ICGEB Research Grants awarded under the 2019 Call for applications

**Title:** Ferroptosis-like cell death in plants  
**Principal Investigator:** Dr. Gabriela Pagnussat, Instituto de Investigaciones Biologicas – CONICET, Universidad Nacional de Mar del Plata, Argentina  
**ICGEB Reference No.:** CRP/ARG19-06  
**Abstract:** Plants are continually exposed to various environmental stresses. As they are unable to escape, tolerance to changing conditions is critical for plant growth and survival. In this context, regulated cell death plays a critical role for specific responses to both abiotic and biotic stresses. We recently discovered that a process similar to the iron-dependent cell death pathway, named ferroptosis, which was first observed in tumour cells, takes place in plants in response to heat stress. Notably, if ferroptosis is prevented by using canonical inhibitors, plants can endure otherwise lethal conditions. Although we found that there are some morphological and biochemical features conserved between animal and plant ferroptosis, plant cells have particular characteristics and responses, so the molecular mechanisms underlying this process in plants are still unknown. In this project we aim to study such mechanisms using biochemical, genomic and molecular tools. As suppressing ferroptosis allows plants to cope with high temperatures, these studies open a new alternative for researchers to study innovative biotechnological approaches for crop protection during times of extreme temperature fluctuations, which are increasingly likely to affect diverse plant species as a result of climate change.

**Title:** Engineering pro-vitamin A rich orange eggplant: Potential to reduce vitamin A deficiency in developing countries  
**Principal Investigator:** Dr. Abdun Noor Muhammad Iftekhar Alam, National Institute of Biotechnology, Dhaka, Bangladesh  
**ICGEB Reference No.:** CRP/BDG19-02  
**Abstract:** Vitamin A deficiency (VAD) has been one of the world’s major human health problems for a long time. Among various approaches, fortification of major food crops with pro-vitamin A (carotene) is considered the most feasible solution. Eggplant is a vegetable consumed in significant quantities in regions where VAD is highly prevalent. Thus, we propose the development of carotene-fortified eggplant through genetic engineering. We will express two rate-limiting enzymes, phytoene synthase (Psy) and phytoenedesaturase (CrtI), through genetic transformation. The genetically modified eggplant is expected to produce high amounts of carotene in the fruits. We will also verify the amount of bio-available pro-vitamin A in various cooked dishes made from the transgenic plants. Successful bioengineering of eggplant would have the potential to combat VAD in developing countries.

**Title:** Mining the soybean leaf microbiome for disease-suppressive microbes  
**Principal Investigator:** Dr. Paulo José Pereira Lima Teixeira, Department of Biology, “Luiz de Queiroz” College of Agriculture (ESALQ) University of São Paulo, Piracicaba, Brazil  
**ICGEB Reference No.:** CRP/BR19-05 EC  
**Abstract:** Soybean is the most important crop in Brazil and exportation of this commodity is a driving force of Brazilian agriculture and economy. Asian Soybean Rust (ASR), however, severely threatens soybean production in Brazil. There are no commercially available cultivars that are fully resistant to ASR and this disease is mainly controlled through routine applications of fungicides, which is a costly practice with potential environmental impacts. In recent years, it has become evident that plants establish intimate relationships with commensal microbes that form complex microbiomes on or within them. In this project, we will define the composition of bacterial communities colonising soybean leaves, to understand how ASR affects the plant microbiome. We will also assemble a collection of soybean-associated bacteria to search for strains that can prevent the establishment of...
Title: Low cost and variability-tolerant cell-free biosensors for RNA viruses
Principal Investigator: Dr. Fernando Federici, Pontificia Universidad Catolica de Chile, Santiago, Chile
ICGEB Reference No. CRP/CHL19-01
Abstract: We propose the development of ratiometric cell-free toehold sensors (CFTSs) in low cost E. coli TX-TL crude cell extracts for the detection of RNA viruses. Ratiometric CFTSs will be tolerant to variability, delivering more robust readouts. This challenge will be addressed by: (i) implementing CFTSs in self-manufactured transcription/translation (TX-TL) cell extracts that are optimised for RNA & DNA stability and for the use of low cost energy regeneration reagents; (ii) studying, identifying and correcting the sources of variability in TX-TL cell-free reactions through mathematical modelling and Ratiometric Dual Analysis; and (iii) engineering novel TX-TL-based Ratiometric CFTSs for the detection of PVY RNA virus, as a proof-of-concept. Implementing CFTSs in self-manufactured cell extracts would allow cheaper design-build-test cycles for prototyping sensors in developing countries. We expect this project to develop foundational knowledge on CFTS engineering, as well as enhancing local capacity and advanced resources for cell-free synthetic biology.

