewed by any of the following bodies (please select all that apply)?

- Funder

2. Is The University of Manchester collaborating with other institutions on this project?

- No - only institution involved

3. What data will you use in this project (please select all that apply)?

- Acquire new data

Antibiotic resistance phenotypes (CSV) and bacterial growth curves (CSV), genomic data of bacteria (FASTQ and derivative analysis files), flow cytometry data (FCS3)

4. Where will the data be stored and backed-up during the project lifetime?

- University of Manchester Research Data Storage Service (Isilon)

5. If you will be using Research Data Storage, how much storage will you require?

- 1 - 8 TB

Genomic data and flow cytometry data are large files, justifying the need for more than 1 TB of space.

6. Are you going to be working with a 3rd party data provider?

- No

N/A

7. How long do you intend to keep your data for after the end of your project (in years)?

- 5 - 10 years

Questions about personal information

Personal information, also known as personal data, relates to identifiable living individuals. Special category personal data is more sensitive information such as medical records, ethnic background, religious beliefs, political opinions, sexual orientation and criminal convictions or offences information. If you are not using personal data then you can skip the rest of this section.

Please note that in line with data protection law (the General Data Protection Regulation and Data Protection Act 2018), personal information should only be stored in an identifiable form for as long as is necessary for the project; it should be pseudonymised (partially de-identified) and/or anonymised (completely de—identified) as soon as practically possible. You must obtain the appropriate ethical approval in order to use identifiable personal data.

8. What type of personal information will you be processing (please select all that apply)?

- No sensitive or personal data

9. Please briefly outline how you plan to store, protect and ensure confidentiality of the participants' information.

No participant data, including any confidential data, will be collected

10. If you are storing personal information (including contact details) will you need to keep it beyond the end of the project?

- Not applicable

11. Will the participants' information (personal and/or sensitive) be shared with or accessed by anyone outside of the University of Manchester?

- Not applicable

12. If you will be sharing personal information outside of the University of Manchester will the individual or organisation you are sharing with be outside the EEA?

- Not applicable

13. Are you planning to use the personal information for future purposes such as research?

- No

14. Who will act as the data custodian for this study, and so be responsible for the information involved?

Danna Gifford

15. Please provide the date on which this plan was last reviewed (dd/mm/yyyy).

2026-01-07

Project details

What is the purpose of your research project?

The purpose of this project is to determine whether predatory bacteria can be improved and stabilised as biocontrol agents by explicitly incorporating evolutionary processes into their design and evaluation. By studying co-evolution between *Bdellovibrio bacteriovorus* and plant-pathogenic bacteria across laboratory, plant and greenhouse systems, the project will identify the traits, constraints and ecological consequences that determine whether evolutionary engineering can deliver durable, biologically based crop protection.

What policies and guidelines on data management, data sharing, and data security are relevant to your research project?

Data management plan- BBSRC

All applications seeking research grant funding from BBSRC must submit a data management plan. This should include concise plans for data management and sharing as part of the research grant proposal, or provide reasons why data sharing is not possible or appropriate.

The plan will be included in applications as a separate mandatory attachment.

The page limit for the plan is maximum one side of A4.

You must use this document to cover the plans for data management and sharing. Use of this space allocation for any other purpose will result in withdrawal of the application. BBSRC reserves the right to withdraw proposals that do not adhere to these guidelines.

What to include

BBSRC recognises that plans for sharing data will vary according to the type of data collected. Data sharing should be driven by scientific benefit and should also be cost effective. Data should be shared using established standards and existing resources where this is possible.

You may wish to include details of:

- data areas and data types – the volume, type and content of data that will be generated, for example experimental measurements, models, records and images
- standards and metadata – the standards and methodologies that will be adopted for data collection and management and why these have been selected
- relationship to other data available in public repositories
- secondary use – further intended or foreseeable research uses for the completed datasets
- methods for data sharing – planned mechanisms for making these data available, for example through deposition in existing public databases or on request, including access mechanisms
- proprietary data – any restrictions on data sharing due to the need to protect proprietary or patentable data
- timeframes – timescales for public release of data
- format of the final dataset.

See our data sharing policy for full guidance.

Assessment of the data management plan

An application's data management plan will be assessed by reviewers and BBSRC standard research grant Research Committees or assessment Panels. Standard (sometimes known as 'responsive') grants are open to a wide range of research and approaches within BBSRC's remit.

The plan will be considered separately from the scientific excellence of the proposed research; however, an application's credibility will suffer if peer review agrees the statement is inappropriate. In the case where a highly-rated proposal has an inappropriate data management plan, research committees and panels may choose to offer conditional awards or provide specific feedback to the applicants. Appropriate plans are expected to be those where the proposed data sharing activities are in-line with current best practice in the field and both the scientific and cost benefits are

Responsibilities and Resources

Who will be responsible for data management?

The project lead, Dr Danna Gifford.

What resources will you require to deliver your plan?

