DMP du projet "Soil biodiversity and suppressiveness of soil against plant diseases and insect pests"

Plan de gestion de données créé à l'aide de DMP OPIDoR, basé sur le modèle "Science Europe - DMP template (english)" fourni par Science Europe.

Plan Details

Plan title

DMP du projet "Soil biodiversity and suppressiveness of soil against plant diseases and insect pests"

Deliverable

Version

Final version

Plan purpose/scope

In WP1, soils of contrasting suppressiveness capacity were compared, with the objective to determine (i) whether soils identified as suppressive dozens of years ago were still suppressive, (ii) the influence of geographic location and soil type on suppressiveness, (iii) the effect of soil management on suppressiveness properties, and (iv) whether new suppressive soils could be identified by screening, i.e. following standard pathology plant tests under greenhouse conditions.

In Task 1.1, we compared soil composition in relation to suppressiveness, by considering standard soil analysis data [Lyon, Lausanne, Braunschweig] as well as soil organic matter quality, which was characterized by a GC-MS profiling method on soils from different countries, i.e. Switzerland, France, Serbia [Lyon].

In Task 1.2, we assessed plant protection from disease and plant metabolomics, under growth chamber conditions, with half of the pots inoculated with a pathogen [Lyon, Lausanne, Braunschweig]. This was done with soils from Switzerland, France, Serbia and Germany. Pathosystems included tobacco and the black root rot pathogen *Thielaviopsis basicola*, as well as wheat and the pathogens *Fusarium graminearum* (for soils not previously characterized with an established pathosystem) or *Gaeumannomyces graminis* var *tritici*. Disease symptoms were monitored [Lyon, Lausanne, Braunschweig], and pathogen survival was estimated (quantitative PCR, especially for *Fusarium graminearum* in 30 Serbian soils) for a range of soils [Lyon]. Plant physiological status was characterized by metabolomic profiling (HPLC-DAD-QTOF MS), which was carried out in the case of both tobacco and wheat [Lyon].

In Task 1.3, the taxonomic biodiversity of the rhizosphere community was assessed for plants growing with/without pathogen inoculation in soils from Switzerland, France, Serbia and Germany. This was done by metabarcoding (Illumina MiSeq) of bacteria [Braunschweig] and fungi [Halle], using 16S rRNA genes and ITS regions, respectively. In addition, in one trial, a focus was also put on the diversity of arbuscular mycorrhizal fungi [Halle].

In Task 1.4, the functional diversity of the microbial rhizosphere community was investigated by shotgun metagenomics targeting soils from Switzerland, France and Germany, planted with tobacco or wheat, and inoculated or not with a root pathogen [Lyon]. Total DNA from the rhizosphere was sequenced using Illumina NovaSeq 6000 technology.

WP2 dealt with the significance of suppressiveness under global change. For this objective, we considered that global change leads to multifaceted modifications in agroecosystems, which are likely to impact directly or indirectly on the suppressiveness capacities of the soils. They include changes in climatic conditions, cropping systems and

farming practices, crop genotypes, prevalent pathogens and insect pests, and the diversity of the plant-beneficial microbiome. A crop relevant under global change scenario in all European regions and considered in this project was wheat.

In Task 2.1, the goal was to assess disease suppressiveness with an emerging crop (wheat) and pathogen (*Fusarium graminearum*). This is an extension of Task 1.2, here in the case of soils suppressive to disease of another crop (tobacco, in Switzerland and France), or soils representative of a geographically heterogeneous area (Serbia). Soil fungistasis was assessed [Lyon], and/or plant health was monitored in soils grown with wheat and inoculated with the pathogen [Lyon, Lausanne, Braunschweig].

In Task 2.2, suppressiveness towards insect pests affecting an emerging crop (wheat) was studied, to determine whether suppressiveness could extend also to the case of insect pests [Lausanne, Changins]. This necessitated extensive method development and optimization, and was carried out with a focus on the cereal leaf beetle *Oulema melanopus*, a leaf-feeder that targets wheat [Lausanne, Changins]. This was completed with metabarcoding analysis of plant-associated microorganisms and chemical analysis of key plant metabolites involved in plant defense responses [Lausanne].

In Task 2.3, the effect of arbuscular fungi on disease suppressiveness was assessed in the tobacco-*T. basicola* pathosystem. We used suppressive and conducive soils from Switzerland [Lausanne], in which arbuscular mycorrhizal fungi were inoculated [Halle, Lyon]. Resistance to *T. basicola* (disease symptoms) was recorded, along with mycorrhizal colonization of wheat plants [Halle, Lyon].