Title: Structural and functional study of Hepatitis A Virus 2C protein and its role in virus replication
Principal Investigator: Dr. Sheng Cui, Institute of Pathogen Biology, Chinese Academy of Medical Science, Beijing, China
ICGEB Reference No. CRP/CNIN19-02
Abstract: Hepatitis A virus (HAV) spreads via contaminated foods, causing millions of cases of hepatitis infection. HAV outbreaks can erupt explosively and lead to devastating consequences. Despite the availability of an effective prophylactic vaccine, HAV still contributes to mortality, largely because there is no effective drug. HAV belongs to the Picornaviridae, and although the structure of the HAV capsid has been solved, it provides limited insights into the replication of HAV, and the role of the nonstructural protein in replication remains enigmatic. In this research proposal, we focus on HAV 2C protein: 2C plays a central role in virus replication and participates in almost every aspect of the virus life-cycle, hence it is a potentially important drug target. In this project, we aim at: (i) investigating the functions of HAV 2C; (ii) determining its high-resolution structure; and (iii) validating the structural findings via mutagenesis. Knowing the structure of HAV 2C will allow virtual screening for drug leads, and should eventually assist in the development of antiviral drugs.

Title: Uncovering developmental and transcriptional mechanisms of the early synthesis of cytotoxic, antimicrobial, and cardiotoxic bufadienolides in toads
Principal Investigator: Dr. Jennifer Lynn Stynoski, Clodomiro Picado Institute, University of Costa Rica, San José, Costa Rica
ICGEB Reference No. CRP/CR19-04_EC
Abstract: A class of steroids called bufadienolides have shown enormous potential as natural products to treat and diagnose cancer, microbial and fungal infections, preeclampsia, and heart disease. Bufadienolides are synthesised in the glands of toads as chemical defences against predators and pathogens, and have long been delivered in crude toad venom as traditional medicine, with diverse detrimental side effects. The development of these into targeted therapeutic tools is limited by a lack in our understanding of the biosynthetic and genomic pathways underlying the production and activities of bufadienolides in animal tissues. Using four different Costa Rican toad species, whose bufadienolides vary in their degree of toxicity, we propose to identify: (i) when and where bufadienolide biosynthesis starts and (ii) the changes in gene expression that are associated with their initial biosynthesis in toads. Understanding how changes in gene expression allow toad cells to make bufadienolides will give us the foundation necessary to research and produce specific therapeutic targets in transgenic models in the future.

Title: Piperine for the prevention of breast cancer
Principal Investigator: Dr. Rama Ibrahim Khalaf Mahran, Department of Pharmacology, Faculty of Medicine, Suez Canal University, Ismailia, Egypt
ICGEB Reference No. CRP/EY19-04_EC
Abstract: Breast cancer is the first cause of cancer deaths among the North African women, including Egyptian women. Prevention of breast cancer represents a cost-effective strategy, as an alternative to treatment. Piperine, the spice derived from black and long pepper, has been shown to have anti-carcinogenesis effects. We question whether piperine will effectively prevent breast cancer by targeting human dysplastic breast stem cells. The aims of this project are: (i) to evaluate the preventive efficacy of piperine against breast cancer in human cell line-derived mammary organoids; (ii) to learn how to establish primary human normal, dysplastic, and cancer 3D mammary organoid cultures; and (iii) to grow primary organoids in cultures in Egypt. Mammary organoids will be treated with piperine and the effects of piperine on stem cell self-renewal, stemness, viability, growth and proliferation, and differentiation will be tested. Finally, the molecular pathways by which piperine targets dysplastic stem cells will be identified.

