



Le projet France2030 HARMi « Harnessing Microbiomes for Sustainable Development » a été financé pour une période de 10 ans. Un troisième appel à projets est lancé pour financer 15 projets de recherche, avec une enveloppe totale de 1 815 k€ allouée par HARMi. Un formulaire unique est disponible pour la rédaction des dossiers. Les projets peuvent être déposés par tout chercheur titulaire appartenant à l'un des organismes partenaires en région Bourgogne Franche-Comté (BFC).

Scientifiquement, le projet HARMi est décliné suivant **quatre Work Packages** détaillés en annexe :

WP1. Comprendre l'écologie et la dynamique spatio-temporelle des communautés microbiennes

WP2. Déchiffrer les interactions microbiote-hôte

WP3. Gérer les communautés microbiennes pour améliorer la durabilité et la fourniture de services

WP4. Développer les biotechnologies microbiennes

La priorité sera accordée aux projets de recherche contribuant à un ou plusieurs de ces WPs **en développant des actions innovantes et interdisciplinaires entre laboratoires.**

Types de financements

Quatre types de projets seront financés. **Chacun des 4 types de projets doit présenter un caractère structurant en région BFC en impliquant au minimum deux unités de recherche en BFC.**

▪ Les **projets starters** – Avec un budget de 30 k€ maximum, ils sont ouverts au financement de fonctionnement incluant des gratifications pour 2 stages de Master. **La durée d'utilisation des crédits est de 2 ans.**

▪ Les **projets transversaux** – Avec un budget de 185 k€ maximum, ils sont ouverts au financement de fonctionnement (pour un montant total maximum de 65 k€) et de salaire (2 ans de postdoc ou 3 ans de thèse). Ce type de projet doit inclure le recrutement d'un doctorant ou d'un post-doctorant. **La durée d'utilisation des crédits est de 2 à 4 ans.**

▪ Les **projets internationaux** – Avec un budget de 210 k€ maximum, ils sont ouverts au financement de fonctionnement (pour un montant total maximum de 90 k€) et de salaire (2 ans de postdoc ou 3 ans de thèse). Ce type de projet doit inclure une collaboration à l'étranger qui devra se matérialiser par un séjour du CDD recruté dans le laboratoire étranger (au minimum 1 mois) et l'accueil du PI étranger pour une durée de deux semaines à un mois. Le recrutement d'un doctorant ou d'un post-doctorant est obligatoire. **La durée d'utilisation des crédits est de 2 à 4 ans.**

▪ Les **projets industriels** – Avec un budget par HARMi de 150 k€ maximum en complément du financement du partenariat industriel, ils sont ouverts au financement de fonctionnement et de salaire (postdoc, CDD ou thèse). Le partenariat industriel cofinance impérativement au minimum de 50 % du montant du projet. 30% de l'apport obligatoire industriel doit se faire en numéraire versé à HARMi et le reste peut être apporté en nature¹. Le montant du contrat d'accompagnement d'une thèse CIFRE pourra être comptabilisé dans l'apport en numéraire de l'entreprise concernée (hors subvention ANRT). Les co-financements des entreprises pourront bénéficier des dispositifs de crédits d'impôts liés à la Recherche (CIR et CICO). **La durée maximum d'utilisation des crédits est de 4 ans.**

¹ Par exemple, dans le cas d'un co-financement HARMi de 150 k€, le co-financement minimal par le partenariat industriel est de 150 k€, dont 30% minimum en numéraire (45 k€) et le reste peut être complété en nature (jusqu'à 105 k€).

L'enveloppe totale financée par HARMi pour ce troisième appel à projets est de 1 815 k€ soit environ :

- 180 k€ pour 6 projets starters
- 555 k€ pour 3 projets transversaux
- 630 k€ pour 3 projets internationaux
- 450 k€ pour 3 projets industriels

Modalités de dépôt des projets

Un **formulaire** est disponible à cette adresse : <https://www.umlp.fr/harmi>

Un dossier **unique** et en **anglais**, respectant la **nomenclature HARMi_2026_[Project type]_[ACRONYM]_[PI lastname].pdf**, sera envoyé en **format PDF** à HARMi@umlp.fr

Date limite : 09 octobre 2026 à 13h.

