FRANCE - ARGENTINE : VINGT-SEPTIEME APPEL A PROJETS ECOS Sud - SICyT (2026)

Tableau récapitulatif des projets sélectionnés

Code Projet	Titre du projet	Abstract	Responsable et établissement français	Responsable et établissement argentin
A26B01	Function of leukokinin and tachykinin-related peptide in the regulation of foraging in the honey bees (Apis mellifera)	Behaviour and physiology are orchestrated by neuropeptides acting as central neuromodulators and circulating hormones. A key question is how these molecules coordinate complex and sometimes competing behaviours. This issue is particularly relevant in social insects, where individuals specialize in tasks that support colony function. Our recent collaboration (Dr. de Brito Sanchez, Dr. Arenas, Dr. Farina) showed that carbohydrate satiation, regulated by the short neuropeptide F (sNPF) pathway, shapes nectar and pollen foraging specialization in honey bees (Apis mellifera). Nectar foragers experience a carbohydrate deficit, associated with elevated sNPF levels that promote sugar ingestion, whereas pollen foragers maintain higher baseline satiety. However, the mechanisms regulating pollen collection remain poorly understood. Neuropeptides such as leucokinin (LK) and tachykinin-related peptides (TRPs) are promising candidates, but their role in pollen-related behaviours has not been directly tested. We hypothesize that LK and TRPs modulate pollen foraging by influencing responsiveness and learning to pollen-associated stimuli. Combining behavioural assays, electrophysiology, and molecular analyses, this project will identify how these signalling pathways regulate task-specific motivation. This research will provide new insights into the neuroendocrine mechanisms underlying foraging specialization, contributing to our understanding of colony organization and the evolution of social behaviour in insects. It will also be relevant to agroindustry, particularly to beekeeping and pollination services, by improving our understanding of the mechanisms that regulate the allocation of foragers to resources essential for colony performance.	**DE BRITO SANCHEZ Maria Gabriela** Sorbonne Université, Campus de Jussieu - UMR8246 Institut de Biologie Paris-Seine Batiment B- 5eme etage 9 Quai Saint Bernard 75005 Paris maria-gabriela.de_brito_sanchez@sorbonne-universite.fr	**ARENAS Andres** Universidad de Buenos Aires, Intendente Güiraldes 2160, Pabellón 2, Piso 4º, Lab. 48 bis. Ciudad Autónoma de Buenos Aires, Buenos Aires aarenas@bg.fcen.uba.ar
A26B02	Time for TEAS : Transposable Elements Alternative Splicing as a Regulator of their Mobilisation and a Determinant of Plasticity in Plants	English Transposable elements (TEs) are mobile DNA sequences that can reshape plant genomes by generating new heritable variation. Although TE silencing by DNA methylation has been extensively studied, transcription alone does not predict mobilisation, implying post-transcriptional checkpoints remain poorly understood. This project investigates whether alternative splicing (AS), the selective usage of splice sites to generate multiple mRNA isoforms from a single pre-mRNA, acts as a regulatory layer controlling TE mobilisation in plants. We propose that AS partitions TE transcripts into productive states (cytoplasmic, translated, mobilisation-competent) and non-productive states (nuclear-retained, degraded, or translationally repressed). Addressing this hypothesis would require a rare combination of expertise in TE biology and AS. The Quadrana laboratory (IPS2, Paris-Saclay) contributes a comprehensive atlas of TE transcripts and products, sensitive transposition assays, and long-read sequencing expertise. The Petrillo laboratory (IFIBYNE-CONICET-UBA, Buenos Aires) contributes expertise in AS regulation by environmental signals and the SuB3 method for simultaneous nuclear/cytoplasmic fractionation of RNA and protein. Together, the two teams will define the compartment-resolved landscape of TE alternative splicing isoforms in Arabidopsis thaliana and Solanum lycopersicum, identify isoforms associated with protein production and transposition, and test whether manipulating isoform balance causally alters mobilisation. Results will extend TE control models beyond transcriptional silencing and provide a mechanistic framework relevant to plant breeding and genome engineering.	**QUADRANA Leandro** Université Paris Saclay - CNRS 9213 - INRAE 1403, Bat 630 rue de Noetzlin, 75000 Paris. leandro.quadrana@cnrs.fr	**PETRILLO Ezequiel** Universidad de Buenos Aires – CONICET, Pabellón IFIBYNE (UBA-CONICET), Calle Interna Ciudad Universitaria UBA. petry1@gmail.com