Title: Comparative lipidomics for development of Mycobacterium tuberculosis-based lipid biomarkers
Principal Investigator: Dr. Feven Tigistu-Sahle, Ethiopian Biotechnology Institute, Addis Ababa, Ethiopia
ICGEB Reference No. CRP/ETH19-05_EC
Abstract: Mycobacterium tuberculosis (Mtb) has been a major problem for human health, particularly in low-income countries. Development of a new treatment for tuberculosis is critically needed. Mtb releases a variety of bioactive lipids during infection, including lipidic inclusions. Further, Mtb-induced lipid inclusions are both a potential disease marker and a potential therapeutic target. Comparing lipidomic profiles of infected samples with healthy samples may help in identifying novel lipid biomarkers for tuberculosis infection and disease progression. These lipid biomarkers may provide new insights into the mechanism of pathogenesis and may represent potential targets for the development of new therapeutic strategies.
**Abstract:**

*Mycobacterium tuberculosis* (Mtbc) is the causative agent for Tuberculosis (TB), a leading cause of death globally. A quarter of the global population is estimated to be latently infected with Mtbc, meaning that their immune system can effectively contain this infection, to remain healthy. Of these latently infected individuals, fewer than 10% progress to active TB infection during their lifetime. Very little is known about the factors that determine these risks and there is lack of effective biological markers to differentiate the latent from active infections. Several studies have established the role of lipids in Mtbc survival within the host environment and during its progression to the active state. This project aims to use modern analytical methods to compare the lipid profiles of Mtbc at different stages of infection, to identify novel lipid molecules for use as biomarkers. The discovery of reliable biomarkers will advance treatment options through the rapid and accurate identification and differentiation of individuals with latent and active Mtbc infections.

**Title:**

Examination of the interaction between *Candida* and oral squamous cell carcinoma cells on the level of extracellular vesicles

**Principal Investigator:**

Mohamad Aimanuddin Mohtar, UKM Medical Molecular Biology Institute (UMBI), UKM Medical Centre, Kuala Lumpur, Malaysia

**ICGEB Reference No.:**

CRP/HUN19-01

**Abstract:**

According to our previous findings, oral squamous cell carcinoma (OSCC) patients are characterised by having increased yeast abundance in their oral cavity, compared with healthy individuals. Therefore, in this project we aim to explore the nature of an possible interaction, between local yeasts, (represented by *Candida* species) and oral tumour cells *in vitro*. Our purpose is to investigate yeast-tumour cell interaction at the level of extracellular vesicles (EVs), as EVs have recently been reported to be major mediators of intercellular (and inter-kingdom) communications. In this project, we also aim to thoroughly examine the physical interaction between tumour exosomes and *Candida* cells, as well as examining the effect of *Candida* EVs on OSCC cells. We plan to use OMICs analyses, biochemical assays, flow cytometry and microscopy experiments to better understand the molecular bases of the potential information transmission between fungal and cancer cells at the level of extracellular vesicles.

**Title:**

A molecular and immunological investigation of leishmaniasis from unusual foci of cutaneous and visceral disease in India and Nepal

**Principal Investigator:**

Dr. Manju Jain, Central University of Punjab, Bathinda, India

**ICGEB Reference No.:**

CRP/IND19-01

**Abstract:**

Leishmaniasis is caused by transmission of the Leishmania parasite through the bite of infected sandflies, which results in Cutaneous Leishmaniasis (CL), causing skin lesions, and Visceral Leishmaniasis (VL), a deadly systemic disease. The different clinical outcomes result from the interplay between the infecting Leishmania species and the host's immune status. Recently, the disease has spread to newer areas, where it shows atypical characteristics: such that the *Leishmania donovani* species, which typically causes visceral disease (VL), now causes cutaneous disease (CL). We propose to study two, newly-emerging, atypical foci of leishmaniasis - one in Himachal Pradesh, India, and the other in the western Hilly and Terai regions of Nepal - to understand why *L. donovani* has changed from being a deadly VL-causing parasite to being a less dangerous CL-causing parasite. *L. donovani* will be isolated from cutaneous lesions in these areas of India and Nepal, and genome sequencing will be performed to identify gene variants that may be associated with atypical cutaneous disease. Immunological correlates in VL and CL patients will also be investigated.

