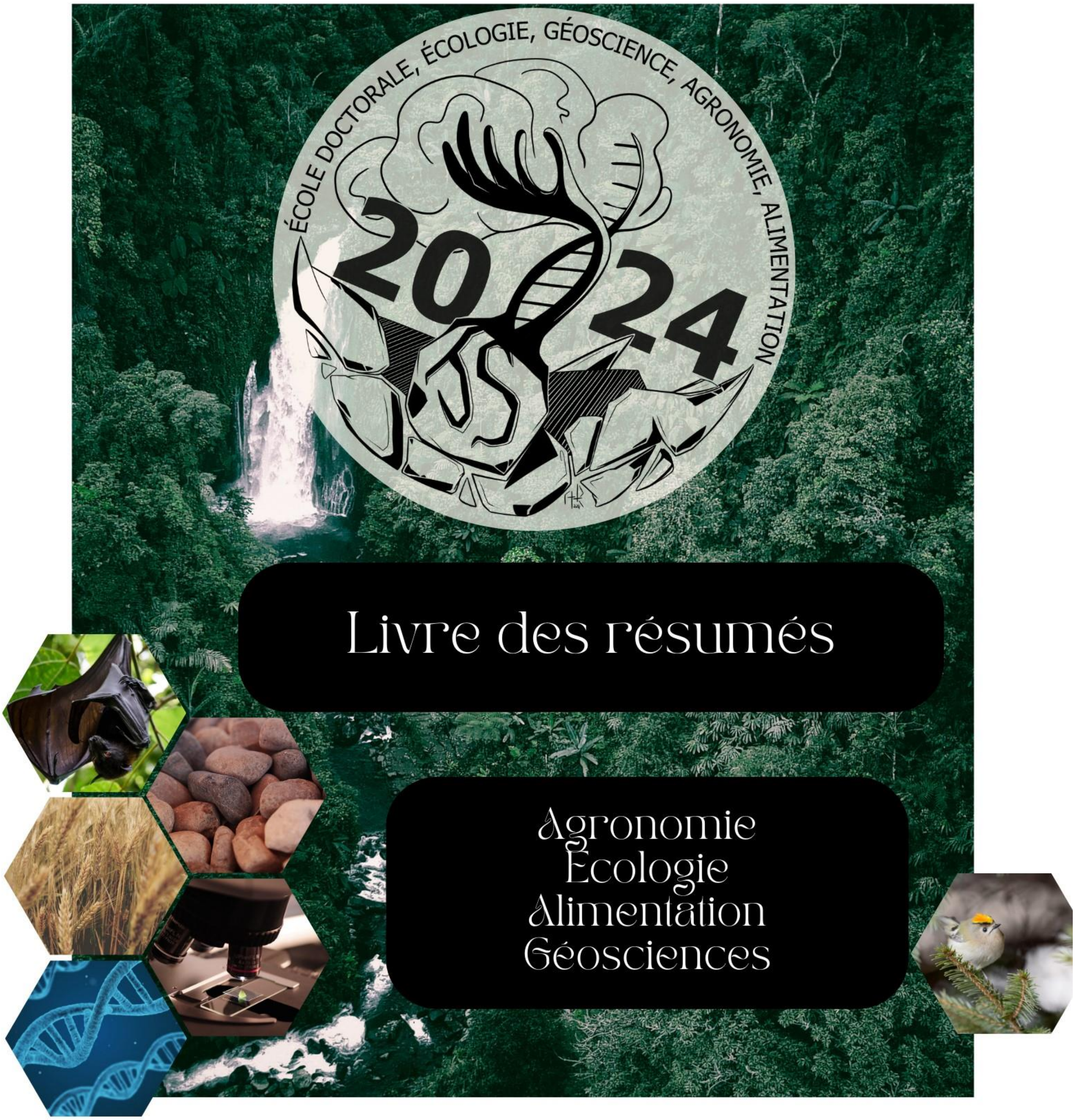
COLLEGE DOCTORAL BRETAGNE
ECOLOGIE GEOSCIENCES AGRONOMIE ALIMENTATION

21 AU 23 MAI

JOURNÉES SCIENTIFIQUES

STATION BIOLOGIQUE DE PAIMPONT



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Présentations orales

1ère session (9h20-10h20, 22mai)

Effects of supplementation with vitamin E or plant extracts on redox and immune status in early lactating dairy cows

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Early lactation is a period for oxidative stress and inflammation, which can lead to cell damage in dairy cows. Our objective was to investigate the influence of dietary supplementation of vitamin E or plant extracts, on redox and immune status of dairy cows. Forty-five Holstein cows, including 23 primiparous cows, were classified into 3 groups and followed from 3 weeks before to 12 weeks after calving. The 15 cows of the control group were fed an unsupplemented diet, the 16 cows in the vitamin E group received 3,000 IU/d 3 weeks before and 1,000 IU/d for 12 weeks after calving, and the 14 cows in the plant extract group received 10 g/d for 12 weeks after calving. Plasma redox status were analysed by spectrophotometry and HPLC methods. Plasma cytokines were analysed after an *ex vivo* challenge of whole-blood cells with heat-killed *Escherichia coli*. Blood neutrophils were analysed by flow cytometry to measure their production of reactive oxygen species under *ex vivo* stimulation. Data were analysed with a mixed model including supplementation, parity, week. Plasma α-tocopherol was higher in vitamin E group than in the other groups. Milk yield, plasma H2O2, plasma antioxidant capacity and plasma glutathione peroxidase activity were not influenced by the supplementations. Erythrocyte glutathione peroxidase activity tended to be higher and plasma malondialdehyde tended to be lower in vitamin E group than in the other groups. Vitamin E and plant extract groups had lower plasma cytokines: CCL4 for plant extract group, IL-6 as a tendency for vitamin E group, and IL-8 for both antioxidant treatments. Both supplemented groups had lower MHCII+ neutrophil percentage, and lower ROS production than the control group. Our study showed that antioxidant nutritional strategies in healthy cows can affect the redox and immune status and may improve antioxidant capacities and reduce the inflammatory response.

Mots-Clés: antioxidant intake, antioxidant response, immunity, lactation onset

Secretion of capsular polysaccharides and DNases by Mycoplasma species infecting ruminants, swine and poultry

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Several species belonging to the genus Mycoplasma are causal agents of infections in ruminants, swine and poultry, leading to economic losses in these production sectors. The project exovirulome aims at clarifying the role that could be played by several mycoplasmal secreted elements in the host-pathogen interactions and whether these elements are shared across different Mycoplasma species. We focused on two elements: (i) the polysaccharidic capsule knownto help escaping phagocytosis by neutrophils, macrophages or dendritic cells and (ii) DNasesthat help bacteria to escape trapping by the Macrophage Extracellular Traps (METs) through degrading the DNA constitutive of the METs. The secretion of these two components by dif- ferent Mycoplasma species infecting swine, poultry and ruminants was studied. The study ofthe CPS secretion by biochemical and genomic approaches contributed to detect production of a capsule made of β(1-6)glucan in the avian pathogen M. iowae like in ruminant mycoplasmas, andrevealed an uncommon β-glucan. Concerning the DNases' secretion, a protocol able to detect cell-linked and free enzymes secreted by mycoplasmas as set up. Secretion of DNAses by the swine-pathogen M. hyopneumoniae and the avian-pathogen M. gallisepticum was confirmed, andsecretion by M. hyorhinis and M. flocculare (for the swine), by M. iowae, M. synoviae and M. pullorum (for the poultry) was evidenced. These enzymes will be identified by zymography and their role in METs escape and mycoplasmal survival in macrophages will be assessed.

Mots-Clés: Mycoplasma, capsular polysaccharides, DNases, interactions host pathogen

Decreased in lactose percentage in milk related to mammary inflammation and metabolic disorder in early lactation of dairy cows

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Lactose is the least variable component of milk compared to fat and protein levels during lactation. However, it can be affected by metabolic disorders (MED) or mammary inflammations (MI) in dairy cows. Two studies examined the combined effect of these factors on lactose content (LC) at the beginning of lactation (5-100 days). The first study, conducted in Canada, analyzed 6,479 samples of cisternal milk from quarters of 380 cows. The second, in France, involved 975,981 milk test-day records from 441,070 cows. MIs were classified based on somatic cell counts (SCC), and MEDs by the concentration of β-hydroxybutyrate (BHB) in milk. A mixed linear regression model, accounting for the specificities of each study, was developed. In both studies, a decrease in TL was observed during MI, which was more pronounced as SCC increased. In the French study, MEDs were associated with a decrease in TL. When MI and MED occurred simultaneously, a greater decrease in TL was observed in both the Canadian and French studies compared to MI or MED alone, suggesting a potential additive effect. This effect was observed despite the different protocols used in these two studies using different protocols (quarter milk vs. milk from the milking of the four quarters) and at different intervals (15 days vs. 1 month). These results show that an early lactation metabolic disorder may be associated with a decrease in TL, the magnitude of which depends not only on MED but also on the inflammatory status of the udder. Therefore, a combined analysis of these two criteria is necessary. These findings reinforce the importance of further investigation into the kinetics of TL evolution in early lactation, with the aim of developing an animal health indicator.

Mots-Clés: Lactose, Mammary inflammation, Metabolic disorders, Dairy cow

How many preys does a predator eat in a day?

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Very few interactions are as decisive as trophic interactions to understand the structure and dynamics of ecological communities. Works on food webs have recently benefited from the development of molecular analyses, especially DNA-based analyses such as PCR-diagnostic or Metabarcoding, that greatly facilitate the description of food webs, and can provide novel insights on diet diversity and food preferences. However, despite commendable efforts, molecular analyses remain largely **qualitative** (presence/absence of predation interaction). Furthermore, the decay of molecular evidence of prey consumption is specific to the predator-prey pair, which impedes the **quantification** of absolute prey consumption rates based on prey detection **frequency**. Previous works have circumvented this issue by empirically adjusting detection frequencies according to the half-life of the prey's DNA calibrated on voracity experiments. Here, we propose a **Hierarchical Bayesian Model** that integrates field detection frequencies and laboratory assessment of detection rate decay into a new mechanistic framework to infer posterior probability distributions of the predation rate in the field. The model provides an estimate of the slope and intercept of the decaying detection curve and an estimate of **the number of prey items consumed by a predator per day**, hereby referred to as **predation intensity**. Moreover, each parameter is broken down into a prey, a predator and a pair effects which allow information to be leveraged from widely observed predator species to inform and improve estimates on rare species. Through a case study with 27 carabid beetles' species preying on 5 types of preys in agricultural fields (wheat and beet), we used our model to investigate the main drivers of predation intensity at species scale (i.e. traits such as predator diet or size) and at community scale (i.e. characteristics such as community size or alpha diversity).

Mots-Clés: Modeling, Trophic Interactions, Predation Intensity

Effects of three grazing methods on different services provided under French production conditions.

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Agriculture, including European livestock systems, is central to climate and environmental issues. In this context, grasslands offer potential solutions by providing various services to society: production of fodder for ruminants, of course, but also storage of organic carbon in soils, maintenance of a high level of biodiversity, maintenance of open and diverse landscapes, etc. The provision of these services can vary depending on how the grasslands are used, particularly through grazing in agricultural systems. An innovative grazing method (adaptive multi-paddock grazing) from North America has potential to provide numerous benefits, including carbon sequestration, while maintaining grass production. The objective of this thesis is to compare three grazing methods on a range of services provided (animal performance, grazing performance, carbon sequestration, biodiversity, work and economy), under French conditions. The study is conducted directly on 18 commercial farms throughout France. Three grazing methods, two widely practiced in France and one innovative, were tested (continuous grazing, rotational grazing, adaptive multi-paddock grazing) on suckler or dairy heifers and their attached grassland. A total of six systems for each grazing method were monitored for three years. This work provides an overview of current and innovative grazing methods in France, with an approach based on a bouquet of services, in order to consider the future of grazing systems.

Mots-Clés: Grazing systems, ecosystem services, AMP grazing, continuous grazing, rotational grazing, livestock, carbon sequestration, biodiversity, zootechnical performance, workload, economy, grazing performance

Study of biodegradable plastics in anaerobic digestion

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Introduction

According to EU recommendations, biowaste from household, public and private establishments should not be incinerated or landfilled anymore but separately collected and recycled in composting or anaerobic digestion (AD) (EEB.org). Consequently, the amount of biowaste treated in codigestion with manure in agricultural biogas plants will increase. In order to facilitate the biowaste collection process, biodegradable plastics are sometimes used as biowaste containers. Nevertheless, stakeholders from AD facilities report a partial degradation of these biodegradable plastics, still poorly described in literature. The aim of this study is to understand better the mechanisms of degradation of biodegradable plastics by making some links between material properties and the biological process in AD.

Methodology

Biodegradable plastics selected for the study are those which are likely to be found in AD fa- cilities namely the poly(3-hydroxybutyrate-co-3-hydroxyvalerate (PHBV), and a composite bag based on starch and polyester, the Mater-bi® (Novamont® Italy). All experiments were setup by using the Biochemical Methane Potential test (BMP) as a technique to evaluate thebiodegradability of a substrate in AD (Nachod et al., 2021). The degradation of plastic pieces of PHBV and Mater-bi® were monitored by analyzing the material properties and the associated microbial communities at different stages of the biodegradation process. Methane productionwas monitored by pressure measures and gas chromatography. Plastic degradation was assessed by Scanning electron microscopy (SEM), spectroscopy FT-IR, size exclusion chromatography. Microbial communities were characterized by high throughput 16S rDNA sequencing.

Results & Discussion

PHBV reached high percentages of degradation while Mater-bi® displayed poor degradation. Analysis of the plastic pieces of PHBV and Mater-bi® submitted to BMP tests showed a re- duction of their physical properties and molecular weights as biodegradation progressed. Char- acterization of the associated microbial communities is in progress and will be presented. EEB,

Mots-Clés: biodegradable plastics, anaerobic digestion, microbial communities, material properties

Optimisation of selection schemes for laying hens breeding

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The egg industry is facing structural changes: since 2017, a European movement called *End the cage age* has initiated an end to the rearing of animals in cages. In France, the consequences of this movement quickly became apparent. In the meantime, egg consumption and production are steadily increasing for years, meeting the growing demand from consumers. To meet theegg industry's production needs in the new social and environmental context, breeding programs have to be optimized in relation with the challenges that the laying hens breeding systems haveto face. The objective of our study was to assess the impact of the conversion of breeding systems from pedigree-based selection in cages systems to genomic selection in alternative systems. The objective was to maximize the genetic gain in egg quality and laying performance traits while minimizing inbreeding in the population. The breeding programs were modelled with the R package MoBPS during an international mobility to Wageningen University & Research. The breeding programs were evaluated using a synthetic indicator that takes into account changes in genetic gain in relation to changes of the population inbreeding rate.