A26B03	Multi-omics characterization of enriched bovine and	Efficient lignocellulosic biomass conversion is essential for ruminant nutrition, as it enables the transformation of plant-derived substrates into metabolizable energy. It is also highly relevant for industrial applications, as this process can be applied to produce value-added compounds such as volatile fatty acids and fermentable sugars for biofuels. However, this process remains challenging due to the inherent recalcitrance of lignocellulose. Rumen microbial ecosystems constitute a rich yet underexplored source of lignocellulose-degrading microorganisms and	**MORGAVI Diego** INRAE Auvegne-Rhône-Alpes, Centre de Theix, 63122 St. Genès	**CERON CUCCHI María** Esperanza Laboratorio de Microbiología Ruminal y Cambio Climático Instituto de

	buffalo rumen consortia for the discovery of novel lignocellulose-degrading enzymes and microbial interactions	enzymes. This project aims to characterize two simplified microbial consortia isolated from bovine rumen that exhibit strong cellulolytic activity, alongside consortia derived from buffalo raised in subtropical environments. This comparative approach will provide insights into host- and environment-specific microbial adaptations and their impact on fiber degradation efficiency. An integrated multi-omics strategy will be applied, combining electron microscopy, enzymatic assays, and high-throughput sequencing to investigate the structural and functional basis of lignocellulose degradation. Functional performance will be assessed through volatile fatty acid production and gas measurements (total gas, methane, and hydrogen). Shotgun metagenomics will enable community characterization and reconstruction of metagenomeassembled genomes, allowing the evaluation of metabolic potential. Particular emphasis will be placed on identifying carbohydrate-active enzymes, cellulosomal systems, and polysaccharide utilization loci to identify novel enzymatic mechanisms. Key microbial members will also be isolated to better understand ecological interactions. This project will advance knowledge of rumen microbiomes and support the development of innovative biotechnological applications through international collaboration and training activities.	Champanelle. diego.morgavi@inrae.fr	Patobiología/Instituto de Patobiología Veterinaria, Instituto Nacional de Tecnología Agropecuaria UEDD INTA-CONICET, CICVyA INTA Castelar Dr. Nicolás Repetto 2751 (B1686LQF) Hurlingham, Buenos Aires. ceroncucchi.maria@inta.gob.ar
A26E01	"Next-Generation NanoBioinks : Integrating Antibiotic Nanocrystals into 3DBioprinted Scaffolds for Enhanced Mechanical Integrity and Controlled Antimicrobial Delivery"	Chronic wounds suffer from antimicrobial resistance. This project integrates pure antibiotic nanocrystals into 3D-bioprinted bioinks. Acting as nano-reinforcements and sustained-release reservoirs, these crystals enhance scaffold mechanics while preventing biofilms. We synthesize stable nanocrystals, embed them in biopolymer matrices, and validate mechanical strength, antimicrobial efficacy against S. aureus/P. aeruginosa, and cytocompatibility. This approach reduces systemic antibiotic use, bridging solid-state chemistry and biomedical engineering for localized therapy.	**RIETVELD Ivo** Université de Rouen Normandie, Place Blondel, 76821, Mont Saint Aignan. ivo.rietveld@univ-rouen.fr	**DESIMONE Martin** University of Buenos Aires, Junin 956. (1113). Ciudad Autónoma de Buenos Aires. desimone@ffyb.uba.ar
A26E02	Thermal and Active Avalanches in Disordered Materials	Disordered systems often respond to external perturbations through intermittent collective events known as avalanches. While these phenomena are well understood in the absence of fluctuations, their behavior at finite temperature or in the presence of internal activity remains largely unexplored. This project aims to investigate how fluctuations enable the emergence of correlated avalanche dynamics in disordered systems. The main focus is on thermally activated processes, where temperature allows the system to escape metastable states and explore complex energy landscapes. A central objective is to characterize the spatial and temporal scales of dynamical heterogeneities and to understand how large-scale correlations develop. In parallel, the project will study systems in which barrier crossing is driven by internal activity, as in active matter. In contrast to thermal fluctuations, activity introduces intrinsically non-equilibrium effects that may lead to qualitatively different avalanche dynamics. Comparing these two mechanisms will help identify both common features and fundamental differences. The project combines numerical simulations and theoretical approaches, and relies on the complementary expertise of the French and Argentinian teams. Beyond its fundamental scope, it addresses key questions related to the mechanical response of disordered materials, including slow relaxation and failure under sustained stress.	**ROSSO Alberto** CNRS / Universite Paris-Saclay, LPTMS, Bat 530 Univ. Pris Saclay. alberto.rosso74@gmail.com	**FERRERO Ezequiel** Centro Atomico Bariloche, Av Bustillo 9500 Bariloche. ezeferrero@gmail.com