**Title:**

Determination of signal flow in cellular systems using the yeast fat regulating network as a model

**Principal Investigator:**

Dr. Bader F. Al-Anzi, Kuwait Institute for Scientific Research, Safat, Kuwait

**ICGEB Reference No.:**

CRP/KWT19-01

**Abstract:**

We have used genetic, proteomic and physiological methods to characterise a protein network that regulates fat storage in yeast. In this network, the contribution of a given structure to its overall signalling output can be determined by simply measuring fat in cells missing that structure. Thus, it can provide empirical parameters to computationally model signal flow within a cellular network. We have succeeded in showing that the importance of each protein to network output is dependent on a topological parameter called Katz centrality. However, it is also important to establish the amount of signalling carried by individual protein connections. To rephrase what we are attempting to do: if these connections are highways, how much traffic are they carrying? This goal will be achieved by following a multidisciplinary approach utilising Mass Spectrometry, yeast strains that cannot form a given protein connection, a variety of metabolic assays, and computational analysis. The acquired data will be used to build a predictive signal flow model.

**Title:**

CRISPRi genetic screen in identifying surfaceome addiction in glioblastoma multiforme

**Principal Investigator:**

Dr. Mohamad Alimanuddin Mohtar, UKM Medical Molecular Biology Institute (UMBI), UKM Medical Centre, Kuala Lumpur, Malaysia

**ICGEB Reference No.:**

CRP/MYS19-04, EC

**Abstract:**

Glioblastoma Multiforme (GBM) is the deadliest disease of the central nervous system. GBM-diagnosed patients have a low survival rate, averaging 12-15 months’ life expectancy. Current standard-of-care therapies have provided poor efficacy in treating GBM. Our analysis, utilising the public genomics database, revealed that many genes encoding the cell surface proteins (termed surfaceome) are highly expressed in GBM, suggesting their importance in GBM pathogenesis. Thus, the general aim of this study is to identify novel oncogenic drivers within the cell surface sub-proteome that support GBM growth and progression. This will be achieved via the utilisation of a CRISPRi genetic screen targeting the most significantly upregulated components of the GBM
surfaceome. The candidate hits from the screen will be functionally validated using cell-based and mouse model experimental assays. This study will facilitate the discovery of novel oncogene addictions in GBM that could potentially be targeted in the clinic, either individually or as part of a combination therapy.

**Title:**
Paleogenomic characterisation of human pathogens spanning the Native-European contact in Latin America

**Principal Investigator:**
Dr. María C. Ávila Arcos, International Laboratory for Human Genome Research, National Autonomous University of Mexico, Querétaro, México

**ICGEB Reference No.:**
CRP/MEX19-03

**Abstract:**
Understanding the genetic makeup of pathogens involved in major pandemics is crucial for informing strategies to face the potential devastating effects of a reintroduction. Ancient DNA studies have revealed the causes of major epidemics and the genetic makeup of some ancient human pathogens. This is of interest in places like Mexico and Argentina, where a large fraction of the Native population died as a consequence of devastating outbreaks caused by pathogens introduced during European colonisation, some of which still pose epidemiological threats today.

In this project we will (i) extract ancient pathogen DNA from archaeological remains from Mexico and Argentinian Patagonia to reveal the extent of pathogen diversity present in each region, before and after European colonisation; (ii) reconstruct whole genomes and resolve their phylogenetic relationship to other strains to unveil the evolutionary patterns of endemic versus introduced infectious diseases; (iii) identify genomic changes associated with pathogenicity and host-pathogen interactions in the ancient strains.