L'adresse électronique du déposant sera utilisée pour tout contact ultérieur. Un courriel d'accusé de réception sera émis vers le déposant après la soumission du document. Le projet doit être visé par les directeur(ice)s des unités.

Critères d'évaluation

La recevabilité des projets sera d'abord examinée par le *Management and Monitoring Team* (MMT). **Pour être recevables, les projets devront être en adéquation avec les objectifs d'HARMi (cf annexe) et impliquer des chercheurs affiliés à des établissements partenaires d'HARMi (e.g. UMLP, UBE, CNRS, INRAE, L'Institut Agro Dijon, CHUB, CHUD) et appartenant au minimum à deux unités de recherche en BFC pour tous les types de financements : starters, transversaux, internationaux et industriels.** Le MMT évaluera également l'éligibilité des projets sur la base de leur caractère structurant en BFC (en particulier les ETP permanents impliqués dans les différents laboratoires/équipes hors personnel technique et personnel de plateforme ET la description du « **partnership** » dans le formulaire de réponse).

Les projets retenus seront ensuite envoyés pour évaluation à des experts extérieurs puis classés par l'*International Advisory Board* (IAB) d'HARMi sur la base des évaluations.

Les principaux critères guidant l'évaluation sont :

- le caractère interdisciplinaire/transdisciplinaire et structurant en région BFC, la qualité scientifique et la complémentarité des expertises
- l'originalité, l'ambition du projet en lien avec les objectifs d'HARMi et sa faisabilité
- l'impact scientifique, économique ou sociétal, la pérennisation éventuelle des activités au-delà de l'échéance du projet.

Un même chercheur ne peut être coordinateur que d'un seul projet financé par HARMi.

Suivi des projets

Les projets lauréats seront suivis durant leur déroulement par le MMT, et les porteurs de projets s'engagent à fournir les indicateurs qui leur seront demandés annuellement. Concernant les publications scientifiques issues des projets, les lauréat(es) s'engagent (i) à déposer le texte intégral des manuscrits acceptés dans l'archive HAL au plus tard à la date de publication, (ii) à mettre en oeuvre les principes FAIR (*Findable, Accessible, Interoperable, Reusable*) dans la gestion des données de recherche et (iii) à mentionner le soutien et la référence du projet selon l'exemple :

"This research was funded by the HARMi (HARnessing Microbiomes for sustainable development) project (ANR-21-EXES-0014) under the France 2030 program managed by the ANR"

Seules les publications et les communications scientifiques ayant mentionné cette référence pourront être comptabilisées dans les résultats du projet.

Calendrier de l'appel à projets

- 30 Avril 2026 : Diffusion de l'appel à projets
- **09 octobre 2026, 13h** : **Date limite de soumission des projets**
- Mars 2027 : Classement des projets par l'IAB
- Avril 2027 : Annonce des résultats
- Avril-Septembre 2027 : Finalisation administrative et financière des projets

Contacts

Pour toute question sur cet appel à projets, vous pouvez contacter les gestionnaires du projet : harmi@umlp.fr

Annexe

WP1: Understanding the ecology and the spatio-temporal dynamics of microbial communities

Microorganisms are ubiquitous and form diverse communities driven by biotic and abiotic factors. Despite their tremendous importance for global health and ecosystem functions, microbial diversity is still poorly described and is not on the biodiversity–conservation agenda. Identifying the factors influencing microbial communities and their activities in various environments is of fast-growing interest due to the huge potential of translating such knowledge into practical outcome. Thus, a deeper knowledge of the ecology of microbial communities is key for new approaches that will allow us to steer and/or engineer microbial communities and their functions for our own ends, as described in WP3 and WP4. It is also critical for predicting the emergence and spread of antimicrobial resistance as well as of pathogens under the One Health approach or the impact of human activities and climate change on ecosystem services. Research in BFC encompasses a wide range of environments *e.g.* food, peatlands, marine to continental paleo-ecosystems, wastelands, agroecosystems, surface water, groundwater, wastewater networks, but also hospitals and other managed ecosystems like cellars and food factories. It therefore holds a great potential for breakthrough insights into the factors shaping microbial communities across a unique range of ecosystems and timescales thanks to fossil records, which are offering a window into the origin and evolution of microbes. In this WP, we will join forces to achieve 5 specific objectives:

Task 1.1 Characterizing microbial communities and their roles in ecosystem functions through time

Microbial ecology, population biology, and microbial metabolism are keys to better understand how microorganisms interact with each other and other organisms and how they are affected and affect their environment. Despite recent and rapid technological advances, little is known about the diversity of microbial communities and the processes driving their assembly and their functions across environments and timescales. Here the deliverables are (i) *estimates of microbial diversity and composition in modern and fossil ecosystems*, (ii) *the list and highlights of the main factors shaping microbial communities and their functions in a range of ecosystems*, and (iii) *the assessment of the linkages between microbial community composition and functions*.

Task 1.2 Assessing the impact of human activities on microbial communities and ecosystem functions

Anthropogenic activities have steadily escalated and are impacting almost every habitat on Earth. Efforts to identify their implications for living organisms have typically focused on large organisms. Yet, a major concern is that changes in microbial communities due to anthropogenic activities cannot only affect their contributions to ecosystem functioning but also larger organisms. The deliverables of this task are (i) *the evaluation of the impact of human activities such as urbanization, agriculture, health, industry and their subsequent pollution on microbiomes and their consequences for ecosystems functions as well as larger organisms*, (ii) *recommendations and guidelines to reduce detrimental impacts of human activities*, and (iii) *the assessment of the capacity of microbial communities to adapt to these changes through resistance and resilience mechanisms*.

Task 1.3. Understanding the ecology and evolution of antimicrobial resistance (AMR)

This ground-breaking task will be developed conjointly with Task 1.2. Increasing use of antimicrobials in human medicine, animal farming, agriculture and food spur the emergence, selection, and spread of drug-resistant pathogens with a high societal burden. The subsequent environment pollution with antimicrobials but also with agents selecting antimicrobial resistant microorganisms (biocides, heavy metals) could also favour the emergence and spread of AMR. In line with the global action plan of the AMR of the World Health Organization and using the broad range of expertise within HARMi to tackle the interdependent human, animal, and environmental dimensions of AMR, *the deliverables in this task are (i) a collection of data and tool to limit antibiotic prescription (control and monitoring of human consumption, vaccination, rapid diagnostic test in primary care, training of prescribers, and sociological approach to prescription)*, (ii) *the characterization of the molecular mechanisms underlying AMR*, (iii) *the identification of conditions that favour the emergence and the spread of AMR*, (iv) *the detection of emerging resistance mechanisms and emerging resistant pathogens*.

Task 1.4. Deciphering how microbial pathogens spread and eco-epidemiology of infectious diseases

The prevention of infectious diseases requires the full understanding of past and current microbial pathogen spreads. However, the literature in the domain is mostly descriptive and often neglects the identification of the drivers of the pathogen spread. The HARMi consortium brings together clinicians, agronomists, microbiologists,

ecologists, bioinformaticians, and historians in a unique way to understand the spread of microbial pathogens in a One Health approach. We wish to examine the spread of pathogens (e.g. *Escherichia coli*, *Pseudomonas aeruginosa*, *Echinococcus multilocularis*, *Human Papillomavirus*) with genome-based state-of-the-art typing methods (using collections from long periods, multiple environments and geographic locations) and to decipher the spatio-temporal dynamics of infectious diseases. *The deliverables of this task are (i) the identification of microbial features and conditions in environments and hosts that drive the pathogen spread, (ii) predictive models of the risk of emergence and resistance of pathogens at several spatio-temporal scales, and (iii) tools to anticipate and control the current and future outbreaks.*

Task 1.5. Unravelling the impact of changing climate on microbial communities and their activities