We expect genomic selection to be more efficient than pedigree selection in terms genetic gain. However, we hypothesized that genomic selection would lead to a greater increase in inbreeding than pedigree selection. Next, multiple combinations of selection age for males and females will be tested to arrive at the optimal breeding program.

Mots-Clés: Genetic, layers, egg, breeding program

Agent-based modelling: a novel approach to understanding High Pathogenicity Avian Influenza (HPAI) spread in French poultry farms through the integration of socio-economic factors

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Since 2015, the French poultry industry has been facing considerable challenges due to recurring outbreaks of High Pathogenicity Avian Influenza (HPAI), which has led to major health, economic and social consequences. These repeated outbreaks highlight the need for a deeper understanding of the virus's transmission mechanisms. This project aims to address this need by integrating socio-economic factors, environmental factors and epidemiological processes into a single model in order to explain the introduction and spread of HPAI in French poultry farms. It also seeks to assess the effectiveness of a range of control measures.
An agent-based spatio-temporal epidemiological model is being developed using the Gama platform, which has proven efficient for dealing with similar issues in human health. The model will represent poultry farms as agents with specific attributes such as farming system, and risk perception. The agents will operate within an environment that will take into account various elements, including spatial representation. This will allow for precise localisation of farms and an understanding of movements between farms. The agents' environment will also incorporate different environmental and socio-economic factors that affect all agents. For the environmental factors, an analysis of the 2022-2023 outbreaks identified variables such as proximity to partic- ular risk zones as potentially significant in the occurrence of the outbreaks. The socio-economic and epidemiological components are ongoing, drawing on both literature data and a field study involving interviews with concerned stakeholders.

This innovative project will contribute to a paradigm shift in infectious animal disease mod- elling, moving from simplistic epidemiological models to more complex systems that aim to to better reflect the reality seen in the field. It will not only enhance our understanding of HPAI dynamics but also facilitate the identification of optimal control strategies.

Mots-Clés: Agent, based models, HPAI, socio, economic factors

2ème session (11h30-12h30, 22mai)

Unpredictable Arbuscular mycorrhizal Fungi (AMF): Effects of ten AMF strains on four plants of the Asteraceae family.

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Plants are known to tightly interact with arbuscular mycorrhizal fungi (AMF). AMFs provide several advantages such as increased nutrient uptake, or improved biomass. However, less is known about the AMF effects on a plants multi traits scale, especially the different trade-offs in the allocations of resources that can occur as a result of these interactions. Moreover, these trade-offs can be a result of the AMF-plant pair, as the effects of one AMF can be different on different plants.

In this experimental greenhouse study, we inoculated four Asteraceeae plants species with ten AMF isolates, in a factorial design. We assessed how the AMF inoculation affects growth, root, photosynthesis and floral traits, and the trait syndromes of plants. We also assessed the differ- ences of effects between the AMFs on plants traits.

AMF inoculation effects on plants varied from positive to neutral to negative, depending on the trait measured. Biomass allocation to roots decreased in the majority of inoculated plants, while the allocations to photosynthesis or flowers increased depending on the AMF or the plant. Differences between each AMF have also been observed, whether taking into account each trait separately, or the trait syndrome. Some effects of trade-offs between vegetative or reproductive growth also occurred for plants inoculated with one or another AMF isolate. Although some consistency has been observed for a given AMF's effects on different plants, more has to be done to be able to predict a precise effect of an AMF on plant traits.

These results show that to be able to understand AMFs effects on plants, we should not just focus on biomass production, but trait variations and resource allocation trade-offs are at least as important. Moreover, further knowledge about AMFs functional traits or ecological strategies is needed to be able to predict an AMF's effect on plant traits.

Mots-Clés: Arbuscular Mycorrhizal Fungi, plant traits, resources allocation, roots, photosynthesis, flowers

Exceptional mud-debris landslides in Karongi area, western Rwanda: an investigation of cause factors.

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Rwanda, in equatorial-eastern Africa, is the most densely populated country on the continent (> 550 pop/km2). Its west is regularly affected by landslides that kill people and destroy crucial infrastructures. This region is characterized by steep slopes (resulting from the activity of the western branch of the East African Rift), clayey soil, and intense rainfall. Therefore, assessing landslide hazards represents a priority including mapping and understanding their potential causes and consequences. However, the current state of knowledge in Rwanda is limited by the lack of field data and fails to monitor active landslides and characterize the population vulnerability.

This study focuses on a specific catastrophic landslide event in the eastern Kivu ridge in the Karongi district (western Rwanda), that generated 750 landslides over about 100 km2 during a single night (7th May 2018) and killed 18 people. We combined field data, satellite images, and climate models (CHIRPS and ERA5-Land) to describe and analyse this event and better under- stand its origin. The Karongi area event was favored by an unusual 2-months near-continuous rainfall during March (228.70 mm) and April (232.78 mm) compared to the other 41 years of the considered period (1981-2022). The thin clayey soil supported by a basal gravel layer and resting on steep schist-dominant bedrock slopes favored waterlogging and sliding. The final mechanism of waterlogging landslides was a violent thunderstorm. The wind- and thunder-sourced vibra- tions probably lead to thixotropy of the water-saturated soil. Not a single parameter but the coupling of continuous rainfall, steep slopes, water-logged ground, and violent thunderstorms explains this catastrophic event.

Keywords: Landslides, Karongi, Rainfall, May-2018, Rwanda

Mots-Clés: Keywords: Landslides, Karongi, Rainfall, May, 2018, Rwanda

Assembly of the water primrose mitochondrial genome

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Invasive exotic species are one of the major sources of biodiversity loss. Among these species, the water primrose is an aquatic plant, which is invasive in France. The water primrose name actually refers to two species: *Ludwigia grandiflora* subsp. *hexapetala* (*Lgh* ; decaploid : 2n=10x=80) and *Ludwigia peploides* subsp. *montevidensis* (*Lpm* ; diploid : 2n=2x=16). In France, *Lgh* displayed an ability to colonize terrestrial environments, particularly wet meadows, giving rise to two distinct morphotypes: aquatic and terrestrial. For a better understandingof genetic processes involved in the acclimatization of water primrose to the terrestrial envi- ronment, it is necessary to generate genomic resources, missing for those two species. We first chose to assemble organelles genomes, easier to do than the nuclear genome. These assemblies were realized using two sequencing techniques known as "long reads" and "short reads". The mitogenomes each consisted of two circular molecules, called M1 and M2, with a size of 544 and 167 kb for *Lgh* and 555 and 167 kb for *Lpm*. M2 molecules were colinear between the two specieswhile numerous reorganizations were observed between M1 molecules. A total of 266 and 294 repeated sequences were identified, representing 7 and 7.4 % of *Lgh* and *Lpm*, respectively. The majority of these repeats were between 30 and 59 bp in size (192-220). Sequences originated from the chloroplast were also present. They contained around 20 genes and represented 6.1 %of each mitogenome. We also demonstrated the existence of alternative forms of M1 molecules due to intramolecular recombinations mediated by large repeats (> 1 kb). These plastomes and mitogenomes will be used for further transcriptomic analysis to better understand the invasive abilities of these species.

Mots-Clés: Mitochondria, Ludwigia, acclimatization, mitogenomes, organelle

Prevalence of two endosymbionts in range expanding Zodarion spiders

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Limits of species geographic ranges are dynamic in space and time through continuous local immigration and extinction processes. Yet, numerous species with major changes to their original range, i.e. shifts, contractions or expansions, have been reported in the recent decades, mostly explained by passive population movements due to climatic changes or introductions. However, the possibility of intrinsic causes such as endosymbiotic implications have not been thoroughly considered yet, despite the potential of these microbial agents to profoundly affect the biology of organisms, in particularl arthropods that are frequent hosts. Here, we described the prevalence of two widespread endosymbionts, *Wolbachia* and *Cardinium*, in the unstudied quickly range expanding spider *Zodarion rubidum* Simon, 1914, and investigated the relationship between geographic range size and prevalence in seven additional *Zodarion* species. Based on specimens of *Z. rubidum* we collected across Europe, we used specific primers to detect each endosymbiont and interpolated their prevalence levels over space using ordinary kriging. We found that both endosymbionts are widely present across *Z. rubidum* populations, but do not show any distribution pattern that would correlate with the expansion of the spider species. Moreover, we did not find any effect of the size of geographic range using seven *Zodarion* specieson the prevalence of *Wolbachia* and *Cardinium*. We discuss the possible explanations for sucha wide distribution of endosymbionts and question their potential impact on spider population dynamics and distribution.

Mots-Clés: **Cardinium, Wolbachia, Dispersal, Arthropod, Geographic range, KriginG**

Dynamiques multi-taxons d’une succession écologique après perturbation: Etude d’un réseau de carrières.

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Dans un contexte d’augmentation des perturbations anthropiques, la compréhension des successions écologiques post-perturbation permet d’envisager les différentes trajectoires possibles lors de la réhabilitation.
Le temps après perturbation et les caractéristiques de l’habitat sont des filtres environnementaux qui influencent la dynamique de succession des communautés. Ces deux facteurs influencent la coexistence des espèces. Une meilleure compréhension des mécanismes de succession le long de gradient d’année depuis perturbation est possible en déterminant l’importance de l’âge du milieu et de l’habitat local. Notre étude vise à comprendre l’impact direct et indirect de l’âge de réhabilitation sur la dynamique des communautés animales après une perturbation. Nos modèles d’études sont des carrières alluvionnaires, qui après exploitation suivent une dynamique de succession.

Nous avons utilisé les 15 ans de données de suivi standardisé de biodiversité du programme ROSELIERE. Nous avons sélectionné 38 carrières alluvionnaires de la moitié Nord de la France, nous permettant d’obtenir un gradient temporel après réhabilitation allant d’avant exploitation à 30 ans après perturbation. L’étude s’est portée sur les dynamiques de successions de 3 groupes taxonomiques : oiseaux, chauves-souris et papillons de jour. Pour chaque groupe, trois indica- teurs de structures des communautés ont été testés, la richesse spécifique, l’indice de Pielou ainsi qu’un indicateur de spécialisation des communautés.
Nos résultats montrent un effet de l’âge depuis perturbation différencié entre taxons, ainsi qu’un effet direct et un effet de l’âge médié par l’habitat local sur la durée de réhabilitation. Ces différences de réponses sont ensuite discutées face aux enjeux de la réhabilitation des carrières alluvionnaires.

Mots-Clés: Multi, taxon, Carrière, Succession Écologique, Écologie de la conservation, Écologie des communautés.

Thermal tolerance of cereal aphids might differ along a longitudinal gradient

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To resist climate change, insects may evolve through rapid local adaptation and/or plasticity. Basal thermal tolerance and the plastic/acclimated thermal tolerance of individuals can reflect their evolutionary potential. To figure out the impact of climate change on the evolution of thermal tolerance, thermal performances can be studied using a space-to-time substitution approach along geographic longitudinal gradients with varying temperatures. Using the three main species of cereal aphids, the Bird cherry-oat aphid *Rhopalosiphum padi*, the English grain aphid *Sitobion avenae*, the Rose-grain aphid *Metopolophium dirhodum,* we tested heat (CT max),cold tolerance (CT min), thermal breadth(CT max- CT min)and their hardening capacity of individuals from 106 clonal lines collected along a European gradient in Spring and autumn 2022. Our first results showed basal thermal tolerance followed the longitudinal gradient; heat tolerance increased with the duration of high temperature (accumulative hours with temperature > 30◦C in summer 2013-2022) and thermal breadth increased with local seasonality, which would be seen as a case of local adaptation. Basal thermal tolerances of the three species S.avenae, M.dirhodum and R.padi presented similar pattern but the level of plasticity (of individuals) differed among species, seasons and localities, indicating that selection pressures varied along the gradient. Our study emphasizes the need for future research investigating evolution processes of thermal tolerance in a climate change context.

Mots-Clés: Thermal tolerance, Plasticity, Climate change, Ecology, Cereal aphid guild

Diversity, transmission and function of the microbiota of a root phytophagous insect

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Gut microbiota of phytophagous insects can contribute to the detoxification of toxic compounds produced by plants and thus to the adaptation of the insect to its host plant. *Brassicaceae* produce isothiocyanates, which can be detoxified by bacteria carrying the *saxA* gene. However, the involvement of insect gut microbiota in the detoxification of isothiocyanates produced by *Brassicaceae* remains understudied. Here, we describe the diversity, composition, acquisition and impact on insect fitness of the cabbage root fly (*Delia radicum*) microbiota. We performeda laboratory experiment where *D. radicum* faced contrasted environments, with a gradient *saxA* abundance. These contrasted environments are represented by rapeseed (*Brassica napus*) genotypes that differ in glucosinolates (directly implicated in the production of isothiocyanates) concentration and on soils that differ in microbiota diversity. We combined the measure of the insect fitness with a metabarcoding approach to exhaustively describe the microbiota communities of the soil, the roots and the insect at different life stages. This DNA-based approach was completed with a molecular approach to carachterize *saxA* abundance and diversity in the environment as well as in insect microbiota. We demonstrated horizontal transmissions in bacterial communi- ties: three bacterial genera (*Pseudomonas*, *Serratia* and *Acinectobacter*) known to harbour the *saxA* gene were shared between the insect, the soil and the root microbiota. Insects have abetter fitness in environments with high glucosinolates concentration. Our results indicate that *D. radicum* deals with the isothiocyanate toxicity and its microbiota contains bacterial genera able to detoxify toxic compounds released by *B. napus*.

Mots-Clés: glucosinolates, isothiocyanates, life history traits, cabbage root fly, microbial communities

Genetic diversity and soil fitness of Listeria monocytogenes in the pig manure recovery sector

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Livestock production intensification in Europe raises local eutrophication issues due to effluent discharge. Manure treatment techniques were developed to reduce soil nitrates pollution by nitrification-denitrification and/or produce methane as energy, promoting a circular economy. Their endpoint is land spreading of the processed manure, potentially reintroducing pathogens in the environment and the food chain. Pathogens flows between pig manure, environment and food sectors are poorly understood, especially for *Listeria monocytogenes* (*Lm*). *Lm* is a ubiquitous foodborne pathogen and the causative agent of listeriosis. Most of the strains are grouped into hypervirulent or hypovirulent clonal complexes.

By adopting a "One Health" approach, this project aims to acquire a systemic and innovative picture of *Lm* fluxes from these manure management chains to the food system, and identifying new genetic elements involved in soil survival.

We therefore assembled and sequenced a collection of 371 *Lm* strains isolated in France from pig faeces and slurries, denitrification and anaerobic digestion treatments. Their pangenome was analysed, virulence and resistance markers and plasmidic content were characterized using bioinformatics tools and their diversity was compared to clonal complexes found in the food sector. Soil survival phenotyping of the strains allowed us to emulate their persistence capacity in soil after land spreading. These results were used to conduct pan-Genome-Wide Association Studies (GWAS), allowing us to discover new genetic elements linked to soil survival in the *Lm* species.