**Title:**
Next generation diagnostics and characterisation for emerging viruses and virus-like agents of pome and stone fruits in Montenegro

**Principal Investigator:**
Dr. Jelena Zindovic, Biotechnical Faculty, University of Montenegro, Podgorica, Montenegro

**ICGEB Reference No.:**
CRP/MNE19-01

**Abstract:**
New emerging viruses and virus-like pathogens, as well as new variants of existing pathogens, pose a serious threat to agricultural production. The availability of metagenomic analyses through Next Generation Sequencing (NGS) has made accessible whole plant and pathogen genomes, and has become a powerful tool in the diagnosis of unknown plant diseases. The goal of this project is to acquire the knowledge, skills and competences in using the state-of-the-art NGS technologies to detect and characterise existing and emerging viruses and virus-like agents of pome and stone fruits, and to contribute to the development of their disease management in Montenegro.

**Title:**
Diagnostic, prognostic and predictive biomarkers for bladder cancer management

**Principal Investigator:**
Prof. Zivko Popov, Research Center for Genetic Engineering and Biotechnology “Gorgi D. Efremov”, Academy of Science and Arts of the Republic of North Macedonia (MASA), Skopje, North Macedonia

**ICGEB Reference No.:**
CRP/MKD19-02

**Abstract:**
Bladder cancer (BC) is one of the most common types of cancer worldwide, and molecular defects associated with the initiation of the carcinogenic process in this type of tumour has great clinical importance. Different molecular changes have been found in the tissue samples of patients with BC, which could be used as markers for non-invasive early diagnosis, as well as being potential prognostic and/or predictive biomarkers for patient management.

The main aim of this project is the determination of the molecular (DNA, RNA, protein) changes in the early stages of the disease, present in the tissue and/or blood of patients with bladder cancer. The potential use of the observed molecular changes as diagnostic, prognostic and predictive markers for clinical management of this disease will also be evaluated.

**Title:**
Design and test of in vitro and in vivo applicators for the use of electromagnetic energy against the Malaria parasite

**Principal Investigator:**
Dr. Lorena Michelle Coronado, INDICASAT AIP, Panama City, Panama

**ICGEB Reference No.:**
CRP/PAN19-01

**Abstract:**
Our group has successfully developed the use of microwave non-thermal irradiation in in vitro tests as a potentially effective malaria treatment, acting by inhibiting the growth of the causative parasite, P. falciparum. We are now at the challenging point when it is necessary to design and build applicators for the delivery of this energy in an effective and safe way in vivo. To achieve this task it is necessary to study the dynamics of blood movement using a fluid moving setup that simulates real blood circulation, with the application of microwaves at a given point of the circulating system. When the right parameters to achieve killing are achieved, tests will be carried out on mice infected with malaria.

Our objective is to design, build and optimise applicators for the treatment of malaria using electromagnetic energy. The aims of this project are: (i) to design and test an applicator to be used against P. falciparum, based on parallel plates; (ii) to design and test an applicator to be used against P. falciparum, based on constant fluid; and (iii) to test the applicators against malaria in an in vivo model.

**Title:**
Are prion (PrP) and MARCKS proteins functional partners in vivo? MARCKS proteins as potential components of prion and Alzheimer’s neurodegenerative pathways

**Principal Investigator:**
Prof. Edward Málaga-Trillo, Universidad Peruana Cayetano Heredia, Lima, Peru
Abstract: Alzheimer’s, Parkinson’s and prion diseases result from the cunning ability of toxic proteins to hijack biochemical signals normally used by neurons to communicate. One such signalling pathway involves the modulation of cell adhesion and neurotransmission by the prion protein (PrP) and its control over Src-family kinases (SFKs). This mechanism is only partially understood, as PrP can interact with other molecules whose involvement in neurodegeneration remains unclear. Among these, MARCKS proteins are of special interest because, like SFKs, they associate with neuronal cell membranes and participate in the control of cell adhesion and neurotransmission. This proposal assesses the potential role of MARCKS proteins as, as yet unrecognised, downstream mediators of PrP neurotoxicity, complementary to SFKs. Using a combination of genetic, cell biological, biochemical and behavioural approaches in zebrafish embryos, we will examine the formation of functional PrP/SFK/MARCKS complexes, their involvement in neuronal physiology and their contribution to prion and Alzheimer’s neurodegeneration.