Backup storage provided by The University of Manchester Research IT (Isilon) and publicly accessible databases (European Nucleotide Archive, Figshare).

Data Collection

What data will you collect or create?

Type of study

The studies encompass laboratory experimental evolution with *Bdellovibrio bacteriovorus* (Bd) and *Pseudomonas syringae* pv. tomato (Pst) bacteria. This will involve allowing bacterial populations to evolve and measuring associated changes in predator/prey co-evolution dynamics, predation efficiency (for Bd), predation resistance (for Pst), general growth phenotypes and genomes (for both species).

Types of data

a) Quantitative data on bacterial growth and population characteristics from laboratory experiments. This will include the genomic mutations in bacteria within isolates, bacterial phenotyping (e.g. growth rate produced by spectrophotometer, predator lysis).

b) Qualitative data on new resistance mutations arising during laboratory experiments. This will include genomic sequencing data produced by Illumina short read sequencing.

Format and scale of the data

Raw data will be stored in open formats (e.g. text-based CSV, R data objects, FASTQ). Data initially output into proprietary formats will be immediately exported to open formats. Open-source analysis tools will be used for downstream analysis of data to ensure reproducibility (e.g. R, breseq). New software generated will be stored in open-source repositories (e.g. GitHub). The use of open formats will facilitate data sharing and long-term data accessibility.

How will the data be collected or created?

Methodologies for data collection / generation

Standards for data collection will be set at the beginning of the project, but will be continually reviewed to ensure that best practices are being followed. This will include e.g. how often data points are collected, the criteria for inclusion in the study, and how negative and positive controls will be included to detect potential mistakes in experimental work. A schema for associating laboratory notebooks with collected data will be made to ensure that the correct metadata is associated with raw data.

Data quality and standards

To ensure data quality, data will be collected by skilled researchers with the appropriate training to use relevant research equipment. The equipment used has checks to ensure data integrity at the point of collection. Data quality will further be maximised through the use of appropriate statistical experimental design to minimise the possibility of spurious results arising due to stochastic noise. At the point of collection, data will be collected by skilled researchers trained alongside metadata on the machine used for collecting data. Data checksums will be used to ensure that files copied from local RDM provisions to public repositories are done so faithfully.

Documentation and Metadata

What documentation and metadata will accompany the data?

Metadata standards and data documentation

Metadata includes documentation of methods and procedures used to conduct experiments and collect samples. This metadata will be stored with the data, and also available in all resulting

publications. This will be stored alongside the databases, which are flexible and allow free-form text documents to be stored alongside data formats e.g. CSV.

Ethics and Legal Compliance

How will you manage any ethical issues?

We do not anticipate any ethical issues arising from the data. Any ethical issues will be managed through referral to departmental or institutional ethics committees.

How will you manage copyright and Intellectual Property Rights (IPR) issues?

Data and publications will be released under Creative Commons Licence 4.0 (CC-BY). External users will be bound by this licence, which is designed to facilitate reuse without restrictions, as long as the original contributor is acknowledged.

Storage and backup

How will the data be stored and backed up?

Data will be stored to meet the standards of UK GDPR. In the short and medium term (i.e. before publication), data will be stored using The University of Manchester's dedicated Research Data Storage (RDS) facility, which offers 8 TB of backed-up data free at the point of use to research groups. On publication, bacterial phenotyping data will be stored alongside publications in open access databases (e.g. Dryad or Mendeley Data), although there is no community agreed/formal data standard. Bacterial genomic data will be stored in the European Nucleotide Archive (ENA, http://ebi.ac.uk), which allows storage of project metadata. The ENA is one of the community agreed databases for genomic sequence data.

How will you manage access and security?

The project lead (Dr Danna Gifford) on the project will make the decision to supply data. In principle data will be freely accessible without a need for a formal request. Data will be stored in publicly accessible repositories and databases.

The main risk to confidentiality is through unauthorised access to raw data, which can occur if data is stored on a device accessible to the general public. This risk will be mitigated by encrypting the hard drives of laptop computers, preventing access to data without a username and password. Further, the use of VPN via Global Connect will be used to access data on RDM servers. Both of these procedures are part of The University of Manchester's standard IT policy.

Selection and Preservation

Which data should be retained, shared, and/or preserved?

Upon publication, raw data will be made available in a public repository (e.g. Dryad or GitHub) as appropriate. Useful unpublished data will be made available in a public repository on conclusion of the project.

What is the long-term preservation plan for the dataset?

Data will be maintained in an established repository (European Nucleotide Archive for genomic data, Dryad for other types of data, GitHub for software pipelines).

Data Sharing

How will you share the data?

Before publication of an associated manuscript, data will be made available upon request to the project lead. When publication of an associated manuscript/preprint has occurred, data will be made available in a public repository with a doi made available in the publication.

Are any restrictions on data sharing required?

There are no anticipated restrictions on sharing data generated.