Mots-Clés: Listeria monocytogenes, genomics, manure recovery, GWAS

3ème session (14h00-16h00, 22mai)

Assessing dependences among variables that describe environmental and productivity performances of dairy farms using statistical copula methods

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In the context of climate change, one major issue for farms is to increase their environmental performances without decreasing productivity too much, while ensuring food security and sufficient farm revenue. Farms emit several types of greenhouse gases (GHGs), whose multiple sources are influenced by many interacting factors on the farms and in their environments, which make farms and their dynamics more difficult to understand. This raises the issue of how to adequately model the multiple interactions of on-farm and environmental factors in order to improve understanding of farm performances. To this end, we investigated the ability of statistical methods based on copula models to capture complex dependence structures among multiple variables. The research was performed in several steps with an increasing degree of complexity. First, we analysed the correlation between two variables as a function of another explanatory variable. We then studied bivariate copulas as building blocks of tree structures to map multivariate dependences among more than three descriptive variables of farms. Finally, we explored copula-based regressions to explain outputs of farms, considering the type and shape of bivariate dependence structures. This presentation focuses on only the third part of the thesis research – copula-based regressions – to assess trade-offs between milk production and emissions as a function of management practices. The method was applied to a dataset of management practices, emissions and productivity of 2347 French dairy farms surveyed in 2013. We first fitted copula-based regressions to milk production per cow and total GHG emissions per livestock unit separately, and then assuming conditional dependence between them. Subsequently, we explored whole-farm mitigation scenarios to decrease GHG emissions without decreasing milk productivity too much. We then assessed the utility of capturing interactions among practices and outputs of farms in order to develop effective mitigation scenarios.

Mots-Clés: copula, based regression, complex dependence structure, dairy farm, environmental performance, milk production, whole, farm mitigation scenario

Contribution of porcine organoids to the study of molecular host-virus interactions of transmissible gastroenteritis virus

Ludivine Percevault * [1,2], Lionel Bigault [1,2], Maxime Berthaud [1], Aurélie Le Roux [1], Pierrick Lucas [1], Léon-Charles Tranchevent [1], Damien Le Gloahec [1], Gérald Le Diguerher [1], Frédéric Paboeuf [1], Daniel Dory [1], Yannick Blanchard [1], Maud Contrant [1]

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The cellular culture (*In Cellula*) and/or the animal experimentation (*In Vivo*) are the standard methods to study the host-virus interactions. However, they have methodological and ethical limitations respectively. Interestingly, the organoids, produced by the differentiation and self-organization of the stem cells, recapitulate the cellular diversity and the structural elements of the organs from which they are derived and represent an alternative to *In Cellula* and *In Vivo* methods. The Viral Genetic and Biosafety Unit has implemented the production of porcine intestinal organoids (PIO) and developed a protocol for infecting these organoids with porcine transmis- sible gastroenteritis (TGEV) alphacoronavirus. This TGEV/PIO system is currently used fora comparative study of host-virus interactions in the three systems: organoids, *In Vivo* and *In Cellula*.

Two TGEV strains were used for the experiments, one adapted to cell culture thanks to passages in series and the other poorly adapted. In detail, intestinal jejunum organoids and piglets were infected with the same viral genomic load (10E8 N gene copies), and Swine Testis (ST) cells withthe same MOI as the organoids. For each model, infection kinetics were performed and cellular RNAs harvested for RNAseq analysis of host-virus interactions.

Viral genomic quantification by RT qPCR showed different infection dynamics between the two viral strains in organoids, with a 2-log difference in production between the two strains in favor of the cultivable strain. This difference in dynamics was also observed by immunofluorescence targeting the viral N protein. On the other hand, In *vivo, RT* qPCR revealed an average of 10E10 N gene copies per jejunum sample for the circulating strain, compared with 10E6 for the cultured strain. A transcriptomic analysis is currently performed to compare host-virus interactions in the three experimental models.

Mots-Clés: Organoids, Virus, Host, virus interactions

Contribution of livestock to organic agriculture: modelling nitrogen flows at the national scale

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The European Green Deal aims to expand the area of organic agriculture (OA) to 25% of agricultural land by 2030, compared to 9.9% at present. Recent studies that proposed scenarios for expanding OA have shown that nitrogen would be a major limiting factor (Barbieri et al., 2021), as the only source of nitrogen available to OA is biological nitrogen fixation by legume crops. In all scenarios, the number of livestock decrease compared to the present number, but livestock are necessary due to their dual function as a source of animal protein for food security and as a vector of circularity of nitrogen flows to cropland (Billen et al., 2021). There is an interest in knowing the current state of nitrogen flows to OA at the national scale and highlighting the contribution of livestock to them to understand OA's capacity to develop within biophysical constraints.

We calibrated the ALPHA model (Chatzimpiros and Harchaoui, 2023) based on national statistics and surveyed data to assess current nitrogen flow metabolism in the national organic agri-food system of France, which has the largest area of OA in Europe.

The main inputs of nitrogen to OA in France were biological nitrogen fixation (51%), followed by atmospheric deposition (27%), conventional manure (11%) and imported feed (11%). The current population of organic livestock does not make it possible to meet the nitrogen needs of organic crops, so approximately 35% of the manure used to fertilize organic cropland came from conventional livestock. Imported feed was used mainly to meet the nutritional requirements of monogastric animals (38% of total feed nitrogen) and, to a lesser extent, ruminants (5%). These results highlight the degree to which OA depends on external nitrogen input, which may limit its development.

Mots-Clés: organic agriculture, livestock, fertilization, nitrogen balance

Sink/source driven metabolic acclimation to drought in winter oilseed rape leaves

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Winter Oilseed Rape (WOSR) is the second most cultivated oleaginous crop in the world, however its grain yield is threatened by climate change. Indeed, drought negatively impacts WOSR growth by reducing photosynthesis and accelerating senescence. These ultimate changes will have direct consequences on the sink/source relationships and metabolism of WOSR, which remain to be determined. To investigate these metabolic regulations, we applied 18 days of progressive water shortage and analyzed both sink and source leaves of WOSR during vegetative growth. At different time points, we evaluated both senescence and water status of WOSR leaves, combined with absolute quantifications of leaf primary metabolites (amino acids, organic acids, sugars, polyols). Overall, our findings indicate that older leaves undergo accelerated dehydration and senescence during drought, while sink leaves maintain their water content. Metabolitesin source leaves tend to be maintain or decrease with drought progression, leading to proline accumulation and activation of genes involved in remobilization through glutamine and sucrosein sink leaves. Sink leaves accumulate most metabolites, particularly proline, consequently with a decrease in glutamate. Sugar metabolism is also affected, with transient accumulation followed by reductions in starch, glucose, and fructose, suggesting activation of energetic metabolismand osmotic adjustment. However, no significant changes are observed in glutamine and sucrose content, despite gene activation, raising questions about remobilization efficiency in WOSR. Bothleaf ranks show limited regulation of TCA cycle enzymes or metabolite content, except for citrateand malate in leaf 11, suggesting carbon utilization for proline accumulation in this leaf rankand raising questions about its metabolic origin. Overall, these findings provide insight into the metabolic dynamics of key compounds in sink and source leaves during drought.

Mots-Clés: Drought, Brassica napus, Metabolomics, Sink/source relationships

Natural deep eutectic solvents (NaDES): a possible link to understand seed desiccation tolerance?

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One of the main challenges for crop production facing climate change is to identify the molecular, genetic and physiological determinants of plant tolerance to drought and desiccation. In desiccation-tolerant organisms, accumulation of compatible solutes forming hydrogen bonds is part of the mechanism that protects cells from damage caused by dehydration. Furthermore, Natural Deep eutectic solvents (NaDES) are mixtures formed between biobased hydrogen bond donor and acceptor compounds. The formation of these mixtures is characterized by a very marked decrease in their melting points creating liquid phases at low physiological temperature. These liquids mixtures are considered as an emerging class of green solvents especially for natural substances extraction. However, some NaDES ingredients are compatible solutes found in drought/desiccation-tolerant organisms, leading to scientific curiosity about their putative involvement in water stress and desiccation resistance. Despite the absence of any evidence of *in-vivo* NaDES formation, some studies suggest that they may replace water to maintain cellular machinery and protect certain macromolecules under high osmotic constraint. The aim of this work is to explore the reality of the existence of eutectic mixtures and their contribution to desiccation tolerance in developing oilseed rape (*Brassica napus* L.). We first identified potential NaDES ingredients in the metabolic composition of the seeds determined by LC/GC-MS and NMR technologies. The spatial distribution of these compounds in different compartments of the seed was also determined by DESI mass spectrometry imaging. Some new seed-based eutectic mixtures have been prepared and qualified for their molecular interactions by NMR and cold ionization mass spectrometry. Putative occurrence and physico-chemical properties of these eutectic mixtures have been addressed during different phases of seed maturation and desicca tion. At the moment, we are also prospecting, through in vitro studies, stability and activity of enzymes such as glutathione reductase and ascorbate peroxidase in these new biobased NaDES.

Regrouping affects cows’ social position at the drinker

Ellynn Nizzi *† [1], Ophelie Dhumez [1], Aline Le Croizier [1], Catherine Hurtaud [1], Anne Boudon [1]

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Social dominance between cows in the same group can affect their drinking behavior. In competition for water, some dominant cows may monopolize access to the drinker, limiting access for subordinates. Furthermore, regrouping of cows is a common practice on farms and can challenge established hierarchies and affect subordinates, resulting in poorer welfare and even suboptimal performance. This study aimed to investigate the effect of two regrouping situations on the established social hierarchy between cows at the watering place.
The study was conducted with 39 lactating Holstein cows. The experiment was divided into two periods. During the first ”*large group*” period, cows were housed altogether and then divided into 4 groups (”*small group*” period). Dominance scores were assigned to each cow based on replacement analysis. The group was then divided into 4 homogeneous groups. Each group consistedof 3 dominants, 4 intermediates, and 3 subordinates. Then, during the *small group* period, the position of the cows in new social categories per group was redetermined.

During the *large group* period, 524 replacements were recorded at the drinkers. During the *small group* period, 106, 116, 101, and 213 replacements were recorded at the drinkers in groups 1, 2, 3, and 4, respectively. Group 3 had the lowest number of replacements, associated with marked differences in dominance scores, allowing clear identification of dominants and subordinates. In contrast, Group 4 had the highest number of replacements and small differences in dominance scores, making it more difficult to discriminate between dominants and subordinates. We also found considerable variability in cows’ social position between the two periods.
Our results suggest that regrouping affects the social position of the cow and that the group may determine the time required to establish a stable hierarchy. These results highlight the importance of well-managed regrouping and well-monitored regrouped cows, especially subordinates.

Mots-Clés: social behavior, agonistic interaction, social scale, cattle

Novel application of phosphor thermometry to investigate the heat transfer in analog porous media

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The study of heat transport in porous media often neglects the impact of the structural heterogeneity of aquifers on their hydraulic and thermal properties. This work introduces a novel application of phosphor thermometry to porous media, aiming to closely examine the validity of existing thermal transfer models under diverse conditions, with a specific focus on the impact of strong Local Thermal Non-Equilibrium (LTNE) effects. The experimental approach involves monitoring the temperature-dependent luminescence properties of solid phosphor particles that are advected by the flow. Through the integration of light sources and cameras, quantitative spatialized and time-resolved measurement of the fluid's temperature field is achieved. Such a measurement is crucial for characterising coupled flow and heat transport processes at the pore scale in transparent analog porous media, overcoming interference limitations (point measurements, perturbing flow etc) associated with current experimental techniques.

Building upon the prior proof-of-concept with YAG:Cr3+, a thermographic phosphor with a temperature sensitivity exceeding 0.3%/K, we will present recent efforts focused on addressing porous structures with thermal conductivity akin to rock matrices, establishing a Péclet number contrast mirroring that of natural aquifers. The current experiments use a modulated light source, recording measurements at 5 kHz during continuous injection of an aqueous solution with different temperatures. The achieved precision, standing at 1.52±K so far, was determined at spatial and temporal resolutions of 600 μm and 0.5 seconds. The experimental results serve to assess the validity of existing models through parallel numerical analysis and simulations, replicating experimental conditions in terms of porosity, solid particle size, and Darcy flux. This work aims at leveraging phosphor thermometry as a robust tool towards using laboratory experiments for advancing knowledge on coupled flow and heat transport in permeable media.

Mots-Clés: phosphor thermometry, heat transport, porous media, LNTE, temperature, experimental technique, tracer, heat transfer, heat, aquifers, subsurface

La serpentinisation du Massif de Ronda (Espagne): interactions fluides-roches-déformations

Bastien Audran * [1], Philippe Boulvais [1], Yannick Branquet [1], Pierre Gautier [1], Marc Ulrich [2], Guillaume Raymond [3], Georges Beaudoin [3], Daniel Layton-Matthews [4], Maëlys Bévan [1], Evelyne Leduc [4], Rémi Coltat [5]

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La serpentinisation est un processus ubiquiste d'altération hydrothermale des roches ultramafiques. Les péridotites du Massif de Ronda forment le plus vaste affleurement de manteau sous-continental, à travers le monde. De nombreuses études ont été conduites sur la déformation à haute température et la pétrologie des roches mantelliques afin de mieux contraindrele(s) mécanisme(s) d'exhumation du massif. Néanmoins, peu de travaux ont traité en détail le processus d'altération hydrothermale, pourtant omniprésent à l'échelle du massif. Nos travaux visent à caractériser les interactions fluides-roches-déformations à l'origine de la serpentinisation des péridotites. Trois étapes de serpentinisation successives, dominées par la lizardite, ont été identifiées dans le Massif de Ronda. La première étape consiste en une serpentinisation pervasive pseudomorphique des péridotites, en proportion variable (_~15-_~90%). La seconde étape correspond à des couloirs serpentineux localisés, composés de bastite, chrysotile et de magnétite. La troisième étape est associée au développement d'une cataclasite à ciment et veine de serpentine et de magnétite ; contemporaine de l'infiltration de filon magmato-hydrothermal entre 23 et 19 Ma. L'analyse structurale des veines de serpentine syntectonique suggère une phase d'étirement horizontal multidirectionnel d'échelle régionale. L'analyse des isotopes stables de l'oxygène et de l'hydrogène montre une faible dispersion autour des valeurs _~+5.0‰ et _~-79‰, respectivement pour les 3 étapes de serpentinisation. Cela suggère que les conditions d'interactions fluides-roches seraient similaires ou bien que les signatures isotopiques de l'étape 1 seraient préservées au travers des étapes 2 et 3. Auquel cas l'origine du fluide serpentinisant de l'étape 1, en considérant un rapport fluide/roche dominé par le fluide entre 100 et 300° C, pourrait être d'origine crustale. Les couples isotopiques d18Oserpentine–d18Omagnétite indiquent une température de cristallisation autour de 180 ± 50 °C des serpentines de l'étape 3. La serpentinisation des péridotites de Ronda, largement peu étudié, se révèle être contemporaine de l'exhumationdu Massif.