Title: Development of bacterial inoculants for biological control of plant pathogens
Principal Investigator: Prof. Djordje Fira, Faculty of Biology, University of Belgrade, Serbia
ICGEB Reference No.: CRP/SBR19-02
Abstract: Biological control of plant pathogens has become an important alternative to the extensive use of chemical pesticides in modern agriculture. The aim of the proposed project is to identify the best strains for the formulation of biocontrol inoculants from the existing laboratory collection. In our previous work, we have already characterised several strains of genus Bacillus at a genetic and biochemical level, including the basis of their strong activities against important fungal and bacterial plant pathogens in experiments both in vivo and in vitro. Therefore, the focus of our research will be on several objectives: (i) to test the biocontrol capacity of selected strains in greenhouse and field trials on crops most important for Serbian agriculture; (ii) to expand the existing collection with Gram-negative bacteria, including their molecular and biochemical characterisation and determination of anti-pathogenic activity; and (iii) metagenomic studies of plant samples during their treatment with biocontrol agents, in order to determine the dynamics of plant microbiome and its influence on plant growth.

Title: Regulation of intracellular complexes formed by dipeptide repeats from C9ORF72 mutation
Principal Investigator: Dr. Boris Rogelj, Faculty of Chemistry and Chemical Technology, University of Ljubljana, Slovenia
ICGEB Reference No.: CRP/SVN19-03
Abstract: Progressive neuronal loss is a key feature in several forms of dementia and movement disorders. One signature microscopic feature that can be observed post-mortem in the brains of patients diagnosed with these diseases, is the abnormal aggregation of certain proteins. In Frontotemporal Dementia (FTD) and Amyotrophic Lateral Sclerosis (ALS) this protein is TDP-43. The most common mutation in ALS and FTD is in the C9ORF72 gene and leads to disease causing aggregations of TDP-43. The mutation in C9ORF72 gene results in formation of toxic RNAs or proteins, whose direct linkage with the disease still needs to be determined. With this proposal we aim to identify the set of proteins that interact with C9ORF72 toxic proteins in living cells, to examine whether the interactions lead to TDP-43 aggregation and to determine how these interactions could be used to attenuate their toxicity.

Title: ValtitaCHO: Faster and cheaper manufacturing of biopharmaceuticals using next generation “super” CHO cell lines generated using a novel directed evolution and synthetic biology strategy
Principal Investigator: Dr. Deepak Balaji Thimiri Govinda Raj, CSIR Biosciences, Pretoria, South Africa
ICGEB Reference No.: CRP/ZAF19_05_EC
Abstract: The biopharmaceutical industry is rapidly growing and is crucial to the well-being of global citizens. Biotherapeutics offer significant advantages and we now have the theoretical toolkit to treat almost all diseases. Significant challenges exist in transferring it to a viable solution. Currently over 70% of the commercial biotherapeutics are manufactured using Chinese Hamster Ovary (CHO) cells, but it is widely acknowledged that in their current format this is unlikely to continue. As the complexity increases, the economics of current CHO-based biomanufacturing further deteriorates and, as we prepare for more futuristic applications, the CHO expression system needs to be significantly improved or to be completely replaced. The key objective of this project is to generate “super” CHO cell lines for improved biopharmaceutical production. Herein, we describe an approach to utilise all of the knowledge generated to date on CHO cells and to evolve this to develop a cell line more fit for purpose, in terms of both cost and production capacity.