Climate change is pivotal and encompasses scientific, social, political, economic and ethical aspects. As climate is predicted to continue to change with more extreme weather events, little is known about the impact of climate change on microbiomes across ecosystems. However, due to the key role of microbes in biogeochemical cycling, this knowledge is important for predicting the impact of climate change on ecosystem functioning. *The deliverables are: (i) the characterization of the resistance and resilience of microbial communities to short term and long-term climatic changes using modern and fossil ecosystems, (ii) the evaluation of the effect of changes in microbial communities on other organisms and hence their ability to respond to climate change, and (iii) the assessment of the capacity of microbes to trigger climate feedback loops.*

WP2: Deciphering microbiota-host interactions

All organisms establish tight interactions with a tremendous diversity of microorganisms during their lifespan. These interactions cover the whole spectrum of costs and benefits, from symmetrical benefits for both partners (mutualism) to highly asymmetrical cost/benefit ratios (parasitism). Host–microbiome interactions are increasingly recognized as determining many host life history traits such as behavior, reproduction, physiological processes, and susceptibility to disease. This paradigm shift led to the emergence of several concepts to describe the intertwined associations between hosts and their associated microbiota such as the holobiont, which is the assemblage of the host and its microbiota forming together a discrete ecological unit. However, even in well-studied organisms, the consequences of microbiome variation for host processes are poorly known. Deciphering the ecological and evolutionary processes underlying the assemblage of the holobiont has far-reaching consequences for i) our understanding of host health and nutrition, and ii) harnessing the microbiota to improve host health, well-being or performance. The unique combination of expertise within HARMi has high potential and offers many new opportunities for breakthrough insights into the rules governing the assemblage of the holobiont and the consequences for host health and fitness across a broad range of biological models (plants, animals, humans). This represents an unprecedented effort to evaluate the generality of the ecological and evolutionary processes that govern the holobiont across living organisms with the following objectives:

Task 2.1. Inferring the co-evolutionary interactions between the host and the microbiota

The construction of the holobiont follows ecological processes that drive the acquisition of the microbiota during specific life stages, its maintenance during lifespan and its transmission. These processes shape the strength and the nature of the selective forces that hosts exert on the microbiota, and vice-versa, giving rise to eco-evolutionary feedback loops that have not been sufficiently studied in the context of the holobiont. In this task, we will investigate the eco-evolutionary dynamic of the interactions between microorganisms and their hosts, underlying the construction and maintenance of the holobiont, in order to have a better insight into the short and long-term consequences of microbial exposure on host health and fitness. *The deliverables of this task are (i) the identification of the processes involved in the recruitment and transmission of microbial guilds under different selection pressures, (ii) the understanding of the co-evolutionary interactions between microbes and their hosts, and (iii) the assessment of the factors contributing to microbial speciation according to the ecological niche offered by the host.*

Task 2.2. Understanding how the microbiota affects host health under different ecological conditions

Despite obvious differences, both plants and animals have evolved a large repertoire of pathogen recognition systems that trigger an “immune response”. Accumulated evidence also shows that the microbiota plays a role in protecting its host towards different threats including infection by pathogens. The importance of the microbiota

for host nutrition through nutrient availability or acquisition also spans across plant and animal kingdom. In this task, we will therefore mobilize our broad range of expertises for an integrated view of the processes underlying the provision by the host microbiota of key auxiliary services such as bioprotection and biostimulation, which are knowledge keys for WP3 and WP4. *The deliverables of this task are (i) the comprehension of the role of microbial stimulation on the immune system across host species (bioprotection), (ii) the assessment of the strength of the protection against biotic (pathogens) and abiotic stressors (bioprotection), and (iii) the identification of the role of microbial stimulation on host nutrition, with a specific focus on animals and plants (biostimulation)*

Task 2.3. Assessing the link between the microbiota and host life history traits and aging