WP3 focused on the analysis of disease and pest suppressiveness in field situations, with the objective to characterize to which extent growth chamber results obtained in WP1 and WP2 match true field situations in farmer's plots managed under current agronomic practices, i.e. with field heterogeneity, microclimatic fluctuations, and field-specific management (crop genotypes, cropping techniques, etc.). However, preliminary investigations in plots, using farmer's fields, pointed that the occurrence of insect damage on roots was difficult to identify and fluctuated too greatly according to soil properties, farming practices and weather conditions [Changins], which rendered connections with suppressiveness properties problematic. Consequently, the focus was put on a long-term field facility in Germany providing more controlled conditions, and enabling also a comparison of current versus future climatic conditions.

In Task 3.1, crop health was studied by monitoring disease symptoms visually under current versus future climatic conditions, with also a comparison between conventional and organic farming [Halle, Lausanne, Changins]. Barley was the rotation crop during the assessment. Symptoms on barley leaves, for the dominant fungal diseases, were also assessed at one plant growth stage by image analysis approaches.

In Task 3.2, crop damage caused by insect pests was monitored [Lausanne, Changins]. Image analysis was used (as in Task 3.1) to assess feeding damage by the dominant herbivorous pest insects.

In Task 3.3, metabolomic profiling was carried out at two plant growth stages [Lyon], in order to assess plant physiology in relation to the climate × farming conditions implemented. The same methodology as in Task 1.2.

In Task 3.4, the taxonomic diversity of rhizosphere microbial communities was assessed by metabarcoding [Braunschweig, Halle], as done in Task 1.3, and their functional diversity investigated by shotgun metagenomics [Lyon], following the methodology in Task 1.4.

Fields of science and technology (from OECD classification)

1.6 Biological sciences

Language

eng

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Identifier type	DOI
Associated documents (publications,reports, patents, experimental plan...), website	• Manure amendments and fungistasis, and relation with protection of wheat from Fusarium graminearum : https://doi.org/10.1016/j.apsoil.2024.105506 • Microbial diversity in soils suppressive to Fusarium diseases : DOI 10.3389/fpls.2023.1228749 • Natural plant disease suppressiveness in soils extends to insect pest control : https://doi.org/10.1186/s40168-024-01841-w

Project Details

Project title Soil biodiversity and suppressiveness of soil against plant diseases and insect pests

Acronym SuppressSOIL

Abstract

SuppressSOIL - Soil biodiversity and suppressiveness of soil against plant diseases and insect pests

Context

Soils can be disease-suppressive or disease-conductive, meaning that the level of disease development varies across soils when a virulent pathogen and suscep- tible host are present. This is especially relevant in regard to root diseases caused by phytopathogenic fungi on crop plants. The link between soil biodiversity, dis- ease suppressiveness and the range of deleterious organisms that are controlled by this mechanism is poorly understood, especially in a context of global change directly affecting crops and pathogen/pest importance.

Main objectives

SuppressSOIL aims at developing integrated knowledge on the relation be- tween soil biodiversity and crop protection in France, Germany and Switzerland. SuppressSOIL will compare soils of contrasting suppressiveness status and soils under different agricultural management regimes to identify novel indicators of soil biodiversity and define management strategies that improve crop health in soils with poor or no suppressiveness properties.

Main activities

SuppressSOIL will work towards this overall objective by:

- Filling current knowledge gaps on suppressiveness, based on analyses of soil, microbial (taxonomic and functional) biodiversity, and crop physiology;
- Assessing the significance of suppressiveness under global change scenario, by considering emerging crop species, diseases and insect pests;
- Determine the applicability of project findings to agronomic conditions, based on monitoring of phytopathogens & insect pests in fields, as well as crop protecting microbiota and crop plants.

  The project will rely on chemical analyses of soil organic matter and crop phys- iological markers, molecular assessments of microbial biodiversity and field analyses of soil management effects on crop health, as well as experimen- tal designs such as growth chamber pot trials of crop protection mechanisms.

  In addition, SuppressSOIL will interact closely with agricultural stakeholders, so that project results and conclusions are deeply rooted in the socio-political context of the project. Specific activities are planned to engage a diverse range of stake- holders, including:

- Farmers and farmer organisations are engaged already, helping to identify sup- pressive soils and providing a recent history of pest and diseases in different sites. This will directly guide the selection of field sites and facilitate the monitor- ing of crop health status;
- Professional media, networks and federation will be mobilised to disseminate pro- ject results in replicable contexts, including through the involvement of farmers and agricultural advisors in technical workshops and visits of each case-study site; Policy-makers at regional and national levels will receive communications and concrete examples drawn from the project that could be used to guide the im- plementation of farming practices fostering soil biodiversity, ranging from indi- vidual-level decisions to regional- and national-level decision making that can materialize into farming policy, especially in a context of global change.