A26H01	Challenges in the Control and Surveillance of a Zoonotic Disease (Bovine Tuberculosis) in France and Argentina : A Comparative and Multidisciplinary Approach.	Among the many infectious animal diseases, bovine tuberculosis (Mycobacterium bovis) is characterized by the management challenges and long-term control efforts it imposes on a wide variety of animal health governance systems, across very different geographic and production contexts. In Argentina, it causes economic losses in the cattle sector, which plays a major role in the national agro-export system, and it also has a non-negligible impact on human health. In France, a country officially declared disease-free, certain regions are experiencing steadily increasing prevalence rates that could jeopardize this status and the continuation of livestock exports. This project aims to identify the factors that hinder efforts to eradicate the disease by focusing on how control and surveillance tools are implemented by different stakeholders (farmers, veterinarians, government services, slaughterhouses, etc.) responsible for its management. Through a comparative and interdisciplinary analysis (geography, economics, and veterinary sciences) of the "cuenca lechera" in Argentina and mountain farming systems in the Pyrenees, the objective is to understand how key actors perceive the problem and implement the prescribed regulations, as well as the reasons why they may bypass, circumvent, or find them ineffective. The project thus proposes a perspective that is simultaneously territorial (sociospatial factors influencing the spread of the disease), social (the collective construction of the tuberculosis issue), and economic (market dynamics, information asymmetries, and the impact of health regulations on the formation of value chains).	**GISCLARD Marie** INRAE, UMR 1248 AGIR, 24 chemin de Borde Rouge – BP 52627- Auzeville 31326 Castanet-Tolosan marie.gisclard@inrae.fr	**DEL VALLE ASIS Inés** Universidad Nacional de Córdoba, Facultad de Ciencias Económicas, Escuela de Graduados. Córdoba. ines.asis@unc.edu.ar
A26H02	Development Banks and the Sevilla Commitment : Financing Sustainable Development and the Climate Transition.	This project examines how public development banks can contribute more effectively to financing sustainable development and the climate transition, in line with the Sevilla Commitment adopted in 2025. It starts from the idea that sustainable transformation requires long-term and affordable finance, especially in developing countries, where weak financial markets and external shocks constrain investment. This proposal forms part of a broader research programme on public development banks and sustainable development finance. That broader programme is organised around three interconnected objectives: studying credit mechanisms for green and development projects; analysing stable and sustainable funding sources for public development banks; and examining how cooperation among multilateral development banks, national development banks, and other institutions can strengthen green finance. Within that broader programme, this specific proposal develops two joint research strands between the Universidad Nacional de Córdoba and the Université de Lille. The first analyses whether credit interventions by public development banks displace private lending or generate complementary effects on private banks. The second studies whether national development banks benefit from lower funding costs in debt securities markets than commercial banks.	**BREI Michael** Faculté des sciences économiques, sociales et des territoires, Université de Lille, Campus Cité Scientifique (Bât. SH2 - Bureau 115), 59650 Villeneuve d'Ascq. michael.brei@univ-lille.fr	**Schclarek Curutchet Alfredo** Universidad Nacional de Córdoba, Facultad de Ciencias Económicas, Córdoba. alfredo.schclarek@unc.edu.ar