Plants and animals exhibit a tremendous variation of age-specific investment into life history traits. Evolutionary ecology traditionally viewed this variation as the result of age-specific risk of mortality due to extrinsic factors. However, we know now that the community of microorganisms living on and within the host also goes through age-specific changes in terms of diversity, composition and functions. A pending question is whether these changes are due to a senescing host providing deteriorated environmental conditions or whether they are due to synergistic effects between the host and the microbiota, potentially accelerating age-associated decline in performance. In this task, we wish to infer the role that the microbiota might play in shaping age-specific life history traits, including age-associated disease and mortality, which opens fascinating perspectives on the possibility to rejuvenate or to treat age-associated diseases of the host by acting on its microbiota. *The deliverables of this task are (i) the identification of age-specific changes in microbiota diversity, composition and function in host species with different pace of life, and (ii) deciphering the link between late-age dysbiosis and host aging and mortality*

WP3: Managing microbial communities for enhanced sustainability and service delivery

Agricultural and industrial activities are using compounds that can persist and transfer to almost all the environmental compartments, which leads to the pollution and degradation of water, air and soil resources, therefore threatening both environmental quality and human well-being. Agriculture is also an important contributor to greenhouse gas emissions that are causing climate change, which threatens food production and security. Harnessing microbes holds great potential to provide solutions to key challenges related to conservation, restoration, sustainable use of ecosystems, climate change action, as well as food safety, security and sensory properties. Indeed, microbes can degrade or stabilize contaminants that pose environmental and human risks and play critical roles in crop production as well as in the safety and stability of all foods, whether they are a necessary processing component (as with fermented foods) or whether they deteriorate the shelf life and safety of fresh foods. Therefore, we are aiming in this WP at breakthroughs in several R&D fronts related to the management of microbial communities with the specific objectives:

Task 3.1. Microbial bioremediation/biodegradation

In Europe, there are more than 650 000 polluted sites, including agricultural soils, industrial and commercial wastelands. For instance, almost all the arable lands have been or are exposed to chemical pollutants. Recycling, landfilling, incineration and pyrolysis are currently used to reduce the pollution of already contaminated sites. However, these methods are expensive and have adverse effects on the environment. One can take advantage of the great microbial metabolism versatility for ecosystem restoration through biodegradation and biostabilization processes. The expertise and tools of BFC in the restoration of multi-polluted soils are covering a wide range of contaminants (e.g. pesticides, trace elements, polycyclic aromatic hydrocarbons, chlorinated compounds, PCBs, and emerging overlooked contaminants such as plastics and PFAS) but is fragmented between partners. We will combined our expertise in this task for the following deliverables *(i) a fact sheet of key microbial players (i.e., strains, genes, metabolic pathways) in biodegradation and stabilization processes based on culturomics and genome-scale metabolic modeling, (ii) a report on simplified microbial consortia for improved contaminant remediation, and (iii) a guidance document on the microbial-based solutions implemented at field scale to restore multi-contaminated environments using synergistic effects of microbes and plants for phytoremediation.*

Task 3.2. Promoting sustainable agriculture in a changing climate

According to the directive 2009/128/EC of the European Parliament for sustainable use of pesticides, the plan "Ecophyto II+" aims at reducing the use of plant protection products by 50% by 2025. In Europe, the annual cost of damage caused by excess nitrogen fertilizers is estimated at 70-320 billion €. In this context, microbes offer an alternative with a great potential for green agriculture. Thus, microbes can act as biocontrol against pathogens to decrease the use of pesticides. Microbes are not only key players in nutrient cycling but can also directly or indirectly provide these nutrients to the plant, therefore reducing the reliance of fertilizer inputs. *The deliverables of this task are (i) the development of microbial-based biologically integrated farming for reducing chemical inputs as well as the impact of climate change by maximizing the benefits of biotic interactions, (ii) the development of microbial-based methods to improve plant nutrition and growth as well as their capacity to withstand climate change (e.g. drought), and (iii) guidelines on the implementation of agronomic approaches that influence N-cycling microbial communities to improve N-use efficiency and N-retention in agroecosystems.*