Mots-Clés: Massif de Ronda, serpentinisation, interaction fluide roche déformation, isotopes stables, analyse structurale

Can isotope analysis trace the sources and pathways of plastic pollution in soils?

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Plastic production is still growing, reaching 400.3 Mt in 2022. Much of plastic waste ends up in the environment. Studies have demonstrated the presence of plastic waste in many environmental compartments, including soils. The main sources of plastics in agricultural soils are the use of plastic mulch and the soils amendments as sewage sludge and compost. Once in soils, plastics can undergo degradation processes, including UV-light degradation, mechanical breaking, chemical and biological processes. In soils, limited data on plastic degradation is available. Plastics are polymers made of monomers, of different types, the most common ones being polyethylene and polypropylene. To give them particular properties, additives are used for i.e. flame retardants, colorants, fillers, light stabilizers, etc. Some metals are used as additives, mainly within pigments. Plastics degrade into smaller particles such as microplastics (MPs) and nanoplastics (NPs). Both MPs and NPs can be transferred through different environmental reservoirs, and eventually interact with contaminants, including metals and organic molecules. Due to the potential harmful effect of these particles a better understanding of plastic fate in soils is needed. Everyday plastics of different types, shapes and colours were collected. Plastics were identified thanks to ATR-FTIR: they were mainly polyethylene and polypropylene. Major and trace elements were also measured and investigated in order identify new proxies of plastic origin and pathways in soils. In addition, the isotopic compositions of copper, lead and carbon were determined for some plastic samples to decipher the potential range of metal isotopic composition among the plastics, and identify possible isotopic fractionation during plastic degradation. The first results (i) present large range of both C, Cu, Pb isotopic compositions, and (ii) suggest that plastic degradation does not modify the Pb isotopic composition, which can be used as a source proxy.

Mots-Clés: plastic waste, soils, degradation, isotopes

Anévrisme tectonique ? Modélisation numérique couplée des interactions entre érosion et tectonique au sein des syntaxes himalayennes

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En contexte orogénique, la dynamique des reliefs résulte de la compétition constante entre l'activité tectonique et l'érosion. L'érosion de la surface d'un orogène peut aussi impacter les processus tectoniques, par le biais des déplacements de masse qu'elle engendre et ainsi modifier l'état des contraintes. Le massif du Nanga Parbat-Haramosh (NPHM), situé dans la syntaxe Ouest Himalayenne et culminant à plus de 8000 m (avec des reliefs locaux proches de 7000 m),en est un exemple frappant. Dans le cas du NPHM, le fleuve Indus incise le massif, avec destaux d'érosion moyen de 4 à 5 mm/an, enlevant alors une grande quantité de matière pouvant induire une modification significative de l'état des contraintes tectoniques, une remontée rapidede la croûte continentale et du manteau sous-jacent, induisant des taux de surrection élevés.Ces rétroactions, qui permettraient d'expliquer l'anomalie du relief du NPHM, ont été décritesà travers le modèle de l'anévrisme tectonique (Zeitler, 2001). Mais ce modèle conceptuel n'a pour l'instant pas été confronté à une validation par une approche de modélisation numérique. L'objectif de notre étude est donc de revisiter ce modèle de l'anévrisme tectonique en utilisantle modèle numérique thermomécanique MDOODZ en 2D possédant une surface libre et prenant en compte la rhéologie visco-élasto-plastique des roches. Les simulations réalisées, de dimensions150x500 km, intègrent une croûte continentale et un manteau lithosphérique, et sont forcéespar l'incision d'une vallée d'une largeur de 1km. Dans un premier temps, ces modèles se font sans raccourcissement tectonique, puis dans un second temps nous ajoutons un raccourcissement tectonique afin d'étudier son effet sur la formation du relief et le comprtement mécanique de la croûte.

Mots-Clés: Modélisation numérique, Anévrisme tectonique, Erosion, tectonique, Hymalaya

Évolution morphologique du fleuve Niger moyen au Quaternaire : de Tombouctou à Gao.

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Le fleuve Niger est un fleuve africain majeur qui coule vers le Nord-Est au travers du Mali avant de tourner brutalement vers le Sud-Est et de se jeter dans l'océan Atlantique au Nigeria. Il a formé un Delta interne fossile (cône alluvial de taille régionale), entre Ségou et Tombouctou. Dans la région de Tombouctou à Taoussa, le fleuve Niger parcourt plus de 300 km de l'Ouest vers l'Est et l'origine de ce tracé reste très peu connue.

Deux questions se posent : 1) l'origine du changement de la direction du fleuve Niger, 2) existait-il un système endoréique dont la capture aurait eu lieu au Quaternaire ?

Les modèles numériques de terrain utilisés pour les traitements de topographie ont permis de restituer la morphologie du Niger moyen à partir des cartes des paléo-rivières, des terrasses alluviales, des cordons littoraux et des dunes. Le tracé des profils en long des paléorivières ont été réalisés afin de déterminer le sens d'écoulement et les zone d'érosion par les rivières.

Les profils en long des rivières mettent en évidence la pente de Tombouctou vers Taoussa et du Nord du Mali vers le fleuve Niger. Les terrasses alluviales sont organisées en plusieurs étages. Les cordons littoraux constituent une limite entre le fleuve Niger et les dunes actuelles. Celles-ci sont datées de l'Holocène et orientées Nord-est Sud-ouest.

L'analyse morphologique et des paléodrainages mettent en évidence une vallée ancienne orientée Est-Ouest faiblement recreusée par le Niger actuel. Cette vallée a été temporairement remplis par un grand lac connecté à l'océan atlantique par la rivière Tilemsi. Ce lac présentait des niveaux différents selon les conditions climatiques qui ont contrôlé l'ennoiement plus ou moins important de cette vallée et potentiellement un endoréisme temporaire. Des dunes plus anciennes recoupées par des cordons littoraux sont recouvertes par des dunes actuelles, permettant de caler l'âge.

Mots-Clés: Fleuve Niger, morphologie, système endoréique, capture, paléotopographie, terrasse alluviale.

4ème session (17h00-18h00, 22mai)

Role of competition-exclusion for trace elements in the antifungal activity of lacticacid bacteria

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Dairy products are susceptible to contamination by spoilage fungi, leading to importantfood waste and economic losses. To prevent fungal spoilage, antifungal lactic acid bacteria (LAB) bioprotective cultures are used as an alternative to chemical preservatives and/or as a complementary hurdle technology. Among action mechanisms of these bioprotective cultures, competition-exclusion for trace elements is a newly discovered mechanism which plays an important role in their antifungal activity. In this context, the study aimed at investigating this mechanism in two known antifungal LAB strains, namely *Lactiplantibacillus plantarum* L244 and *Lacticaseibacillus rhamnosus* CIRM-BIA 1759, using a yogurt model. To do so, skimmed milk supplemented or not with a single trace element, including 6 metals (e.g. manganese) and 12 vitamins (e.g. vitamin B1), was fermented with a commercial yogurt starter culture as well as with or without one of the tested antifungal strains. Following fermentation, yogurts were artificially contaminated with different dairy spoilage fungi (*Penicillium biforme*, *Galactomyces geotrichum*, *Mucor racemosus* and *Yarrowia lipolytica*) and fungal growth was evaluated during storage at 10 C.°In yogurts containing the antifungal strains, manganese supplementation suppressed the growth inhibition of the selected *P. biforme* and *Y. lipolytica* isolates, suggesting that manganese depletion was involved in the antifungal activity. In parallel, scavenging of trace metal elements was determined using ICP-MS in cell-free lactoserum obtained from yogurts prepared with or without the antifungal LAB and stored for 7 days at 10 C. The ob°tained results showed that manganese concentrations were significantly lower in yogurt supplemented with antifungal LAB (2 ppb) as compared to the control yogurts (5 ppb), confirming that Mn was indeed scavengedby the antifungal strains. The role of competition-exclusion for Mn in the inhibition of a large diversity of spoilage fungi is currently under study to see whether this mechanism is generic among dairy spoilage fungi.

Mots-Clés: competition, exclusion, lactic acid bacteria, antifungal activity, manganese

SporeBiotech : Implémentation d'une technique iChip pour la récupération de spores bactériennes issues du sol

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La methode de l'iChip permet d'explorer la diversite microbienne en "apprivoisant" les microorganismes incultivables en laboratoire via une etape prealable de culture in situ. L'objectif de cette etude est d'optimiser la methode iChip afin de selectionner uniquement les spores bacteriennes issues de la terre.

Des echantillons de 15g de terre (sol cultive, sol non cultive, rivière) sont recuperes, tamises et dilues dans 30ml d'eau distillee filtree. Puis differentes sonications ont ete testees (60%,1min; 60%,3x1min; 100%,1min; 100%,2x1min; 100%3x1min) afin d'augmenter la recuperation des spores. Après sonication, 3 lavages à l'eau distillee filtree sont effectues suivi d'une centrifugation pour eliminer les debris de terre. Differents paramètres de centrifugation ont ete testes (1000g, 5min; 6300g, spin; 6300g 2min; 6300g, 5min ; 6300g, 10min). 1ml de surnageant est recupere et traite thermiquement (80 C,10 min) puis un denombrement par microscopie à contraste de phase est effectue. La suspension est ensuite diluee à 2 spores pour 90μl dans de la gelose SMS agar à 1%. Cette suspension permet d'ensemencer les plaques iChip (90μl par puit) et incubes 1 semaine, 3 semaines et 6 semaines dans leur environnement respectifs.

L'etude demontre que, pour une recuperation optimale des spores, une sonication 100% 2x1 min suivi de 3 lavages et d'une centrifugation 6300 g spin est adequat pour la recuperation des spores bacteriennes. La campagne de prelèvement iChip des trois sols a permis d'obtenir plus de 300 isolats. L'analyse des resultats après une semaine d'incubation a permis d'augmenter le taux de recuperation de bacteries de 38% comparee à la methode de culture en boite de Petri. Pour confirmer ces premières donnees, une identification des isolats est en cours via le sequençage de l'ARNr 16S. La capacite à sporuler sera egalement confirmee via l'utilisation de tests de sporulation en milieux liquides et/ou solides.

Mots-Clés: Bactéries sporulées, iChip, incultivable, biocontrôle

Role of milk serum proteins in the compressibility and rheological behavior of casein micelles dispersions

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Skim milk is a complex mixture of serum proteins, casein micelles (soft nanoparticles, natural aggregates of caseins), lactose, and minerals dispersed in water. In order to optimize milk processing (separation and concentration via filtration, evaporation, and spray-drying), knowing the properties of milk proteins dispersions is crucial. The current studies rarely account the role of milk serum proteins in the properties of milk protein dispersion. Therefore, the objective was to shed a light on the role of milk serum proteins in compressibility and rheological behavior of mixed dispersions of milk proteins, and protein-protein interactions.
Powders of serum proteins and casein micelles were dispersed in their natural environment: permeate of skim milk ultrafiltration. Compressibility (dependency of osmotic pressure on protein concentration) of mixed dispersions was measured via the osmotic compression technique. Rheological properties (shear thinning index, consistency coefficient and yield stress of suspensions, sol-gel transition concentration, storage and loss moduli of gels) were studied via the steady shear and oscillatory tests. All measurements were done at 20 °C in a wide range of total proteins concentration (0.025 – 0.400 g·g–1) at different values of serum proteins to caseins ratio: *R* = 0.07 – 10.0 g·g–1.

For a given casein concentration, increase of *R* in mixed milk proteins dispersions (a) increased the osmotic pressure (decreased the compressibility), (b) increased the apparent viscosity, (c) shifted the onset of non-Newtonian behavior to higher casein micelles concentration, (d) lowered the yield stress. Oscillation measurements revealed that the sol-gel transition point shifted to higher concentration as *R* increased. At the same time, the relative viscosity of mixed dispersions decreased and flowability improved as *R* increased.
It was concluded that relatively small serum proteins molecules (a) space larger casein micelle particles in the system and (b) lower micelle-micelle interaction (serving as a type of dispersant for casein micelles).

Mots-Clés: casein micelles, colloidal dispersion, serum proteins, membrane filtration, compressibility, rheology, viscosity, sol, gel format

Impact des dynamiques de température sur la sporulation de Bacillus subtilis BSB1

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La sporulation bactérienne permet à certaines bactéries de survivre dans des environnements hostiles. La température et le pH rencontrés lors de la sporulation influencent la vitesse de formation, la quantité et les propriétés des spores produites. Cependant, l'impact de ces facteurs en condition dynamique est très peu été étudié, ce qui est préjudiciable pour des applications dans le domaine environnemental ou industriel, notamment agroalimentaire. L'objectif de cette étude est d'étudier l'impact de la dynamique de température sur la sporulation de *Bacillus subtilis* BSB1. *Bacillus subtilis* BSB1 a été cultivée dans du milieu nutritif en bioréacteur. A intervalles réguliers, des échantillons ont été prélevés, dilués, puis ensemencés dans du milieu gélosé et incubés à 37◦C pendant 24h pour quantifier les cellules totales. Les spores ont été quantifiées après un traitement thermique à 80◦C pendant 10 min. Trois cinétiques de croissance/sporulation ont été réalisées : i) 37◦C, ii) 37◦C pendant 16h, puis à 10◦C, et iii) 37◦C pendant 16h, 10◦C pendant 24h suivi de 37◦C. Les cinétiques sont ensuite ajustées par un modèle pour caractériser la croissance et la sporulation.

Les résultats révèlent une influence significative de la température dynamique sur la sporulation. À 37 ◦C, deux phases distinctes lors de la sporulation ont été observées : une augmentation brusque suivie d'une phase de sporulation progressive. Pour les cinétiques dynamiques, une fois la température a été réduite à 10 ◦C, aucune nouvelle spore n'est apparue. Après 24h à 10 ◦C, le retour à 37 C a entraîné une trajectoire similaire à celle observée sous des conditions de température statique.

Ces résultats soulignent l'importance de tenir compte de ces variations afin de prévoir au mieux la sporulation. Cette approche pourrait être particulièrement utile dans l'industrie agroalimentaire, en ciblant spécifiquement des étapes critiques en termes de température et durée pendant le processus de transformation des aliments pour contrôler la sporulation.