Funding

- Biodiversa : BiodivERsA2018-A-350

Start date 2020-03-01

End date 2024-02-29

Research outputs :

1. Soil composition and metabolomic markers of crop (Dataset)
2. Taxonomic biodiversity of rhizosphere community (Dataset)

Contributors

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DMP du projet "Soil biodiversity and suppressiveness of soil against plant diseases and insect pests"

1. Data description and collection or re-use of existing data

Soil composition and metabolomic markers of crop

1a. How will new data be collected or produced and/or how will existing data be re-used?

SuppressSOIL aims at developing integrated knowledge on the relation between soil biodiversity and crop protection in France, Germany, Switzerland and Serbia. SuppressSOIL will compare soils of contrasting suppressiveness status and soils under different agricultural management regimes to identify novel indicators of soil biodiversity and define management strategies that improve crop health in soils with poor or no suppressiveness properties.
To fill current knowledge gaps on suppressiveness, based on analyses of soil, microbial (taxonomic and functional) biodiversity, and crop physiology; the SuppressSOIL project will characterize analyse data on accumulated metabolites (molecules) and on sequencing data on the diversity of microbial gene alleles (to characterise microbiotes and functional groups) from fungal disease-conducting and fungal disease-suppressing soils or test insects:

- **Soil chemistry**, including soil organic matter quality Potential differences in soil chemistry will be identified by standard chemical analysis and chromatographic profiling of organic matter quality. Soils of contrasting suppressiveness capacity will be compared based on standard chemical analysis (texture, organic matter content, pH, nutrient contents, etc.). Soil organic matter quality, important for suppressiveness, will be assessed using chromatographic profiling of soil organic matter using a HPLC-DAD-QTOF MS and completed (to access also primary metabolites such as sugars, organic acids, fatty acids, etc. together with other low-weight compounds) by gas chromatography). For a more thorough assessment of N-containing compounds important for plant health, amino acid profiling will also be done for selected samples using the Agilent AdvanceBio Amino Acid Solution.
- **Plant metabolomics:** Plant performance/health will be assessed in soils of contrasting suppressiveness capacity, under growth chamber conditions, with half the pots inoculated with a pathogen. Plants will be sampled at a phenological stage crucial for biocontrol interactions. Pathogen abundance (i.e. indigenous strains plus inoculum strain in half the treatments) will be estimated by quantitative PCR and/or disease symptoms will be monitored. Plant physiological status will be characterized using metabolomic profiling, using chromatographic procedures (HPLC-DAD-QTOF MS and/or GC-QQQ MS) validated for various crops (e.g. *Walker et al. 2012; *Chamam et al. 2015) and that can be readily adapted for analysis of other crops.

1b. What data (for example the kind, formats, and volumes), will be collected or produced?

data will be obtained by analytical apparatus such as UHPLC-DAD-QTOF MS/MS and/or GC QQQ MS. Therefore number of files and file formats will depend ont apparatus brand and systems.

Taxonomic biodiversity of rhizosphere community

1a. How will new data be collected or produced and/or how will existing data be re-used?

- **The taxonomic biodiversity of the rhizosphere** (soil influenced by the root) / root microbial community of plants growing with/without pathogen inoculation will be assessed using next generation sequencing (NGS)-based metabarcoding]. Total microbial community DNA will be extracted from rhizosphere/root samples. PCR-based amplicon libraries will be produced using taxon-specific primer sets and sequenced using Illumina MiSeq paired-end chemistry (2 × 300 bp). Bacteria (using primers for 16S rRNA genes), fungi (targeting the ITS2 region), and specifically the arbuscular mycorrhizal fungi (AMF; targeting the 18S rRNA region) will be studied. Sequence datasets will be analyzed using standard procedures in MOTHUR (https://www.mothur.org/) and/or QIIME (https://qiime.org), and assigned to the respective reference databases (SILVA database for bacteria, UNITE

database for fungi) (e.g. see *Schöps et al. 2018). Data analysis will include rarefaction curves, OTU richness (Chao 1) and Shannon's Bray-Curtis similarity index will be computed and microbial communities compared by non-metric multidimensional scaling (NMDS) and non-parametric multivariate analysis of variance (PERMANOVA) to assess differences in community composition. In addition, a particular attention will be paid to taxa with documented role in biocontrol, entomopathogenesis and mycorrhizal behavior, as well as taxa corresponding to fungal/oomycete/bacterial phytopathogens. Co-occurrence network analyses at interkingdom level both on the whole microbial communities and on populations potentially involved in disease suppression will be performed, as complexity and strength of the co- occurrence network may correlate with suppressiveness, especially on the German soils managed to enhance biodiversity. Furthermore, network analysis may provide insights into the core microbiota of suppressive/conducive soils depending on farming practice, identifying potential microbial hubs of importance for suppressiveness.