Task 3.3. Mitigating climate change

Microorganisms are key players in the biogeochemical cycles and are therefore of global importance in the balance between the production and the consumption of greenhouse gases such as CO₂ and N₂O. Shifts in land use since the industrial revolution has resulted in the depletion of soil organic carbon, releasing 50 to 100 GT of carbon from soil into the atmosphere. Agriculture is also the largest source of anthropogenic emission of N₂O due to the microbial transformation of nitrogen fertilizers. On the road to Paris Agreement of the COP21, our main objective in this task is to foster microbial processes that can help minimizing and mitigating greenhouse gas emissions for climate-smart agriculture and geological sequestration of CO₂. *The deliverables are (i) the characterization and datasets of microbial guilds modulating the balance between sources and sinks of greenhouse gases as well as of the underlying processes, (ii) a report on the anthropogenic and the environmental drivers of these microbial communities, and (iii) the identification and the design of management best-practices that can foster microbial sinks of CO₂ and N₂O.*

Task 3.4. Optimizing microbial processes in food and wine production

Microorganisms are also key players in food production processes, during which they engage into synergistic or antagonistic interactions. These interactions between microorganisms but also with their food matrix during fermentation are crucial for the sensory quality (e.g. taste, odor, texture), which is tightly linked to the typicality, and for the conservation of the food/wine products through bio-preservation (i.e. preventing the occurrence of pathogens or toxic/anti-nutritional compounds). A better control of microbial communities within a dynamic food matrix is therefore key for improving fermented food production and solving food safety problems. *The deliverables of this task are (i) optimized control of food quality, (ii) the generation of new ferments with enhanced quality, (iii) the creation of added value to the by-products from agri-food industries (e.g. fruit and vegetable peels (iv) a rationale for limiting food spoilage.*

WP4: Developing microbial biotechnology

Microbial biotechnology has been used to serve mankind since ancient time for food processing before being exploited in other sectors such as agriculture, industry, public health, and medicine. The global microbial culture market (e.g., in agriculture and food industry) is projected to reach 2.8 billion US\$ by 2024. Microorganisms also represent an exceptional source of valuable compounds, metabolites, and enzymes. Henceforth, microbial biotechnology offers opportunities to meet several sustainable development goals. Thus, with an increasing demand for natural bio-products, it now comprises biocontrol agents and enzymes for agriculture, food and medicine, agents for biodegradation of organic and inorganic pollutants, biofertilizers. The large spectrum of interdisciplinary research in BFC on food microbiology, microbial functions in the environment, and on microbe-host interactions has the potential to generate groundbreaking knowledge and tools for innovative microbial biotechnologies by combining our complementary methodologies and experimental approaches. Because it is leading to new products and services therefore opening up new markets, investments in microbial biotechnology are growing and this WP is intended to facilitate transfer and partnership with socio-economic partners. In this WP, we will therefore develop new products, tools, and concepts in microbial biotechnology that can be applied for sustainable agriculture, food safety and security, environmental bioremediation, climate regulation, and human health.

Task 4.1. Characterization and conservation of strains of interest

The other WPs will lead to the isolation of numerous new valuable strains that must be characterized and stored for further use (e.g. as inoculum). For this purpose, we plan to set up a pipeline to characterize and exploit our microbial collection based on the already existing genome analysis capacities of the 2B2S platform, which will be extended to the metabolome and proteome for the identification of novel microbial pathways and bio-active products (including molecules and proteins). These analysis tools will additionally include the capacity to test the activity of targeted enzymes and to solve the three-dimensional structure of targeted proteins. *The deliverables will include: (i) a pipeline for sequencing, metabolomic, and proteomic including bioinformatics for in-depth microbial strain characterization, and (ii) a unified culture repository dedicated to the storage and distribution of environmentally, agriculturally, clinically, and industrially important microbial strains*

