Contents

Invited speakers

Nicholas Chia: A Systems-approach for Differentiating the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers

Multi-omic data and genome-scale microbial metabolic models have allowed us to examine microbial communities, community function, and interactions in ways that were not available to us historically. Now, one of our biggest challenges is determining how to integrate data and maximize data potential. I will present the results of our studies using multi-omics to discern the distinct paths by which the microbiome can influence cancer progression in two subtypes of cancer—deficient mismatch repair and proficient mismatch repair colorectal cancer. As part of this talk, I will demonstrate the ways in which we can test a hypothesis by combining multi-omic data using systems biology approaches on the organismal, ecological, and environmental level and why it is so important to integrate across all three to arrive at real solutions to medical problems.

Patricio Jeraldo: Microbe-metabolite networks inferred from metabolic models can explain observed interactions in the gut microbiome

Background: The link between colorectal cancer (CRC) and the gut microbiome has been established, but the specific microbial species and their role in carcinogenesis remain controversial. Our understanding would be enhanced by better accounting for tumor genetic subtype, microbial community interactions, metabolism, and ecology.
Methods: We collected paired colon tumor and normal adjacent tissue and mucosa samples from patients with CRC. Mismatch repair (MMR) status was classified as either deficient (dMMR) or proficient (pMMR) MMR tumor subtypes. Samples underwent 16S rRNA gene sequencing and, for a subset of samples, targeted metabolomic analysis. dMMR and pMMR microbial communities were then analyzed using a generalized linear mixed effects model. Using community genome-scale metabolic models to generate microbial interaction networks and metabolite predictions, we assessed global network properties and metabolic influence of specific microbes and metabolites within the dMMR and pMMR communities.

Results: We demonstrate distinct roles for microbes in dMMR and pMMR CRC. Sulfidogenic *Fusobacterium nucleatum* and hydrogen sulfide production were significantly enriched in dMMR, but not in pMMR. dMMR microbial communities are predicted to be less stable than pMMR microbial communities, whereas pMMR communities are predicted to be suppressive of CRC-associated *Bacteroides fragilis*. Community stability may play an important role in CRC development, progression, or immune activation within the respective MMR subtypes.
Conclusions: Integrating tumor biology and microbial ecology highlighted distinct microbial, metabolic, and ecological properties unique to dMMR and pMMR CRC. This approach could critically improve our ability to define, predict, prevent, and treat colorectal cancers.

Jim Brunner: Efficient dynamic FBA for microbial communities

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Personalized models of the gut microbiome are valuable for disease prevention and treatment. For this, one requires a dynamical model that predicts microbial community composition and the emergent behavior of microbial communities. Motivated by the goal of creating individualized models from single patient data, we investigate models built from the interactions between microbes and external metabolite. These models, called metabolite mediated models, have the necessary complexity to explain growth experiments involving a set of species grown in pairs and trios. In order to build metabolite mediated models, we use genome scale metabolic models. We may simulate community dynamics using “constraint based analysis", optimizing internal reaction vectors for growth and updating microbial community biomass as well as external metabolite concentration accordingly. This procedure is known as “dynamic flux balance analysis". We present a novel algorithm, using a piecewise ordinary differential equation (ODE) approximation to dynamic flux balance analysis, which increases speed over traditional algorithms. Furthermore, this algorithm is based on a piecewise quadratic ODE, moving the problem into a well-studied framework and allowing us to take advantage of the theory of differential equations.

Minsuk Kim: Revisiting the definition of ecological interactions in community metabolic modeling studies: current approaches, limitations, and future directions

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Genome-scale metabolic models have been considered to be a very useful tool for investigating microbial interactions. Since first proposed by Stolyar et al. (Mol. Syst. Biol. 2007), joint flux balance analysis (Joint FBA) has been widely used by many research groups for inferring ecological interactions between microbes. First, Joint FBA is used to compare growth rates of microbes from individual and co-growth simulations. Then, types of ecological interactions between microbes (e.g., competition, commensalism, and mutualism) are determined based on the differences in growth rates. However, it has recently been discussed that mass balance equations for extracellular metabolites in Joint FBA are inappropriate (Chan et al., PLoS Comput. Biol. 2017). Moreover, here we argue that the ecological interactions defined based on Joint FBA are not very useful for further applications. In this talk, we present a new method that we are developing to address the limitations of Joint FBA. Our method is similar to the SteadyCom algorithm (Chan et al., PLoS Comput. Biol. 2017) in terms of the constraints used in the optimization problems, but is also quite different in terms of the system definition and objective function. Notably, our method can be used to test a mutual invasibility criterion for stable coexistence for a more rigorous definition of ecological interactions. In addition, our method has an advantage over Joint FBA and SteadyCom in that it generates hypotheses that can be experimentally tested in a chemostat. We expect that the method can be applied to tackle clinically important problems such as predicting susceptibility to a pathogen and persistence of probiotics.

Maximino Aldana González: Modeling the role of the microbiome in evolution

When plants and animals appeared on Earth, the planet was already crowded with microbes. Therefore, the evolution of multicellular organisms did not only take place in the presence of microbes but, in many cases, it was possible only with their help. Throughout evolution, microbes and multicellular organisms established long-lasting symbiotic relationships observed to this day. These symbiotic interactions are so strong that some scientists have suggested that the very concept of “individual” has to be reformulated (or extended) in order to incorporate these interdependencies in evolutionary theories. Thus, the concept of “holobiont” (the multicellular host plus its microbiota) has emerged as a unit of selection in evolution. We present an evolutionary model, based on complex network dynamics, showing that the interaction with microbes greatly improves the adaptation of the host to perform new functions. Furthermore, a great microbial diversity is required for the host to develop multiple phenotypes in order to perform different functions. Disrupting these interactions often leads to

non-adaptive states, reminiscent of dysbiosis, where none of the networks the holobiont consists of can perform their respective functions. By considering the holobiont as a unit of selection and focusing on the adaptation of the host to predefined but arbitrary functions, our model reproduces many patterns regarding the emergence of host-microbe symbiotic interactions and predicts the need for specialized diversity in the microbiota. Furthermore, both structural and dynamical complexity naturally emerge in the holobiont as a result of considering it as a unit of selection in evolution.