A26S01	L-Dopa incorporation into tubulin : a potential pathogenic mechanism underlying dyskinesia and cognitive dysfunction in Parkinson's disease	Project Summary Parkinson's disease (PD) is a major neurodegenerative disorder characterized by motor symptoms as well as cognitive and neuropsychiatric impairments. Although L-Dopa remains the most effective treatment, its long-term use leads to L-Dopa-induced dyskinesia (LID) and is frequently associated with cognitive decline. The mechanisms underlying these complications remain poorly understood and may involve processes beyond dopaminergic dysfunction. This project proposes a novel pathogenic mechanism ased on the post-translational incorporation of L-Dopa into tubulin, leading to persistent alterations in microtubule dynamics. Previous work from our teams has shown that L-Dopa-modified microtubules impair synaptic structure and reduce dendritic spine stability in cultured neurons. Building on these findings, we hypothesize that chronic L-Dopa treatment promotes the accumulation of LDopa– modified microtubules in neurons, disrupting cytoskeletal regulation, synaptic function, and neuronal integrity, thereby contributing to both dyskinesia and cognitive deficits. To test this hypothesis, we will combine complementary approaches including PD mouse models, longitudinal behavioral analyses, histological and synaptic studies, proteomics, in vitro reconstitution assays, and the analysis of post-mortem human brain samples. This integrated strategy will allow us to establish causal links between L-Dopa–induced microtubule modifications, synaptic dysfunction, neurodegeneration, and clinical outcomes. By bridging molecular mechanisms with translational relevance, this project aims to identify L-Dopa–modified tubulin as a novel biomarker and potential therapeutic target. More broadly, it will provide a new conceptual framework to understand the long-term complications of L-Dopa therapy in PD, while strengthening Franco-Argentinian collaboration and promoting knowledge transfer.	**PERIS Leticia** Grenoble Institut des Neurosciences U1216 UGA, Chemin Fortuné Ferrini, 38706 La Tronche Cedex, leticia.peris@univ-grenoble-alpes.fr	**BISIG Gaston** Center for Research in Biological Chemistry of Córdoba-National Scientific and Technical Research Council /National University of Cordoba. gastonbisig@unc.edu.ar

A26S02	Gene Therapy in C2F-associated auditory synaptopathy : mapping the inner hair cell vesicular release to auditory nerve firing at single synaptic boutons.	Hearing depends on the precise and sustained transmission of auditory information at inner hair cell (IHC) ribbon synapses in the cochlea. This process is critically controlled by otoferlin, a Ca^{2+} sensor that drives synaptic vesicle fusion. Mutations in otoferlin cause DFNB9, a major form of congenital deafness resulting from defective neurotransmitter release. Although adeno-associated virus (AAV)-mediated gene therapy has recently demonstrated remarkable success in restoring hearing in preclinical models and early clinical trials, its broader application is limited by the substantial phenotypic variability associated with different otoferlin mutations, particularly within the C2F domain. This project addresses a key unmet challenge: understanding how distinct otoferlin mutations differentially disrupt synaptic transmission and determining whether gene therapy can effectively restore neural sound encoding across this spectrum, including forms of hidden hearing loss. We will leverage two novel knock-in mouse models carrying pathogenic C2F mutations that reproduce complementary auditory phenotypes, from severe hearing loss to synaptopathy with preserved thresholds but impaired neural output. Using a cutting-edge dual ex vivo paired patch-clamp approach, we will directly measure presynaptic release and postsynaptic responses at individual IHC synapses. This unique strategy enables a causal and quantitative dissection of synaptic function before and after gene therapy. By linking molecular defects to synaptic and neural coding deficits, this project will define the mechanistic basis of DFNB9 variability and establish a predictive framework for optimizing and generalizing gene therapy strategies for hereditary deafness.	**SAFFIEDDINE Saaid** Institut ReConnect/centre de l'Institut Pasteur, IHU reConnect Inserm U1335, CNRS UMR8252 63 rue de Charenton, 75012 Paris. saaid.safieddine@pasteur.fr	**GOUTMAN Juan Diego** Instituto de Investigaciones en Ingeniería Genética y Biología Molecular "Héctor N. Torres" (INGEBI – CONICET). Buenos Aires. jgoutman@gmail.com