Task 4.2. Developing microbial inoculants and inoculant efficiency optimization

In agriculture, microbes can contribute to crop growth promotion, nutrient uptake, stress tolerance, resistance to pathogens with a global agricultural microbial market is expected to reach 900 million US\$ by 2025. Biostimulation is a widely-practiced bioremediation technology for the management of contaminated sites. It exploits the capability of microbes to degrade and/or detoxify pollutants in the soil. Biostimulation can be influenced by both biotic and abiotic factors, which are determining for example the ability of microorganisms to survive and migrate. In food industry, microbial inoculants contribute to the food flavour as well as its nutritional quality. Many commercial bio-inoculants used in agriculture or bioremediation do not work under field conditions with the efficiency demonstrated in greenhouse or laboratory experiments due to inadequate and/or poor-quality formulation, including poor compatibility and stability of the carriers. In the present task, field and pilot scale trials will evaluate and improve the efficiency of inoculant formulations, which is the crucial issue for successful commercial inoculants. It will innovatively combine the skills of BFC in the fields of agriculture, food production, and remediation with skills in the production of microorganism inocula, leading to the following deliverables: *(i) development of micro-environmental conditions that favour the growth and activity of the bioformulates (ii) a library of bioremediation microbes, which could be used in multi-task microbial consortia for the simultaneous removal of several pollutants/additives with licensing agreements for industrial and environmental agencies, (iii) a report on process for the encapsulation of microbial inoculants using biopolymer-based capsules that can be functionalized and fine-tuned according to their specific application, (iv) the creation of integrated packages of products and services for assessing the impacts of inoculants on native microbiomes as well as ecosystem functions.*

Task 4.3. Engineering of microbial process reactors for the scale up and industrial development

The use of efficient microbes in agriculture, food production and environmental management requires an up-scaling for industrial production of their biomass. Most industrial devices have been designed for common lactic acid bacteria and yeasts. As microbiologists reveal the extreme biodiversity of microorganisms from unknown ecosystems, the need to develop exploitable biomass production devices is emerging. The main challenges in this area concern the formulation of efficient growth conditions that can be integrated into bioreactors. In addition, these conditions must be regulatory and economically viable. The development of efficient growth media is time consuming when based on experimental designs. In this task, a rational approach will be developed to define the optimal conditions for biomass production and stabilization based on the integration of -omics data in the process engineering. Scalability at the industrial level will be a central issue and new pilot reactors will be developed. Stabilization and formulation of microorganisms constitute another challenge for applications. Accordingly, microorganisms need to be preserved during extended periods that separate their production from their use but also formulated in order to target their site of action and resist before reactivation. In this task, the deliverables are *(i) the design of microbial production reactors and stabilized functional formulations based on omics data, (ii) the development of pilot units for the production of microbial biomass, and (iii) the transfer of know-how to industrial partners for rational scale-up production and stabilization processes.*

Task 4.4. Developing cheap tools to track microorganisms and their functions in the environments

While the use of microbial inoculants is increasing, it is still challenging to track the inoculated microbes *in situ* while their persistence in the environment is essential for their success. Tracking native microbial populations in the environment such as pathogens or their functions is also of high interest. In this task, we will develop tools and propose services to track microorganisms (both introduced or native in case of pathogens for example) as well as their functions in relation to the HARMi objectives, leading to the following deliverables : *(i) a guideline*

for sampling and sample preparation for the different methodological approaches that will be assayed and that can be applied by non-scientists (ii) a portfolio of monitoring tools based on Raman spectroscopy, electrochemical sensors and high-throughput real-time as well as digital PCR to quantify microorganisms in situ, (iii) the development of electrochemical sensors for the measurement of specific enzyme activities in situ, and (iv) an integrated service to private companies for quantifying their inoculants after field application.

Task 4.5. Production of microbial metabolites, microbial cell compounds, peptides, and proteins of interest

During the last decade, the biological production of molecules dramatically increased around the world. Microbiological production is an affordable and environmentally friendly alternative to chemical synthesis. It also broadens the spectrum of produced molecules with potential new properties, leading to new technical opportunities. The combination of disciplines such as microbiology, molecular biology, biochemistry, enzymology, and industrial process engineering have allowed the consortium of laboratories of the HARMi project to develop nationally renowned biotechnological facilities. In this task, microbes will be used to produce molecules including peptides and proteins identified as of interest in the other tasks, leading to the following deliverables: *(i) novel microorganisms for optimized molecule production (including non-genetically or genetically modified microorganisms, (ii) the production of compounds with enhanced extraction yield and their ad hoc formulation, and (iii) a molecule/protein purification workflow as well as analyses of their stability and efficiency.*