- **Diversity of microbial functional groups in rhizosphere community.** The functioning of the rhizosphere microbial community will be also assessed, with a focus on three key microbial functional groups important for plant health, such as (i) the producers of 2,4-diacetylphloroglucinol , a secondary metabolite inhibiting a range of phytopathogens) and that triggers induced resistance pathways in plants (Iavicoli et al. 2003; Weller et al. 2012), (ii) the producers of HCN, an antimicrobial compound implicated in biocontrol of pathogens and insect pests, or (iii) the producers of 1-aminocyclopropane-1-carboxylate (ACC) deaminase, a microbial enzyme that modulates ethylene metabolism in plant, thereby alleviating deleterious effects of high ethylene levels upon plant infection, and is important for biocontrol of various diseases. This assessment will be done based on Illumina sequencing of the corresponding marker genes *phlD*, *hcnAB* and *acdS*, following same procedure as for taxonomic markers.

1b. What data (for example the kind, formats, and volumes), will be collected or produced?

NGS data Miseq:
- Raw: fastq.gz; compression due to large file size
- Processes: csv or txt .

All of these formats were chosen because they are suitable for data warehouses and are easily reusable without conversion.

2. Documentation and data quality

Soil composition and metabolomic markers of crop

2a. What metadata and documentation (for example the methodology of data collection and way of organising data) will accompany the data?

Question sans réponse.

2b. What data quality control measures will be used?

Question sans réponse.

Taxonomic biodiversity of rhizosphere community

2a. What metadata and documentation (for example the methodology of data collection and way of organising data) will accompany the data?

PCR-based amplicon libraries will be produced using taxon-specific primer sets and sequenced using Illumina MiSeq paired-end chemistry (2 × 300 bp). Bacteria (using primers for 16S rRNA genes) [Braunschweig], fungi (targeting the ITS2 region), and specifically the arbuscular mycorrhizal fungi (AMF; targeting the 18S rRNA region) and functional groups targeting corresponding marker genes *phlD*, *hcnAB* and *acdS*, will be studied. Sequence datasets will be analyzed using standard procedures in MOTHUR (https://www.mothur.org/) and/or QIIME (https://qiime.org), and assigned to the respective reference databases (SILVA database for bacteria, UNITE database for fungi, and in-house databases for functional groups). Data analysis will include rarefaction curves, OTU richness (Chao 1) and Shannon's Bray-Curtis similarity index will be computed and microbial communities compared by non-metric multidimensional scaling (NMDS) and non-parametric multivariate analysis of variance (PERMANOVA) to assess differences in community composition. In addition, a particular attention will be paid to taxa with documented role in biocontrol, entomopathogenesis and mycorrhizal behavior, as well as taxa corresponding to fungal/oomycete/bacterial phytopathogens.

2b. What data quality control measures will be used?

Question sans réponse.

3. Storage and backup during the research process

Soil composition and metabolomic markers of crop

3a. How will data and metadata be stored and backed up during the research?

The raw data generated will be saved on the servers of the French lab for the duration of the analysis. The analysis scripts will be saved and shared between the collaborators, then published at the end of the work.

In the end, the raw and processed data (cleaned and analysed) will will be freely accessible after publication of the data.

3b. How will data security and protection of sensitive data be taken care during the research?

Data are safely stored in house on a bioinformatics server which is daily saved.

Taxonomic biodiversity of rhizosphere community

3a. How will data and metadata be stored and backed up during the research?

The raw data generated by service providers will be saved on the servers of the French, Swiss and German laboratories for the duration of the analysis. The analysis scripts will be saved and shared between the collaborators, then published at the end of the work.
In the end, the raw and processed data (cleaned and analysed) will be deposited in the dedicated databases and will be freely accessible after publication of the data.

3b. How will data security and protection of sensitive data be taken care during the research?

Data are safely stored in publicly available repositories but also in house on a bioinformatics server which is daily saved.

4. Legal and ethical requirements, codes of conduct

4a. If personal data are processed, how will compliance with legislation on personal data and on security be ensured?

no personal data will be collected

4b. How will other legal issues, such as intellectual property rights and ownership, be managed? What legislation is applicable?