A26S03	Could anti-Müllerian hormone be driving a male equivalent of polycystic ovary syndrome, linking metabolic dysfunction and subtle reproductive impairment ?	Infertility is a worldwide concern, with male factors contributing to 20% to 50% of cases among couples. Declining semen quality has paralleled the increasing prevalence of metabolic disorders, raising the question of how metabolic dysfunction impacts male reproductive function. This project aims to leverage the complementary expertise of Paris and Buenos Aires partners to determine whether anti-Müllerian hormone (AMH) represents a link between metabolic dysfunction and male reproductive alterations in the male equivalent of polycystic ovary syndrome (PCOS), the leading cause of infertility in women. Although male relatives of women with PCOS often exhibit similar metabolic disturbances, their reproductive function remains poorly explored. We hypothesize that, despite being fertile, these men show subtle sperm alterations caused by chronic metabolic and endocrine imbalances, resulting in suboptimal fertility. Given the central role of AMH in female PCOS pathophysiology, we propose that AMH may mediate the relationship between metabolic status and testicular function. To test this, we will study the development of male reproductive function in Goto-Kakizaki (GK) rats, a spontaneous PCOS model, alongside the onset of metabolic disturbances. We will then translate these findings to humans by assessing the relationships between metabolic disorders, AMH levels, and reproductive function in pediatric and adult cohorts from both countries. Finally, we will evaluate whether blocking AMH can reverse metabolic and reproductive alterations in GK males. This project will clarify links between metabolic syndrome, fertility, and AMH, opening new research and clinical perspectives.	**DI CLEMENTE Nathalie** Sorbonne Université, 27 rue Chaligny, 75012 Paris. nathalie.di-clemente@inserm.fr	**REY Rodolfo** CONICET, Buenos Aires. rodolforey@cedie.org.ar
A26S04	Comparative Analysis of Regulatory T Cell Heterogeneity and Therapeutic Modulation Across Infection, Transplantation, and Cancer.	Regulatory T cells (Tregs) are essential for immune homeostasis but represent a highly heterogeneous and plastic population. Depending on tissue location and disease stage, Tregs can exert potent immunosuppressive activity or acquire tissue-repair functions. This functional versatility is critically involved in chronic infection, transplantation, and cancer, where it can lead either to pathology or protection. This project aims to perform the first cross-disease comparative analysis of Treg heterogeneity, focusing on tumor necrosis factor receptor 2 (TNFR2) as a key marker and regulator of a functional continuum between suppressive and tissue-repair Treg states. By integrating existing bulk and single-cell transcriptomic datasets with in vivo experiments in mouse models of Trypanosoma cruzi infection, allogeneic hematopoietic stem cell transplantation, and pancreatic ductal adenocarcinoma, we will map the spatiotemporal dynamics of TNFR2 expression and associated programs. The project seeks to identify conserved transcriptional modules across disease contexts and to demonstrate that stage-specific TNFR2 targeting can selectively restrain immunosuppressive Tregs while preserving tissue-protective functions. These findings will provide a foundation for TNFR2-based precision immunotherapy across infection, transplantation, and cancer.	**TOSELLO-BOARI Jimena** Inserm, IMRB- I-BIOT, 8 rue du Général Sarrail, CRETEIL. jimena.tosello-boari@inserm.fr	**ACOSTA-RODRIGUEZ Eva Virginia** Facultad de Ciencias Químicas - Universidad Nacional de Córdoba. Centro de Investigaciones en Bioquímica Clínica e Inmunología (CIBICI) – CONICET. eva.acosta@unc.edu.ar

A26U01	Opening a new window on the violent Universe with the Hybrid Elevated Radio Observatory for Neutrinos (HERON).	Our goal is to develop and build in Argentina, by 2030, the next-generation ultrahigh energy neutrino observatory: HERON, a discovery instrument to open a new window to cast light on the workings of the most violent astrophysical sources in the Universe. HERON, a project funded by the ERC and to start around June 2026, will be based on the successful design of a radio antenna array, and its deployment and operation in the San Juan province in Argentina. Within this ERC framework, and in particular over the first two years of the project, CNRS and CNEA will work hand-in-hand to perform site surveys, deploy, and commission the instrument, as well as optimize the Science performances and build prototypes.This ECOS program will be central to launch a successful partnership between France and Argentina, synergistically combining the complementary and necessary knowledge and technical skills on multimessenger astronomy, radio detection, instrument conception, data analysis, and in situ operations.	**KOTERA Kumiko** CNRS, Institut d'astrophysique de Paris, 98 bis bd Arago, 75014 Paris. kotera@iap.fr	**SANCHEZ Federico** CNEA, ITEDA. federico.sanchez@iteda.cnea.gov.ar