Title: Comparative study of Sickle Cell Disease modifiers in Ghana, Nigeria and Tanzania. Investigation of foetal haemoglobin parameters and clinical manifestation
Principal Investigator: Dr. Siana Nkya, Muhimbili University of Health and Allied Sciences, Dar es Salaam, Tanzania
ICGEB Reference No.: CRP/TZA19-01
Abstract: Sickle Cell Disease (SCD) is an inherited blood disorder that is caused by a mutation leading to the synthesis of abnormal haemoglobin and red blood cells (RBC). SCD is clinically characterised by insufficient blood (anaemia), episodes of pain, painful swellings of the hands and feet, frequent infections and delayed growth. SCD patients inherit the sickle mutation with other genetic combinations, which are known as haemotypes. Five SCD haemotypes have been described: Senegal, Benin, Central African Republican, Cameroon, and Arab-Indian. SCD symptoms are different among individuals with different haemotypes.
Foetal Haemoglobin (HbF) is a major modifier of the severity of SCD symptoms; however the levels and distribution of HbF in RBCs is different among individuals with SCD and across SCD haplotypes, leading to the observed differences in SCD symptoms. This study will be one of the first in Africa to systematically compare HbF levels and distribution with clinical symptoms across SCD patients from different geographical locations and with different SCD-haplotypes.

**Title:** The synthesis and testing of novel drugs for the treatment of Diabetes Mellitus  
**Principal Investigator:** Dr. Varma Hemant Rambaran, The University of Trinidad and Tobago, Arima, Trinidad and Tobago  
**ICGEB Reference No.:** CRP/TT019-01  
**Abstract:** Present anti-diabetic medicines on the market still rely on the signalling action of insulin as a means of remedying the hyperglycemic levels in the body. This is a major problem in the case of Type II Diabetes, where the cells’ insulin receptors have become desensitised to the action of insulin and therefore an alternative form of therapy is needed. Vanadyl complexes have had a successful history, as insulin mimetics, in attenuating blood glucose levels, however, a shortcoming is the gastric disorders that are associated with oral administration. To overcome this disadvantage, it has been proposed that a means to avoid such deleterious effects is to optimise or change the specie of binding ligand. The project discussed herein focuses on the synthesis and biological evaluations of two novel vanadyl complexes, with the hope of obtaining at least one drug that will be both pharmacologically effective and safe when used as a diabetes-therapeutic agent.

**Title:** CD300f immune receptors in neuroinflammation and neuroplasticity: role for behavioural alterations relevant for major depression disorder  
**Principal Investigator:** Dr. Hugo Peluffo, Institut Pasteur de Montevideo, Uruguay  
**ICGEB Reference No.:** CRP/URY19-01  
**Abstract:** Depressive disorders affect more than 350 million people worldwide. Recently, increased immune responses and higher levels of inflammatory molecules have been found in depressed patients. The immune system is our defence system, being responsible for identifying and protecting the body against potential threats. However, dysfunctional immune activation after stress exposure can be detrimental, and a condition called neuroinflammation may impact the function of, and communication between, brain cells in areas responsible for controlling behaviours, such as mood and pleasure/reward. Our goal is to study the receptors for CD300f, a molecule present in both immune and brain cells, which is involved in the control of immune activation and in reduction of inflammation. We will use genetically modified mice and human studies to investigate whether CD300f receptors can control the spread of neuroinflammation, and the changes in brain cells, and resultant behaviours relevant for depression. With this knowledge, we can propose new pharmacological strategies to treat depression.

**Title:** Characterisation of a GWAS-derived QTL for yield-related traits in Vietnamese landraces suitable for local rice breeding program  
**Principal Investigator:** Dr. Nqan Giang Khong, Agricultural Genetics Institute, Hanoi, Vietnam  
**ICGEB Reference No.:** CRP/VNM19-03  
**Abstract:** Panicle architecture is one of the key components of rice yield and exhibits a large diversity. To identify the morphological and genetic determinants of panicle architecture, a genome-wide association study (GWAS) using an original panel of Vietnamese landraces, was performed. Twenty-nine stable QTLs associated with several panicle traits were detected over the two years. Interestingly, a new single QTL with co-location of both Spikelet Number (SpN) and Secondary Branch Number (SBN) traits was observed (namely QTL_9), and no functionally characterised genes were co-located in this genomic region of 780 Kb. The aim of this project is to characterise the GWAS-derived QTL9 and the associated genes related to rice yield. The main objectives are: (i) to characterise the QTL9 through bi-parental population; (ii) to analyse the function of candidate genes in Vietnamese varieties by transgenic plants; and (iii) to develop the genetic markers for rice breeding programmes in Vietnam.