Mots-Clés: Sporulation, dynamique de pH, facteurs environnementaux

5ème session (10h00-11h30, 23mai)

Towards selection of more durable resistance to Globodera pallida

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Breeding efforts have been made to create potato varieties resistant to *Globodera pallida*. Currently, most of these resistant varieties carry *GpaVvrn* Quantitative Trait Loci (QTL). However, the resistance conferred by this QTL has been overcome by nematode populations in controlled conditions and in the fields in some parts of Europe. The resistance variability observed in potato genotypes containing *GpaVvrn* may be attributed to additional genetic factors. Newgeneration genotyping technologies, like Genotyping-By-Sequencing (GBS), and advanced statistical models, such as the Multi-Locus Mixed Model (MLMM), have been shown to be effective in refining the detection of genomic variants associated with relevant traits and identifying molecular markers useful for breeding programs.
We developed a GWAS approach using MLMM on a panel of 249 advanced breeding clones which were phenotyped for resistance to *G. pallida* population (Chavornay population) and genotyped using GBS technology (G2PSol H2020 project) and SolCAP array. We successfully identified relevant molecular markers specifically linked to *GpaVvrn* loci. Additionally, we discovered another QTL on chromosome 9, previously unknown in our panel, which likely corresponds to *GpaVI* locus.

Subsequently, we identified sets of SNP markers linked to these two QTL and converted them for PACE (PCR Allele Competitive Extension) technology. The concordance between the SNP genotyping data obtained from GBS and PACE, as well as the genotype-phenotype association at each PACE marker set, were confirmed in a subset of the GWAS panel and in a validation panel. This study led to the development of novel SNP markers closely linked to *GpaVvrn* and *GpaVI*. The genetic regions associated with these markers are derived predominantly from a potato clone which is currently used by breeders. In conclusion/To conclude, this study provides useful tools for breeding potato varieties with a high level of resistance to *G. pallida* by pyramiding QTLs which likely improve durability of resistance.

Mots-Clés: S.tuberosum, G.pallida, GWAS, Resistance, GBS, MLMM, PACE

Understanding Insect Presence in Strawberry Greenhouses : Relative Contributions of Cultural Practices and Environmental Factors

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Despite growing awareness of the damaging effects of conventional agricultural practices on human health and the environment, agriculture remains largely dependent on chemical inputs, raising major concerns about its sustainability. Therefore, it is necessary to explore alternatives capable of preserving yields while minimizing environmental impact. In this context, biological control of pests has been developed in greenhouse crops, generally based on periodic releases of natural enemies. However, the effectiveness of this method is questioned due to the low capacity of natural enemies to regulate pests compared to beneficial insects naturally occurring in greenhouses. For these cropping systems, little research has been conducted on the agronomic and environmental factors that could be manipulated to promote these populations of beneficial native insects and reduce pests. So the thesis aims to (i) evaluate the structure and compositionof arthropod communities in greenhouses, as well as the major spatiotemporal factors that may affect them, and (ii) identify local factors related to practices and the environment that couldalso play a role in their variation.We hypothesized that there is regional variability in insect community composition, mainly due to climatic features and influenced by seasonality, andthat intensive production systems exhibit lower insect diversity than less disturbed systems. In addition, edges and the surrounding landscape are considered major factors influencing arthropod communities in greenhouses. To validate these hypotheses, samples are conducted nationally in strawberry crops in greenhouses in France. The occurrences of major arthropods in crops are examined, and practices and the surrounding environment are characterized. We hope to identify the key factors influencing greenhouses colonization and thus identify risk situations and provide recommendations for more sustainable crop management.

Mots-Clés: Conservation biological control, landscape context, protected cultivation, strawberry crops, natural enemies, insect pests

Plant consumption by aphid-predating coccinellids revealed by DNA metabarcoding.

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Ecological intensification promotes the ecosystem service of biological pest control, notably through the maintenance of natural habitats at the local level, especially when natural enemy habitats are widespread and of good quality at the landscape level. Coccinellids are major natural enemies of the aphid *Eriosoma lanigerum* (Hausmann) (Aphididae) that cause significant damage in apple orchards worldwide. These predators also consume nectar, honeydew, pollen and fruit. Consequently, the availability of these resources on surrounding landscapes may enhance pest control, as in several species they form a significant part of their optimal diet. Establishing trophic interactions between coccinellids, plant resources and aphid prey on different landscape scenarios could help to design strategies for ecological intensification in agricultural systems. DNA metabarcoding allows the detection of trophic interactions in small samples and has proven to be very useful for the study of arthropods diet. We assessed plant consumption by the most abundant aphidophagous coccinellids in apple orchards, along a gradient of compositional heterogeneity at the landscape level. The abundance of *E. lanigerum* and their natural enemies were monitored in 19 apple orchards in central Chile, during 2 seasons. Adult coccinellids were captured directly on the trees, labeled and frozen to later extract DNA from their intestine contents. DNA metabarcoding, using ITS2 region, was carried out to obtain the taxonomic identityof the plants consumed by the coccinellids. Our results show a frequent and diverse consumption of plants by all captured coccinellid species. The three most frequently detected plant species were *Broussonetia papyrifera*, *Ambrosia artemisiifolia* and *Galega officinalis,* common plants found and flowering in the surrounding landscape at the time of collection. The results of this research contribute to identifying the mechanisms by which ecological intensification improves pest reduction, enabling the design of pest-resistant agricultural systems.

Mots-Clés: Biological control, Coccinellids, Aphids, Orchards, Trophic interactions, DNA metabarcoding

Genomic and phenomic predictions help capture low-effect alleles promoting seed germination in oilseed rape in addition to QTL analyses

Marianne Laurencon * [1], Julie Legrix [1], Marie Hélène Wagner [2], Didier Demilly [2], Cécile Baron [1], Sophie Rolland [1], Sylvie Ducournau [2], Anne Laperche† [1], Nathalie Nesi [1]

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Oilseed rape faces many challenges, especially at the beginning of its developmental cycle. Achieving rapid and uniform seed germination could help to ensure a successful establishment, and therefore enabling the crop to compete with weeds and tolerate stresses during the earli-est developmental stages. The polygenic nature of seed germination was highlighted in several studies, and more knowledge is needed about low- to moderate-effect underlying loci in order to enhance seed germination effectively by improving the genetic background and incorporat- ing favorable alleles. A total of 17 QTL were detected for seed germination-related traits, for which the favorable alleles often corresponded to the most frequent alleles in the panel. Genomic and phenomic predictions methods provided moderate to high predictive abilities, demonstrating the ability to capture small additive and non-additive effects for seed germination. This studyalso showed that phenomic prediction better estimated breeding values than genomic predic-tion. Finally, as the predictive ability of phenomic prediction was less influenced by the genetic structure of the panel, it is worth using this prediction method to characterize genetic resources, particularly with a view to design prebreeding populations.

Mots-Clés: Germination, Brassica napus, GWAS, NIRS, Genomic Prediction, Phenomic Prediction

Compounds involved in the different steps of short-distance host plant acceptance in a Brassica specialist

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In phytophagous insects, host plant selection is comprised of two main stages: 1) host plant location and 2) host plant acceptance. The latter stage occurs upon contact and involves surface and internal plant compounds. These compounds, which include primary and specialized metabolites as well as nutrients, are known to play a crucial role in stimulating or deterring key insect behaviors such as feeding and oviposition. The presence or absence of these contact compounds largely determines whether a plant is accepted by an insect. Understanding how specific plant metabolites may affect acceptance is therefore crucial for comprehending plant-insect interactions and their co-evolutionary dynamics, but also for developing innovative strategies for insect pest management based on biologically derived molecules, i.e., antifeedants applied as foliar sprays. The cabbage stem flea beetle, *Psylliodes chrysocephala*, is an insect specialized on the Brassicaceae family that causes significant damage to oilseed rape (OSR) in Europe. The recent reduction in the number of insecticides authorized for its control, together with the widespread occurrence of resistance phenomena to these substances, call for the development of alternative management strategies. To identify compounds that may deter feeding in *P. chrysocephala* lar- vae and adults, we developed a bio-guided fractionation approach involving Brassicaceae plants known for their low level of acceptability compared to OSR. As part of this approach, feeding tests involving foliar extracts are carried out on an artificial substrate to determine the effectof different fractions of the plant metabolome. At this stage, this approach has enabled us to highlight different acceptance mechanisms depending on the insect's stage of development. In- deed, foliar extracts of a same plant were found to have conflicting effects on adults and larvae. Such results demonstrate the difficulty of identifying molecules that could be used as part of an integrative strategy targeting both stages.

Mots-Clés: Chemical ecology, Pest management, Plant insect interactions

Biodiversity-based cropping systems and their long-term agro-environnemental consequences in the context of climate change: a 50-year simulation in western France

Arnaud Delbaere * 1

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Biodiversity-based cropping systems offer a promising solution to the interlinked challenges of food security, environmental sustainability and climate resilience. Crop diversification, by increasing managed and associated biodiversity, harnesses biological and physico-chemical processes that provide benefits over time. However, considering the temporal provision of these benefits in these systems is complicated by the prevailing short-term decision-making in agriculture. Comprehensive, long-term studies require methodological adaptations and the integration of transdisciplinary approaches. Crop models, such as STICS, are useful tools for simulating the complex biogeochemical processes that occur in these systems, thus facilitating a nuanced understanding of their dynamics. This study aims to simulate the long-term functioning of a biodiversity-based cropping system based on high crop diversity, developed in collaboration with agricultural experts.

Using the STICS model, the simulations focus on assessing the impacts on soil nitrogen, leaching and organic carbon stocks. Historical climate data from 1970 to 2020 and IPCC projections under different climate scenarios (4.5 and 8.5) provide the necessary climatic context for the simulations. The diversified cropping system studied was co-designed through participatory workshops with local stakeholders, resulting in highly diversified systems with 16 different species over a six-year cycle. To provide a framework for comparison, reference systems such as the maize-wheat-nitrate-fixing crops commonly found in the Brittany were also modelled. Over a simulation period of 50 years, the dynamics of nitrogen, leaching and organic carbon were analysed under current climate conditions and previously cited IPCC scenarios. Statistical analyses using R software were performed to evaluate the evolution of these variables and to identify temporal patterns.

Preliminary results suggest that under current climate conditions, the diversified system conserves more soil organic carbon than the non-diversified reference system, albeit with higher NO3 levels but increased leaching events.

Mots-Clés: Agroecology, Crop diversification, Long term, Cropping system, Crop model, STICS model, Co, design

Posters

Surface colonization in an O2 gradient - insights from microfluidic experiments

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Bacterial growth and development remains a major topic in research, both for its applications, such as biofouling, clinical research and bioremediation, and for the insight into the fundamental behavior of microbes. Bacteria experience environments with a wide array of characteristics in nature, such as surfaces with different wettabilities, chemical gradients and detrimental toxins which often stress them and affect colonization and growth. Hurdles such as these are most often present in the subsurface, where the heterogeneity of its structure provides ample opportunities for various stressful conditions. These effects and how they relate to both colony formation and biofilm growth have not been thoroughly investigated. Presently, this study aimed to better understand how heterogeneous environments affect early stage colonization and growth of Pseudomonas putida in an oxygen gradient and with two different surface wettabilities. Microfluidics and fluorescent microscopy were used to capture the growth in real time. Our experiments show that Pseudomonas putida microcolony formation is enhanced on hydrophilic surfaces, and that this effect is reversed for the flagella deficient mutant. We have also shown that a gradient of oxygen improves surface colonization when compared to homogeneous conditions. These results imply that bacterial persistence and available appendages significantly affect surface colonization of Pseudomonas putida. Future studies could investigate more closely the exact dynamicsof early stage colonization on the single cell level to better explain how appendages and nutrient limitation force surface attachment.

Viral diversity in freshwater: microviridae as potential bioindicators

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The European directive for bathing water quality only requires the measurement of 2 bacterial indicators of human faecal contamination: E. coli and intestinal enterococci. However, those two bioindicators do not represent the potential presence of all microorganisms such as viruses. Viruses represent the major biological entity on Earth, being estimated at 10^2 in freshwater. Even if viruses are known for their pathogenicity, most of these aquatic viruses are bacteriophages, of which less than 1% have been identified until now. Understanding their diversity and dynamicsis crucial to highlight their implications within an ecosystem such as the Seine River. In thisway, viral DNA from raw water was extracted in several ways and then sequenced using IlluminaMiSeq technology. The raw sequencing data were cleaned and the contigs assembled by SPAdes and MetaviralSPAdes for comparison. The depth, quality and contamination of the viromewere satisfactory. In total, over 90% of the taxa found in the raw water of the Seine were bacteriophages. Of these, the 2 main groups were the caudoviricetes class and the microviridae family. Microviridae were characterised based on their phylogenetic marker: the coding sequence for the VP1 capsid protein. The sequences of new *gokushovirinae*, a subgroup of microviridae ubiquitous in the environment, were annotated and could represent an indicator of the viral dynamics of river water.

Mots-Clés: Virome, Microviridae, Seine, Bioinformatics, Bioindicator

Two-Phase Flow in Geological Rough Fractures to Decipher CO2 Residual Trapping in Fractured Aquifers: An Analog Experimental Study

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Research on multiphase flow in porous media has been very extensive in the last 40 years, at both the pore and the continuum scales. However, a comprehensive understanding of the phenomenology of two-phase flow in geological fractures, encompassing flow regimes (capillary number Ca), fluid properties (viscosity ratio M), and the geometry (aperture fields), remains elusive. We investigate residual trapping of CO2 in fractured reservoirs at the fracture scale, exploring the complex interplay between fracture surface roughness and the displacement of fluid-fluid interfaces. Our approach explores the phenomenology of two-phase flow in fractures, systematically taking into meticulous consideration the fluid properties, flow conditions, and fracture geometry. To this aim, we have developed a transparent fracture flow cell with self- affine rough-walled surfaces and precisely-controlled mean aperture, which can be varied. The fracture wall geometry is generated from numerical models that are consistent with the well- known stochastic geometric properties of geological fractures. A camera allows recording the dynamics of the fluid phases' spatial distribution within the fracture plane. The displacement patterns are characterized as functions of Ca, M, the density difference of the fluids, and the fracture's geometrical parameters. We thus aim to characterize the amount of supercritical CO2 trapped in fractured aquifers as a function of those controlling parameters.

Mots-Clés: Multiphase flow, Fractured reservoirs, CO2 storage, Capillary, Rough surface

Plastic pollution in terrestrial environments : environmental dynamics and ecotoxicity

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The main source of plastic pollution in agricultural soils is the spreading of contaminated compost from household waste.
Once in the soil, these plastics get fragmented into smaller particles, microplastics (MPs) and nanoplastics (NPs) due to degradation and aging. This transformation alters their surface and their physicochemical properties.

Moreover, the smaller the plastic fragments, the more mobile they are in the soil.

Because of their presence in the soil, MPs can have an impact on the structure of the soil. For example, by filling the soil pores, reducing the connectivity between soil pores, or the overall stability of soil aggregates, and even modifying soil permeability.

