
Investigating the soil microbiome to understand soil health and soil ecosystem services

A Data Management Plan created using DMP Assistant

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Project abstract:

Understanding the soil microbiome is essential to the stewardship of ecosystem services provided by soils, such as soil fertility (for food, fibre and fuel production), water quality, resistance to erosion and climate mitigation through reduced feedbacks to climate change. Microbial communities play a central role in virtually every biogeochemical cycle on earth. While soil microbial diversity and activity can be characterized using molecular tools, quantitative linkages to ecosystem function are often difficult. We need a better understanding of microbial activity and ultimately, biogeochemical cycling, in order to predict soil ecosystem responses to changes in climate, vegetation or land management. An array of scientific approaches, including short-term field studies and long-term field experiments will be used to investigate microbial drivers of soil ecosystem services and soil health. Over the next two years, metagenomics and metatranscriptomics (i.e., high throughput sequencing approaches applied to environmental samples) will be used to provide comprehensive and quantitative descriptions of the taxonomic and functional diversity using the total pool of nucleic acids and identify couplings between environmental conditions and the microbial community composition and function. The research will: (1) Assess the impact of sustainable and resilient agricultural practices on the functional diversity of microbes in the plant-soil interface; (2) Estimate tradeoffs of diversified cropping systems by comparing in situ measurements of microbial activity to greenhouse gas emissions under field conditions. . This research will contribute to our understanding of the ecosystem tradeoffs required to maximize productivity in agroecosystems in order to meet the demands of a global population while minimizing impacts on soil, air, and water quality, recognizing that we are also experiencing unseen climate variability and environmental change.

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Data collection

What types of data will you collect, create, link to, acquire and/or record as part of this project?

Primary data collected will be dna sequences aquired from MiSeq analysis of soil metagenomic DNA.

Data collected will be approximately 15 GB.

Sensitivity of the data is non sensitive

Low risk

Preservation

Where will you deposit your data for long-term preservation and access at the end of your research project?

Processed data from this project will be deposited into the Agri-environmental Research Data Repository (<https://dataverse.scholarsportal.info/dataverse/ugardr>) along with relevant supplemental files through a facilitated deposit process managed by the University of Guelph Library. This (Dataverse) system, hosted in Canada on University of Toronto servers, is maintained and backed up by Scholars Portal according to high quality systems standards as part of a larger network of Canadian repositories. Each project is assigned a unique DOI (digital object identifier) which can be used in reporting, sharing, publishing and journal submissions to provide a permanent link to the location of the data. The PI will determine the level of access available to users and the conditions under which the data can be used by third parties

Indicate how you will ensure your data is preservation ready. Consider preservation-friendly file formats, ensuring file integrity, anonymization and de-identification, inclusion of supporting documentation.

Question not answered.

Restrictions

Are you aware of any current or future restrictions on the data used in and/or generated during this project?

No known restrictions

Sharing and Reuse

Will you make data from this project available for sharing?

The following data: metadata, qpcr results, accession numbers for sequence reads will be shared through the Agri-environmental Research Data Repository upon publication of our research findings. Wherever possible, the data and the publication will be cross-referenced using stable links.

Unprocessed sequence reads of from microbial genes obtained in this study will be deposited in NCBI's Sequence Read Archive (SRA) as FASTQ files, and accession numbers will be recorded.

If so, what data will you be sharing and in what form? (e.g. raw, processed, analyzed, final)

Unprocessed raw data

Analysed data on data repository.