All the data is the property of the research laboratories involved in the project. However, following publication of the articles, the data will be accessible to the entire scientific community. Therefore there are no restrictions on the re-use of the data.

4c. What ethical issues and codes of conduct are there, and how will they be taken into account?

There are no ethical or legal issue that can impact data sharing of this project.

5. Data sharing and long-term preservation

Soil composition and metabolomic markers of crop

5a. How and when will data be shared? Are there possible restrictions to data sharing or embargo reasons?

There will be an embargo until the data has been published at least once in peer-reviewed journals.

5b. How will data for preservation be selected, and where data will be preserved long-term (for example a data repository or archive)?

No data must be destroyed for contractual, legal or regulatory reasons.
Raw data, final analysis data and scripts will be kept for the long term. Intermediate data will be deleted.

5c. What methods or software tools are needed to access and use data?

The Galaxy 4 metabolomics workflow management system

5d. How will the application of a unique and persistent identifier (such as a Digital Object Identifier (DOI)) to each data set be ensured?

Question sans réponse.

Taxonomic biodiversity of rhizosphere community

5a. How and when will data be shared? Are there possible restrictions to data sharing or embargo reasons?

The raw and worked (cleaned and analysed) data will be deposited in the dedicated and freely accessible databases after publication of the data. There will be an embargo until the data has been published at least once in peer-reviewed journals.

5b. How will data for preservation be selected, and where data will be preserved long-term (for example a data repository or archive)?

No data must be destroyed for contractual, legal or regulatory reasons.
Raw data, final analysis data and scripts will be kept for the long term. Intermediate data will be deleted.
The raw data (NGS) and scripts will be useful to the scientific community in the framework of other research projects. The NGS data will be deposited on the NBCI databases (SRA).All datasets produced in the context of this project will be made publicly available. Metadata, documentation and code will be made available. All other datasets, typically sequencing datasets,will be made available via NCBI with an identifier and accession numbers also referenced in published articles.

5c. What methods or software tools are needed to access and use data?

Sequence datasets will be analyzed using standard procedures in MOTHUR (https://www.mothur.org/) and/or QIIME (https://qiime.org), and assigned to the respective reference databases (SILVA database for bacteria, UNITE database for fungi) (e.g. see *Schöps et al. 2018). Data analysis will include rarefaction curves, OTU richness (Chao 1) and

Shannon’s diversity. Bray-Curtis similarity index will be computed and microbial communities compared by non-metric multidimensional scaling (NMDS) and non-parametric multivariate analysis of variance (PERMANOVA) to assess differences in community composition

Data not yet published will be available to project members in a direct and unlimited way. The same will apply to data published via SRA or github.
Data under analysis will not have a DOI. Nevertheless, explicit names will be given to the files, which, together with the README files, will ensure their traceability and reuse.
The data published on SRA will have multiple identifiers such as BioProject numbers, BioSamples, etc. The github repository will have a DOI assigned by Zenodo, which will follow the version control allowed by github, if new data needs to be added.

5d. How will the application of a unique and persistent identifier (such as a Digital Object Identifier (DOI)) to each data set be ensured?

All datasets produced in the context of this project will be made publicly available. Metadata, documentation and code will be made available via Zenodo.org or similar website with assigned DOI. All other datasets, typically sequencing datasets, assembled genomes and genes will be made available via NCBI with an identifier and accession numbers also referenced in published articles.

6. Data management responsibilities and resources

Soil composition and metabolomic markers of crop

6a. Who (for example role, position, and institution) will be responsible for data management (i.e. the data steward)?

Gilles Comte, a professor at Lyon 1 University in the Microbial Ecology Laboratory, and Markjolaine Rey, an Engineer of Studies at CNRS, part of the RHIZO Team & CESN Platform located at La Doua site, are responsible for managing the data derived from metabolomic analyses. (french partner of the project)

6b. What resources (for example financial and time) will be dedicated to data management and ensuring that data will be FAIR (Findable, Accessible, Interoperable, Re-usable)?

Question sans réponse.

Taxonomic biodiversity of rhizosphere community

6a. Who (for example role, position, and institution) will be responsible for data management (i.e. the data steward)?

Daniel Muller, Associate Professor at Lyon 1 University, and Danis Abrouk, Engineer at CNRS at the Microbial Ecology Laboratory, will be responsible for data management from microbial metabarcodes and metagenomic data sets and analysis workflow.

6b. What resources (for example financial and time) will be dedicated to data management and ensuring that data will be FAIR (Findable, Accessible, Interoperable, Re-usable)?