Plastics are manufactured with additives, such as metals or substances recognized as endocrine disruptors. Once the plastic is in the ground, these additives can be released during the degradation in the environment.

Plastic fragments in the soil can also interact with other soil contaminants, due to their large specific surface area, their strong hydrophobicity, and their alteration due to aging in the soil. The contaminants with which plastics could interact are, for example, trace metals, antibioticsor even persistent organic pollutants present in the soil. MPs and NPs can therefore increase ecotoxicological risks, by increasing the risk of co-exposure of organisms living in the soil.

To this day, only a few studies quantified MPs in the soil, and none quantified NPs. Research on this topic is still at its infancy.
In this poster, I will first expose the current knowledge on plastic pollution in agricultural soils. Then I will explain the research that I will conduct during my thesis, in order to understand the dynamics and ecotoxicity of the fragments of plastics in terrestrial environments.

Mots-Clés: Ecotoxicology, Plastic pollution, Microplastics, Nanoplastics, Soils

Aged or senescent: How ageing is affecting life history traits and cold tolerance in summer-acclimated vs winter-acclimated Drosophila suzukii

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An insect population is a highly dynamical structure which individually-based biological processes, from birth to death, progress through time. Almost all species show clear signs of ageing across diverse traits including physiology, body structure and molecular pathways. This process called senescence, is commonly associated with a decline in biological function linkedto chronological age. Drosophila suzukii also known as the Spotted Wing Drosophila (SWD)is a major fruitfly pest that lay eggs in soft fruits while still on plants. Overwintering strate-gies in SWD remain unclear and every year, females that develop in early winter are suspectedto sustain under harsh cold conditions and to revive populations in spring. Winter is a very challenging season with low temperature and food availability, implying biological energy real- locations. Cold-acclimation is known to enhance lifespan and cold tolerance at the expense of reproductive capacities. *Drosophila suzukii* displays a large panel of phenotypical and physiolog- ical plastic adaptations to sustain across seasonal temperature variations, yet nothing is known about how winter-acclimation affect life history traits through ageing under spring conditions.The goal of this study is to elucidate the evolution of senescence in summer-acclimated *vs* winter-acclimated males and females and to detangle how evolve starvation resistance and reproductive capacity, through ageing, when brought back to artificial spring conditions. Our results show poor signs of senescence in 90 days old and great capacities in resisting to starvation in winter- acclimated flies compared to summer-acclimated. Moreover, winter-acclimated females show a constant, non-affected by age, number of produced offsprings that remains similar as middle-agedsummer-aclcimated. Yet, it results that winter affects more sperm production than oogenesis as overwintering males show great signs of fertility loss. We conclude that overwintering females, previously cold-acclimated, have capacities to survive 3 months under suboptimal conditions and to contribute in populations outbreaks in the warming season.

In vitro and in vivo characterizations in turkey and mouse of a recent A(H1N2) influenza virus in France originating from swine

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Since February 2020, surveillance of influenza A viruses in swine in France allowed the detection of a new A(H1N2) influenza virus, deriving from a swine lineage which has been initially described in Denmark in 2004. Starting from April 2020, this virus was also detected in 20 breeding turkey farms in western France, which reported egg-drop symptoms, and also in human in September 2021. In the current "One Health" context, considering the crossing of the species barrier by this virus, it is important to evaluate the virulence of this A(H1N2) virus detectedin turkeys and its ability to infect mammals in return. The aim of this study was to character-ize and to compare three A(H1N2) viruses, one as a reference swine virus and two others from turkeys, on avian and mammal models.

A(H1N2) complete viral genomes from turkeys were compared with swine A(H1N2) influenza viruses detected in the same geographical locations, at a similar date. Phylogenetic analyses allowed us to select two turkey viruses: one resulting from swine-to-turkey transmission and one that appears to have circulated within turkey farms. These two viruses plus a representative strain of swine parental virus, were characterized *in vitro* by determining replication kinetics on different cell types belonging to different species. *In vivo* experimental trials were carried out on breeding turkeys and on mice to determine and compare the virulence as well as the tissue tropism of these viruses.

Viruses identified in turkeys were directly related to the swine A(H1N2) genotype. Refined phylogenetic analyses suggested at least three independent transmissions from swine to turkey and a potential circulation between turkey farms. The *in vitro* comparisons of virulence and tropism of the three strains are currently underway. *In vivo* challenges showed that these viruses induce clinical signs in mice but not in turkeys.

Mots-Clés: influenza, barrière d'espèce, dinde, mammifère

Exposure to nanoplastics affects the development and behavior of the fruit fly Drosophila melanogaster

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Global plastic production is rising, now reaching 400 million metric tons per year and becoming a major environmental concern. Plastic waste alteration leads to the accumulation of macro- and meso-fragments which progressively degrade into micro- and nanoplastics in the environment. Numerous studies reported the toxicity of micro- and nanoplastics in aquatic organisms. While terrestrial plastic contamination can be 4 to 23 times higher in comparison to aquatic environments, implications for terrestrial species remains less understood. To fill this knowledge gap, our study investigates the effects of nanoplastics (NP) ingestion on the fitness, development, metabolism and locomotor activity of *Drosophila melanogaster* females. The insects were continuously exposed, from eggs to adults, to a mix of commercial polystyrene NP (20, 80 and 200 nm) at two concentrations (1.05 μg/g and 525 μg/g of food) and compared their control counterparts. Our results show that NP exposure slightly affect fitness and mobility of *D. melanogaster*. The presence of NP may impact the nutritional quality of food, potentially explaining the observed hyperactivity in the flies-a heightened foraging activity aimed at promoting food intake. How- ever, NP did not significantly affect the physiology of the flies. More studies are needed to fully understand the effects of NP on insects.

Mots-Clés: nanotoxicity, emergence rate, mobility, microcalorimetry

Microbial diversity associated with endemic and alien plant species in contrasted fellfield environments in Kerguelen Islands

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Plants evolve in environments rich in micro-organisms that colonize all of their organs: the rhizosphere (fraction of the soil under the influence of the roots), roots, stems, leaves, flowers, seeds, etc. These micro-organisms are transmitted both vertically from generation to generation and recruited horizontally from the pool of micro-organisms in the environment (e.g., air, soil, insects). These microbiomes contribute to functions that are crucial for the life and survival ofthe plant: nitrogen fixation, resistance to pathogens, resistance to abiotic stress. In this way, a plant can be considered as a 'holobiont', made up of the plant and the myriad micro-organisms that interact with it and govern its ability to respond to biotic or abiotic stresses, rather than an autonomous living being. The sub-Antarctic Kerguelen Islands are an ideal open-air laboratoryto study these plant-microbiome interactions because of the relative simplicity of its ecosystems (home to a low diversity of native flowering plant species) due to its geographical isolation. In these islands, fellfields represent one of the ecosystems least affected by anthropic activities and biological invasions, making them an ideal system in which to investigate patterns of biodiversity in intact ecosystems. We hypothesize that, just like plants, the special geographical context ofthe Kerguelen Islands has led to low α-diversity in phyto-microbiomes, resulting in plant species (both endemic and introduced) having less micro-organism species to choose from. We also expect climatic variability along altitudinal gradients to be responsible for a specific patternin microbial β-diversity (*i.e.* lower diversity at higher altitudes). To test these hypotheses,we investigated changes in microbial communities in soil and roots of three plant species, *Poa kerguelensis*, *Pringlea antiscorbutica* and *Poa annua*, along altitudinal transects at three locations in the Kerguelen Islands.

Mots-Clés: Kerguelen, subantarctic, phytomicrobiome, bacteria, fungi, holobiont

Mitigation of greenhouse gas and ammoniac emissions during sewage sludge composting: a statistical analysis

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To follow the ambitions of Europe for the sustainable environmental transition the best practices must be favored for the management of organic wastes. Special attention has to be paid to the reduction of their environmental impact. In this context, a statistical analysis of literature data has been performed to assess the level of greenhouse gas (N2O and CH4) and ammonia (NH3) emissions during composting of sewage sludge, to identify key physicochemical parameters of the initial mixture that might affect gaseous emissions. A corpus was created and analyzed for the following parameters: sewage sludge and composted mixture initial physicochemical parameters (pH, dry matter, total carbon, total nitrogen, C/N), the dry mass ratio of sewage sludge to bulking agent and the duration of composting. The average cumulative values for CH4, N2O and NH3 emissions were 1.37± 2.71 gC.kg-1, 0.13±0.17 gN.kg-1 and 2.23±2.79 gN.kg-1 respectively. The standard deviations show a great variability in the gas emissions, probably due to the variability of the experimental conditions. Few significant and strong correlations have been identified between composting parameters and gas emissions (p-value < 0.05). CH4 emissions were positively correlated to pH of sewage sludge, N2O emissions were positively correlated to the ratio of sewage sludge to bulking agent and to the duration of composting and NH3 emissions were positively correlated to the pH and total nitrogen of the composted mixture. Despite the few significant correlations found, the results highlight that the physicochemical parameters regularly used to characterize composted substrates are not sufficient to explain all of the emissions variability. In order to better understand gas emissions, this study suggests to broaden the range of studied parameters. For example, a systematic and in-depth analysis of the impact of the bulking agent characteristics should be investigated.

Mots-Clés: composting, methane, nitrous oxide, ammonia, sewage sludge

Climate change and fertility

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The impact of climate change on fertility has been investigated across a wide range of taxa, revealing that fertility limits provide more accurate predictions of species distributions than survival limits. However, several questions remain controversial or overlooked, including which sex is more affected and the natural potential for recovery. Hermaphrodites represent a unique model to investigate these questions, as a single individual possess both sexual reproductive systems, circumventing potential cofounding effects present in separate-sex species. However, most studies conducted on hermaphrodites predominantly focus on overall fertility impact rather than sex-specific effects. While Macrostomum lignano, a simultaneous hermaphroditic marine flatworm, stands as a potential candidate, we needed further characterization of abiotic stressors affecting its fertility and potential interactive effects between these stressors. In this study, we assigned worms to control conditions (20◦C; salinity 32‰) or to range of high temperature (35, 37.5, 40 €) and/or salinity (48, 64 ‰) for 8 hours, with one or two shocks to test for the impact of stressor frequency. Following the shock, worms were returned to baseline conditions with a partner to measure their fertility (i.e. number of larvae) and their potential for recovery over time. Worms exposed to heat/salinity shocks are likely to have a decreased fertility compared to control worms. We also expect that the severity of this decline will increase with more intense, frequent and combined stressors. We expect the worms to be able to recover the loss in fertility when returned to baseline conditions after the shock, but their potential for recovery might be negatively correlated with the intensity, frequency and number of stressors. This study establishes the baseline for future work on the short- and long-term effects of climate change on hermaphrodite fertility.

Mots-Clés: global warming, fertility, heatwave, salinity, phenotypic plasticity

Do native and invasive macroinvertebrates differ in key functional traits?

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Many hypotheses on the success of invasive species and the invasibility of ecosystems concern the availability of niche space that the invader can occupy. In order to fill unfilled niche space, or displace native species from their occupied niches, invasive species can benefit from having unique functional traits relative to their recipient communities. Diverse, species rich communities are thought to better fill this functional space and be more resistant to invaders, while simple, species poor communities are predicted to be more susceptible to invasion and to severe effects. Island ecosystems are often made up of species poor communities and are therefore are considered to be some of the most vulnerable to invasion – especially those in remote locations with little historical influence from other regions. Sub-Antarctic islands, like the Crozet and Kerguelen archipelagos, are some such systems. We sampled arthropod communities and functional traits at eight different locations across these two archipelagos to examine how different the traits of invasive species are to their host communities using multiple methods to test the hypothesis that successful non-native species are functionally unique relative to their recipient communities. We discuss our results in the context of residence time and ecological consequences of polar invaders.

Mots-Clés: functional traits, invasive species, polar, insect invasion, niche

Changes in length-at-first return of a sea trout 1 (Salmo trutta) population in northern France

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The resilience of sea trout populations is increasingly concerning, with evidence of major demographic changes in some populations. Based on trapping data and related scale collection, we analysed long-term changes in body length of a sea trout population in the Bresle River, France. From 1984-2022, the length of first-time returning individuals decreased by 1.73 27 mm.year-1 (SD = 0.08), which resulted in the loss of c. 12.3% of mean body length. This decrease results from a decrease in the age at first return, with a gradual loss of the oldest individuals and an increase in the proportion of the youngest. Timing of the return migration advanced drastically, although shorter sea sojourn had little influence on body length. We found little evidence of a decrease in length-at-age, to the exception of the oldest age class, suggesting that growth conditions at sea might not have deteriorated greatly during the study period.

Mots-Clés: age structure, body length, life history, marine growth, migration, sea trout

Evaluation of carbon sequestration scenarios in soils and vegetation applied on metropolitan public policies : application on Rennes Métropole territory

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Among the levers for mitigating climate change, additional carbon sequestration in vegetation and soils is considered one of the most significant, since these two components constitute the main carbon reservoirs in terrestrial ecosystems (Jacobson et al., 2000; IPCC 2022). This lever can be applied to natural and agricultural environments, as well as to urbanized areas, but the means of action for maintaining and increasing the associated stocks differ according to the environments considered, their initial state and local conditions. This work is part of efforts to combat climate change in the Rennes metropolitan area, by identifying carbon sequestration opportunities in urban and peri-urban green spaces. Urban soils have only recently begun to be studied, so very little data exists. One part of this work will therefore focus on estimating the carbon stock in different urban uses (urban meadow, tree park, tree line, forest, natural meadow) through in-situ measurements across the whole of Rennes metropolis. The second part of the project focuses on estimating the carbon stock in urban tree vegetation, using photogrammetric data and physical measurements of tree spaces such as diameter and height to assess above-ground biomass and deduce the carbon stock within them. These two parts will then enable us to assess the dynamics of organic carbon (stabilization/mineralization) between now and 2050, according to scenarios co-constructed with metropolitan stakeholders, combining spatial planning with associated practices.

Mots-Clés: Urban, Carbon, Soil, Vegetation, Digital soil map, Public planning policy

A chromosomal inversion forms parallel clinesof frequency between America and Europe in Coelopa frigida: An adaptation to thermal latitudinal variation?

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Recent advances in sequencing technologies have shown that chromosomal inversions, by forming blocks of linked genes, play an important role in intra-specific diversity. However, the mechanisms that control the spatio-temporal dynamics of these polymorphic supergenes and the evolution of their sequence remain poorly described.

The seaweed fly *Coelopa frigida* is a diptera species distributed on the northern coasts of the Atlantic Ocean. Its genome includes several large polymorphic inversions, one of which showsa latitudinal gradient of frequencies along the American East Coast. This marked distribution pattern suggests a divergent selection of the haplotypes and that the inversion may be involved in adaptation to different thermal contexts.

After confirming the presence of the inversion in European populations, we demonstrated the conservation of its sequence between continents and validated in Europe the efficiency of the molecular marker used to genotype the inversion. Subsequently, we demonstrated that the frequency of the inversion forms two parallel latitudinal clines between America and Europe, providing a strong argument in favor of adaptation to the same environmental gradient.

An experimental approach was then set up, aiming to test the direct link between the inversion and phenotypes associated with the thermal stress response. First, traits involved in cold resistance (supercooling point, chill coma recovery time) were measured in populations sampled at different latitudes. In a second step, different life history traits (development time, viability, fecundity, longevity) were measured at several temperatures in order to test the role of the inversion on fitness variation.

The results already obtained provide an empirical case of parallel distribution of an inversion polymorphism, supporting the prediction that this type of genetic architecture is possibly important in repeated adaptation along environmental gradients.

Mots-Clés: Evolutionnary ecology, Chromosomal inversion, Parallelism, Thermobiology

Mise au point d'outils pour l'étude protéomique de la protéine ORF3 du virus de la diarrhée épidémique porcine

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L'épidémie de SARS-CoV-2, troisième émergence à coronavirus chez l'homme ces 20 dernières années, a dramatiquement remis en lumière l'importance du potentiel zoonotique des *Coronaviridae*. Répartis en 4 genres, Alpha, Beta, Delta et Gamma, les deux premiers sont retrouvés parmi les mammifères et les deux derniers, essentiellement chez les volailles. Les coronavirus partagent une organisation génomique commune avec les deux premiers tiers du génome codant pour le complexe de réplication, suivit par les séquences codantes des protéines structurales. Suivant les genres, une ou plusieurs séquences codant pour des protéines dites accessoires sont intercalées entre les gènes structuraux. A l'exception des Deltacoronavirus, au moins une ORF accessoire est nichée entre les gènes Spicule et Enveloppe. Le produit de l'une de ces ORF, situé entreles séquences codantes des protéine S et E, majoritairement nommée ORF3 et présente chez les Alpha et une majorité de Beta coronavirus, serait directement impliquée dans la virulence et la régulation du cycle infectieux.

La protéine codée par l'ORF3 est essentiellement caractérisée chez les betacoronavirus SARS-CoV-1 et 2. Afin d'étendre nos connaissances sur ces protéines accessoires, nos travaux por- tent sur la protéine ORF3 de l'alphacoronavirus de la diarrhée épidémique porcine (PEDV).Notre équipe développe les outils moléculaires adéquats pour la recherche de ses partenaires pro- téiques, ainsi qu'un protocole d'infection sur organoïdes intestinaux de porcs, modèle cellulaire plus représentatif des conditions réelles d'infection que la culture sur cellule Vero.

La recherche et l'identification des interactants, seront réalisés par spectrométrie de masse, grâce à un système d'expression et de co-immunoprécipitation de la protéine d'intérêt. Un outil de génétique inverse, en cours de finalisation, permettra de valider nos résultats dans un contexte infectieux, et de d'étendre la caractérisation de cette protéine à des souches difficilement cultivables.

Mots-Clés: Virologie, protéomique, relation hôte, pathogène

Assessing the Ground Deformation in the Okavango Graben (Botswana): The Role of Floods and Tectonic Activity

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The Okavango Graben (Botswana) is an active half-graben located at the southwestern terminus of the East African Rift System and represents an outstanding opportunity to understand the early stages of rift opening (1). Global Navigation Satellite System (GNSS) data indicate normal to dextral strike-slip displacements of 1 mm per year (2). However, seasonal rains and floods in the graben generate a cyclic subsidence of up to 2 cm, hindering the interpretation of the tectonic signal (3). GNSS studies provide punctual data on displacements. Thus, to quantify the deformation field over the Okavango Graben, we analyze Interferometric Synthetic Aperture Radar data (InSAR) provided by the FLATSIM service (4). The InSAR analysis follows three steps. (i) Interferometric coherence (a quality indicator of InSAR signals) is used to map flood extents in the Okavango Graben over four years, based on the significant coherence decrease induced by water arrival. (ii) Based on flood extents and water inflows in the Delta, we calculate the hydrologic loading on the lithosphere and derive the resultant flexural elastic response. (iii) The theoretical flexural response to the hydrologic loading is then compared to ground displacement timeseries measured with GNSS and InSAR. Considering the seasonal signals, our objective is to unravel the tectonic from the hydrologic signal in the Okavango Graben.

Mots-Clés: Okavango, Tectonics, Remote Sensing, InSAR, Flood, Rift, Botswana

Pathogen's competitive interactions in a multiple-infection context

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In natura, plants are subjected to multiple biotic stresses including interactions with other organisms (microbes, other plants, insects, mammals) that may have beneficial or detrimental effects. Globally, plants are submitted to these multiple interactions sequentially or concomitantly. Coexistence implies the mutual exploitation of at least one shared limited resource necessary for development and reproduction by at least two individuals, often leading to the establishment of competitive interactions. Ecological theories like niche exclusion, 'tragedy of the commons' and the virulence/transmission trade-off, are useful approaches but experimental observation of the process is too rare and could invalidate general theories. The type of interaction might depend on spatial or temporal distance of parasite species but also on their trophic regime. This inter- action can change life history traits of the competitors (incubation, latency, growth rate) andthen alter their fitness. This study aims to evaluate how sequential arrival and spatial distribu-tion of co-occurrent pathogens modify pathogens development and disease severity. To answer this question, co-infections of a winter pea cultivar plantlets (Escrime) was performed by using three different fungal pathogens: *Peyronellaea pinodes, Ascochyta pisi, and Colletotrichum* sp. Spatial distribution of pathogens was studied by inoculating the two pathogens on two different nodes, whereas sequential arrival of pathogens was studied by delaying the inoculation of the second pathogen 3 or 7 days. Preliminary results show that coinfection led to a change in leaf colonization. Analysis of all the data are in process, and will be presented during the seminar.

Mots-Clés: pathogens interaction, plants multiple infections, coinfection

Vegetated Discharge Areas for Plastic Debris Removal: Deciphering of their Deposition on Various Substrates

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Wastewater treatment plant effluent plays a significant role in the discharge of plastic debris into the oceans. Conventional treatment systems retain between 70% and 99% of microplastics and nanoplastics (Carr et al., 2016). Developments known as vegetated discharge areas (VDAs) could improve this performance through terminal refinement. These zones made up of vegetated basins have several vocations, including filtering residual micropollutants (Boutin et Prost-Boucle, 2012). There is currently no data available on the capacity of these natural filters to retain plastic debris.

This work is a preliminary study, evaluating the performance of two substrates in retaining microplastics. An inorganic substrate conventionally used in ZRVs was tested, along with an organic substrate derived from a waste recycling process. Despite their recognized adsorption properties and nutrient-rich composition, organic substrates are rarely, if ever, used in ZRVs. For the sake of environmental representativeness, the microplastics used were obtained from plastic waste collected on a beach near the North Atlantic gyre. After mechanical fragmentation in the laboratory, microscopic analysis confirms that microplastics are polydispersed in size and polymorphic.

The experiments were carried out in columns, where a flow of microplastics passed through the substrates following two modes. Pulses injections are carried out to compare the substrates retaining performances. Continuous injections are also performed to test the saturation of the substrates. Various parameters are tested, such as the volume of substrate in the column andthe flow rate of the microplastics stream. In parallel, a reliable and robust method for quan- tifying microplastics is being developed using pyrolysis-gas chromatography-mass spectrometry. The substrates selected showed very high microplastic retention performance (70% on average), particularly for the organic substrate (up to 90%). The same experiments were carried out with potassium bromide as a non-reactive tracer, to further characterize the filtering properties of the substrates.

Mots-Clés: Wastewater, Microplastics, Nanoplastics, Depollution, Pyrolyse, GC/MS

Bioenergetic disponibility and potential biomass in a fractured subsurface

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The continental subsurface is likely one of the largest reservoir of microbial biomass on Earth, predominantly comprising autotrophic microorganisms that obtain energy from redox reactions, thereby influencing geochemical cycles. But despite its significance, accurately quantifying and studying the distribution of this deep biomass remains largely uncertain. Here, we have devel- oped a novel thermodynamic modeling approach applied to in-situ geochemical data to estimate the biomass potentially supported in the subsurface. Initially, field data are integrated with thermodynamic calculations to identify and quantify the main energy sources that can support chemolithoautotrophic microorganisms. Our model is based on the estimation of the thermodynamic chemical disequilibrium in the subsurface with the Gibbs free energy from redox reactions. These calculations determine the prevailing microbial metabolism in the subsurface, as well as the amount of bioavailable energy sustaining the microbial community, whether for maintenance or growth purpose. By combining this bioavailable energy derived from geochemical conditions with the energy requirements for microbial maintenance and growth, we estimate the potential biomass supported by this microbial community. This model is applied along various subsurface flow paths to examine the spatial structuring of potential biomass at depth. The results reveal the presence of an energy front at depth where a maximum of potential biomass is observed. This work contributes to a deeper understanding of the microbial life in the subsurface by providing an estimation of the potential biomass based on in-situ geochemical conditions and thermodynamic principles.

Mots-Clés: deep subsurface, thermodynamic, biomass, redox reactions, Gibbs energy

Immune transcriptomic profile in adult female pigs: dominance status has more influence than environmental enrichment

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Assessing animals' affective states is crucial for evaluating the welfare of farm animals, yet practical tools are lacking. In this study, we tested whether the peripheral blood mononuclear cell (PBMC) transcriptome can be used to show variations in sows' affective state. To do this, we compared animals whose emotional states were assumed to differ due to their lives in more or less enriched environments and to their different dominance statuses. Sows (n = 71) were housed in conventional (C) or enriched (E) environments from gestation day 0 (G0) until three weeks before farrowing (G105), after which they were transferred to conventional maternity rooms. From G99 to G103, behavioral analyses were conducted, and dominance hierarchy was evaluated. Blood samples were collected for PBMC transcriptome analysis on G98 and on lactation day 12 (L12). While EE affected only a few genes (31 differentially expressed genes (DEGs) in G98, dominance status significantly impacted the PBMC transcriptome (449 DEGs in G98). Compared with subordinate sows (SUB), dominant (DOM) sows exhibited upregulated inflammatory genes, downregulated B-cell activation, and upregulated plasma cell function. In groups of sows, dominance status is partly related to sow parity, and we compared the effect of dominance with that of parity. Some similar DEGs emerged when comparing different parity animals (high-parity (HP) vs. low-parity (LP)), indicating that some effects of dominance on the transcriptome were in fact more due to age or reproductive cycles than to dominance itself. EE and dominance effects appeared relatively short-term, as DEG numbers decreased on L12 (four DEGs for E vs. C, 25 for DOM vs. SUB). Both EE and dominance status influenced sows' affective states; however, dominance status exerted a more pronounced influence on sows' PBMC transcriptome than did environmental enrichment. In particular, dominance status modulated genes associated with B cells and plasma cell functions.

Mots-Clés: Peripheral blood mononuclear cell, pig, gestation, lactation, social environment, envi-

Effect of Fractures in Bedrock on River Erosion: An Experimental Approach

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Continental landscapes evolve under the action of climate and tectonics, in particular through erosion processes. Erosion by rivers is driven by abrasion and plucking processes. Abrasion polishes bedrock through sediment friction, while plucking removes blocks from the substrate. These erosion mechanisms and erosion rates are influenced by several factors. Among them, bedrock fractures seem to have a strong control. However, the effect of fracture geometry on bedrock river erosion has not been systematically investigated.

Our study investigates the impact of bedrock fractures on erosion mechanisms and rates using an experimental approach. Our setup consists of an erosion mill designed to simulate the erosion of a fractured bedrock in an active river. To simulate our fractured substrates, we use 3D printed plastic (BVOH) artificial fractures placed in concrete disks (17 cm diameter). We use water and gravel and a motorised propeller to simulate the flow of a river and cause erosion ofthe disks. To track the evolution of the disk's topography over time, we photograph the diskwith 4 fixed cameras every 2 minutes of erosion (or 4). This method of structure-from-motion photogrammetry allows us to record the disks erosion dynamics at high resolution. Thirty-six experiments with varying fracture spacings, dips and azimuths were conducted to investigate the effect of fracture geometry.

Our results demonstrate the significant influence of fracture network density on erosion processes. Low density networks promote abrasion dominance, whereas high density networks facilitate plucking episodes. Fracture dip induces asymmetric erosion, favoring plucking on one side and abrasion on the other, with plucking clusters aligned with the flow direction. At the disk scale, abrasion maintains a steady erosion rate, while plucking introduces spatial and temporal variability. These results highlight the importance of incorporating fracture parameters into fluvial erosion models.

Mots-Clés: Experimental, Erosion, Fractures, R

A new approach of Lewontin's Paradox in flowering plants

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Understanding the variation in genetic diversity across species is crucial for conservation efforts, genetic, and agronomical studies. In theory, genetic diversity is positively correlated with population size. However, Lewontin's Paradox, first described in 1974, challenges this notion by highlighting that while there is considerable variation in population size among species, genetic diversity variance appears to be consistently lower, often by an order of magnitude. This paradox persists today, posing challenges to explaining the lack of correlation between population size and genetic diversity. While some hypotheses attribute this discrepancy to the impact of selection on reducing diversity, even at neutral sites, here we want to explore the demographic effects.

In fact, actual genetic diversity, with the addition of other evolutionary forces, is the result of genetic drift (represented by demography) that occurred during millions of generations since the divergence of the population. One hypothesis could be that the current level of genetic drift that populations undergo (referred to as short-term effective size) may not be directly correlated with the total amount of genetic drift experienced by a population (better represented by long-term effective size). This discrepancy between short and long-term effective size could explain in part why we observe such a low correlation between population size and genetic diversity. Also, recent studies have demonstrated that life history traits (LHT) serve as proxies for genetic diversity. One hypothesis could be that LHT are responsible for the dynamics of demography over time, explaining in part this paradox.

To test that hypothesis, I will build an integrative dataset with information about populations' genotypes, LHT, and species ranges for multiple plant species. With that large database, I will then be able to compare demographic dynamics between species by taking into account their LHT but also their species range.

Mots-Clés: Génomique des populations, Bioinformatique, Angiospermes, Génomique

Modelling and monitoring ammonia and greenhouse gas fluxes from grazed grasslands

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The bidirectional exchange of ammonia (NH3) between the biosphere and the atmosphere in grazed ecosystems is influenced by complex interactions among soil, vegetation, animals, and atmospheric conditions. This process involves NH3 exchange through plant stomata/cuticles, and soil surface reactions following urea hydrolysis, influenced by varying environmental and management conditions. Modelling these interactions presents challenges due to their high temporal variability, and is often represented using resistance models. To address this, we adapted the Generation of Ammonia from Grazing (GAG) model, originally developed for a UK grassland, to a grazed grassland affiliated with the Integrated Carbon Observation System (ICOS) at Méjussaume Le Rheu. The site has been monitoring atmospheric fluxes of NH3, carbon dioxide (CO2), water (H2O), nitrous oxide (N2O), methane (CH4), and supplementary ecological data (soil, canopy height, leaf area index (LAI), animal presence, and meteorology) since 2020.

Initial applications of the GAG model revealed its inability to accurately predict grazing-induced changes in atmospheric and plant resistances, resulting in inaccurate NH3 simulation. To im- prove this, we incorporated dynamic LAI and canopy height measurements. Furthermore, we updated the equations associated with these processes improving the representation of plant re- sistances and atmospheric interactions in the model, thus reducing the negative flux biases.
Our ongoing work involves refining soil processes to address the positive post-grazing NH3 flux biases and conducting sensitivity analysis of the GAG model. In the future, we plan to integrate the GAG model with the Basic Grassland (BASGRA_N) model well known for simulating grassland dynamics, to enhance flux simulation for future scenarios. Extensive data collection planned for 2024 will support validation and integration of both models. Through this integrated approach, we aim to advance our understanding of NH3 emissions and their impact on nitrogen and carbon cycling in grazed grasslands, capturing the complexity of the soil-plant-animal-atmosphere system

Mots-Clés: Ammonia grazing grasslands ecology modelling biogeochemistry

From myth to reality: the dawn of fungal carbohydrate SulfoTransferases approaches!

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Sulfation is a fundamental process for a plethora of organisms. It plays a key role in bioactivity of numerous molecules, ranging from small specialized metabolites to large polysaccharide molecules. Glycosaminoglycans perfectly illustrate the importance of sulfation in animals. These are highly sulfated polysaccharides, generally coupled to proteins, involved in both organism development (e.g., cell differentiation) and maintenance (e.g., hemostasis). Sulfation defects can lead to serious or even lethal symptoms (1). The sulfation process requires specificenzymes called SulfoTransferases (STs), which transfer a sulfate (-SO3) group from a donor tovarious hydroxyl (-OH) and amine (-NH2) groups. Nowadays, several families of STs have been defined according to functional and structural characteristics (e.g., Pfam motif) and are widely used in databases (e.g., UniProt). Carbohydrate SulfoTransferases (CSTs) are present inseveral of these families (e.g., St1 and G3St families) and are defined according to many criteriasuch as acceptor substrate specificity (glycosaminoglycans, polysaccharides, glycoproteins or glycolipids), linkage of sulfate (-O or –N) and structural considerations (i.e sulfate position) (2). CSTs have been widely characterized in metazoans and predicted in algae. Surprisingly, no CST has yet been described in the fungal kingdom. However, Fungi represent probably oneof the most diverse group of eukaryotes, with up to 3.8 million species estimated . These organisms have a long and complex evolutionary history, marked by numerous events such as early terrestrial colonization. They have colonized most ecological niches, adapting and developing a variety of lifestyles such as saprobe,symbiont or parasite. By analyzing fungal genomes, we have revealed numerous putative genes encoding CSTs. To strengthen this discovery, phylogenetic analysis and biochemical characterizations ofthe recombinant protein were conducted. Our discovery provides the first insight of fungal CSTs and raises many questions, such as the biological role of these enzymes or their evolutionary origin.

Mots-Clés: Biochemical characterization, fungal evolution, Early Diverging Fungi

Evaluation of the dynamics and impact of nanomagnetites (Fe3O4) on lettuce (Lactuca sativa) in a context of cadmium contaminated soil

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Soil contamination by toxic metals such as cadmium (Cd) is a major issue for our society. For soil remediation, several approaches have been tested. Due to their physicochemical properties and their nanometric size, nanomaterials have been receiving substantial growing attention. Among these nanoparticles, nanomagnetites (NPs-Fe) have great potential for soil remediation. Evaluating the impact and fate of these nanoparticles therefore seems essential. This research aimed to evaluate the effect of nanomagnetites on lettuce (Latuca sativa) and their role as an adjuvant to improve the phytoextraction efficiency of Cd in soil. In this context, nanomagnetites were applied (1.2 g.kg-1 soil) to a Cd contaminated soil (20 mg.kg-1 soil). Four conditions were tested: control, Cd, NPs-Fe and Cd+NPs-Fe. The plants were harvested, weighed, freeze-dried and analysed by ICP-MS after 46 days of exposure to determine metal concentrations. Photosynthetic yield measurements were taken before harvesting and the dynamics of nanomagnetites from soil to plants were studied by measurement of magnetic susceptibility.

The results show a negative impact of Cd and NPs-Fe on lettuce development, with a reduction in biomass of around 50% for each of the treatments alone and over 70% for the Cd+NPs-Fe treatment. While the analyses do not show any difference in Fe content, a significant difference is observed for plant Cd content, which is roughly two times higher under NPs-Fe treatments compared to nanomagnetites-untreated conditions. Concerning the photosynthetic yield, a significant difference is only observed between control and Cd+NPs-Fe. Finally, a magnetic signal is detected in plants with NPs-Fe treatments, indicating the presence of NPs-Fe in plant tissues.
This study showed that at the concentrations tested, nanomagnetites have a negative impact on the development of lettuce, but significantly increase the plant Cd concentration. It could be interesting to study different concentrations of NPs-Fe to complete this work.

Mots-Clés: Iron nanoparticles, Magnetite, Pollutants, Plant, Ecotoxicity, Remediation

Use of virulent Globodera pallida lineages obtained from experimental evolution to reveal candidate regions for the adaptation to potato resistances

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The use of alternative methods to control populations of cyst nematodes has accelerated since the banning of the most efficient nematicides. The pest-resistant plant varieties have also become an indispensable solution to this problem. However, this solution is not without risk, since it has been shown that some nematode populations can overcome these resistances. Inorder to understand the mechanisms of adaptation of the nematode *Globodera pallida* to potato resistances, a combination of phenotypic and genomic approaches has been initiated on lineages obtained from experimental evolutions. The objectives are to identify the genetic basis of *G. pallida* adaptation to (1) different resistance QTLs and (2) to a combination of QTLs. This work involved phenotyping to characterize the level of virulence of selected lineages on potato genotypes carrying different resistance factors. These initial results illustrate the overcome of resistances by virulent lineages after 10 generations. The nematode lineages were then sequenced and analyzed using a GenomeScan approach. This analysis highlighted genomic regions under selection and potentially involved in the adaptation mechanism. First results showed for instance that genes involved in the adaptation to resistant QTLs from different wild Solanaceae are locatedin distinct genomic regions. These results will have an impact on the design of efficient and sustainable management strategies, independent of the use of controversial chemicals.

Mots-Clés: Globodera pallida, adaptation, virulence, phenotyping, GenomeScan

Effects of fish assemblage and practices in freshwater fishpond polyculture among fish farmers: a trophic web modeling approach

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The growing demand for aquaculture products requires a focus on both increasing productivity and the sustainability of the fish farming system. Polyculture is attractive because it can (i) utilize feed waste, (ii) enhance the recycling of nutrients within the system, which (iii) optimizes the efficiency of resource use and (iv) reduces environmental impacts. In France, the fish farming industry is stagnating and needs to be revitalised. The aim of this study was to investigate effects of species associations and feeding practices on the performance of the farming system in terms of productivity, resource use efficiency and recycling. The study was carried out on 11 ponds in 3 regions during the production season in 2021 and 2022. The environmental and production parameters of the ponds were collected for implementation in the trophic relationship model using the "Ecopath" software. The ponds showed variations in primary and secondary productivity. The majority of the ponds, whether fed or not, had a macroinvertebrate ecotrophic efficiency close to 1. This indicates that the fish yield of the ponds could be limited by their productivity. Some of the fed ponds do not optimize the feed intake (feed EE < 0.3), which makes it necessary to reduce it. A recycling parameter, the Finn cycling index, was positively correlated with the efficiency of use of detritus and phytoplankton (R2 = 0.9). The Net fish yield was positively correlated with the Finn cycle index (R2 = 0.6). The Ecopath model is somewhat limited in its consideration of trophic compartments. Nevertheless, the results could be used as a tool for improving fish assemblages in fish farms.

Mots-Clés: polyculture, fishpond, modeling, Ecopath, efficiency, recycling

Déterminer la contribution du microbiote sur la santé des plantes

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Les plantes vivent en interaction avec divers micro-organismes (*i.e.* bactéries, champignons, protistes et oomycètes). Cette communauté d'organismes est appelée microbiote et se trouve sur tous les compartiments de la plante. Ils peuvent être pathogènes, bénéfiques ou considérés comme neutres pour celle-ci. Les micro-organismes bénéfiques permettent une meilleure tolérance au stress abiotiques et/ou biotiques. Une manipulation du microbiote végétal permettra un meilleur contrôle des maladies, une meilleure efficacité de l'utilisation des nutriments par la plante etainsi augmenter la productivité agricole de manière durable en réduisant les intrants chimiques. Cette étude, s'intéresse aux stress biotiques. Les mécanismes impliqués pour la réduction de ce stress incluent des interactions microbiote-ravageur (compétition pour la place et les ressources et production de molécules antimicrobiennes) et la modulation de l'immunité de la plante. L'objectif de cette étude est d'identifier des membres du microbiote fongique qui modulent la santé de la plante par des interactions microbiote-ravageur sur deux pathosystèmes différents : *Rhizoctonia solanii* infectant *Brassica napus* et *Fusarium graminearum* infectant *Triticum aestivum*. Pour cela, des souches fongiques ont été isolées par culturomique de différents champs en France de telle manière que la plus grande diversité soit isolée. Ainsi, leur effet sur le pathogène peutêtre testé. Plusieurs tests vont être effectués pour identifier les souches d'intérêt : (1) des tests d'antagonisme (mise en contact du pathogène avec les champignons isolés) permettant d'identifier les souches en compétition pour la place et les ressources et ceux qui produisent des molécules antimicrobiennes. (2) La réalisation de profils métaboliques permettant d'identifier les sucres consommés par les différentes souches. Cela contribuera à expliquer pour quelles ressources les souches sont en compétition avec le pathogène. (3) Des tests sur plantes pour exclure les souches pathogènes pour la plante. Les premiers résultats du test (1) pourront être présentés lors de ces journées scientifiques.

Mots-Clés: Microbiote, Culturomique, Fungi, Rhizoctonia solanii, Brassica napus, Fusarium graminearum, Triticum aestivum, Santé des plantes

Impacts of heat and salinity stress on inbreeding depression in a free-living hermaphrodite flatworm

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Climate change presents an urgent threat to the survival of many organisms, including through its impact on increasing the frequency and intensity of stressful events. Inbred individuals tend to be more sensitive to stress compared to their outbred counterparts. In otherwords, stress amplifies the magnitude of inbreeding depression. Generally, the more stressful an environment, the greater the increase in inbreeding depression. However, the exact nature of this relationship, and whether it varies depending on the stressor, remains understudied. We plan to conduct a study using *Macrostomum hystrix*, a free-living hermaphrodite flatworm, as our modelorganism. We will expose both outbred and inbred *M. hystrix* individuals at different life stages to varying levels of salinity and heat stress and measure their fitness. *M. hystrix* individuals can self-fertilize (or self) their gametes, and those from primarily outcrossing populations can utilize selfing as a reproductive assurance strategy when outcrossing opportunities are limited. However, selfing can impose severe fitness costs due to inbreeding depression, as it is the strongest form of inbreeding. Understanding how environmental conditions change these costs is crucial because inbreeding depression levels play a vital role in many evolutionary processes like extinction risk, purging of inbreeding depression and mating systems evolution.

Mots-Clés: Inbreeding depression, Climate change, Stress, Mating systems, Self fertilization, Hermaphrodites, Heatwaves, Salinity, Flatworms

How do urban heat islands and vegetation structure shape communities of grassland-dwelling spiders in Rennes ?

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As urbanization progresses worldwide, alterations in habitat and temperature are significant threats for biodiversity. However, understanding their respective impacts on animal community composition is complex due to their correlated nature. In this study, we examined the relationships between taxonomic and functional compositions of spider communities and distinct habitat and temperature gradients, comparing landscape-level factors such as urbanization andthe Urban Heat Island (UHI) effect to local variables including vegetation height, cover, and near-ground temperature. We collected 20,499 spiders representing 137 species across 36 grasslandsin Rennes. In contrast to rural areas, urban sites exhibited characteristics such as short vegetation and intensified UHI, harboring species-poor communities dominated by small, thermophilic species. We found that increased UHI intensity and local habitat simplification, characterized by reduced vegetation complexity, were associated with declines in larger, heat-sensitive species. These findings underscore the predominant role of urban warming, rather than changes in land cover, as a selective force shaping urban arthropod communities. Additionally, our results suggest that landscape-scale UHI, rather than local temperature, acts as a filter for species basedon their functional traits, highlighting UHI's role as a thermal barrier that selects species basedon their ability to tolerate urban heat conditions. Finally, to counteract biotic homogenization,we advocate for the implementation of diverse habitat structures at the local scale within urban green infrastructure.

Mots-Clés: Araneae, arthropod, climate warming, community composition, environmental filter, functional composition, functional traits, urbanization

Contextualization of life cycle assessment methodology to eco-design localized protection systems by airflow in food industries

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Airborne contamination in food production poses significant risks, including the transmission of harmful microorganisms such as E. coli and Listeria, leading to foodborne illnesses and spoilage. Although traditional HVAC systems and UV irradiation are employed for environmental control, their effectiveness is often not monitored, and the food industry has been slow to innovate. In contrast, cleanroom technology, which meticulously controls airborne particles, presents a promising alternative. Although initially expensive and encouraging an uncomfortable working environment, cleanrooms create a safer environment for food production, reducing the need for additives and potentially extending shelf life. Nevertheless, the high energy demands associated with such systems raise sustainability concerns. This study proposes a life cycle assessment (LCA) of three clean air supply systems designed for food production environments, evaluating their environmental impacts. By analyzing scenarios ranging from general ventilation to localized protection systems, the LCA aims to pinpoint the environmental hot spots and compare the sustainability of these systems. The LCA results show two main findings: energy consumption's dominance in the systems' environmental impact and the cleanroom's high environmental cost compared to localized protection systems and general ventilation. However, the study's reliance on a single functional unit," clean, conditioned air," without considering factors like food quality or work environment improvements, is a critical limitation. It risks presenting an oversimplified view that might misguide stakeholders, lacking a comprehensive evaluation. An investigation of the socio-technical landscape of the clean air supply system by multi-level perspective methodology. This study highlights the need for a comprehensive decision-making tool beyond environmental impacts, encompassing multifunctionality, worker welfare, and total ownership costs. The findings advocate for the evolution of LCA into a holistic tool that assesses not only environmental but also social and economic dimensions, thus directing businesses towards more sustainable and responsible practices.