Ayari Fuentes Hernández: Modeling ecological interaction of microbial communities

Microbial communities are defined as an assembly of different microorganisms interacting in a complex environment. There are multiple benefits associated with living in a community, for instance, by communicating and exchanging metabolites, microbial consortia can perform functions collectively that individual cells could not achieve when grown in isolation.

In particular, we study a community composed of individuals that produce and export into the environment essential substrates that the remaining members of the community need to perform critical cellular functions, but are unable to synthesize themselves. In this case, the profile of interaction of the community can be defined as obligate mutualism, and the stable co-existence of all strains can only be guaranteed if every member is present and cooperating. The community's population dynamics, however, is highly dependant on the physicochemical properties of the environment, so, in principle, the strength of pair-wise interactions could be modulated through environmental manipulations. For instance, if one of the exchange molecules is supplemented into the environment, then this substrate ceases to be limiting, and the strength of the positive interaction decreases until a competitive interaction emerges at high concentrations, thus compromising the stability of the community.

In this work, we use a co-culture of multiple strains of Escherichia coli with complementary amino acid auxotrophies and different fluorescent markers, with the aim of evaluating how the profile of interaction of the community changes in response to different media compositions (amino acids and antibiotics) and population structures (initial frequencies of each strain).

Marco Tulio Angulo: Controlling complex microbial communities: a network-based approach

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Controlling human microbiota offers new possibilities to prevent and treat complex diseases. However, the complexity of the human microbiota —in terms of its number of species and the limited knowledge of their interaction mechanisms— makes it very challenging to rationally and systematically design efficient control strategies. In this talk, I will introduce a two-step framework to overcome this challenge based on new mathematically rigorous algorithms. In the first step, we developed an algorithm to infer the ecological network underlying a microbial community. Crucially, this algorithm does not require knowledge of the community's dynamics, allowing us to map a directed signed network that encodes the ecological interactions between species. In the second step, we show how the inferred ecological network enables identifying a minimum set of its "driver species," manipulation of which allows controlling the whole community. Our results provide a systematic pipeline to efficiently drive complex microbial communities towards desired states.

This is joint work with Yang-Yu Liu (Harvard) and Claude H. Moog (L2SN, France).

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Joel Stavans: Stochastic Turing patterns in the development of a one-dimensional organism.

Cells having the same genetic information can behave very differently, due to inevitable stochastic fluctuations in gene expression, known as noise. How do cells in multicellular organisms achieve high precision in their developmental fate in the presence of noise, in order to reap the benefits of division of labor? We address this fundamental question from Systems Biology and Statistical Physics perspectives, with Anabaena cyanobacterial filaments as a model system, one of the earliest examples of multicellular organisms in Nature. These filaments can form one-dimensional, nearly-regular patterns of cells of two types. The developmental program uses tightly regulated, non-linear processes that include activation, inhibition, and transport, in order to create spatial and temporal patterns of gene expression that we can follow in real time, at the level of individual cells. We study cellular decisions,

properties of the genetic network behind pattern formation, and establish the spatial extent to which gene expression is correlated along filaments. Motivated by our experimental results, I will show that pattern formation in Anabaena can be described theoretically by a minimal, three-component model that exhibits a deterministic, diffusion-driven Turing instability in a small region of parameter space. Furthermore, I will discuss how noise can enhance considerably the robustness of the developmental program, by promoting the formation of stochastic patterns in regions of parameter space for which deterministic patterns do not form, suggesting a novel, much more robust mechanism for pattern formation in this and other systems.

Rosana Pelayo Camacho: Leukemia remission in the context of an increasingly complex environment: the global challenge

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Childhood acute lymphoblastic leukemia, one of the leading concerns of global health and the major cause of mortality from disease worldwide, results from alternate waving of normal and leukemic lymphopoiesis, where the uncontrolled production of lymphoid precursor cells within the bone marrow (BM) is the prominent feature. From a multi-factorial, dynamic and interactive biological network perspective, acute leukemias result from the continuous interaction of subjacent genetic elements with microenvironmental factors that contribute to evolution of primitive malignant cells. Unraveling the pathobiological identity of leukemia initiating cells (LIC) and how they relate to microenvironment is essential to develop integral therapeutic strategies or to propose new predictive and prevention routes.

The comprehensive understanding has been considerably delayed due to the high biological and clinical heterogeneity of the disease and the phenotype similarity with the normal stem/progenitor cells LIC exhibit. Moreover, requirements and microenvironmental intercommunication they establish with a hematopoietic niche are poorly known due to lack of models that better replicate structural properties of the bone marrow. Systems biology, including both, theoretical and experimental approaches to model the essential cell-to-cell intercommunication regulating crucial cell fate decisions, has allowed us to dimension the role of microenvironment in the complexity of tumor colonization at the expense of normal blood differentiation.

We have learned that primitive LIC have affinity for hypoxic specialized niches and are highly dependent on interactions with microenvironmental cells and cues. Organoid-like three-

dimensional structures resembling the BM architecture and patient-derived xenotransplantation models have revealed a dysfunctional reticular niche that relates to leukemic burden, while hypoxic niches may protect quiescent leukemia initiating/relapse cells. Developing malignant cells outcompete normal cells and remodel the surrounding microenvironment through release of exosomal TLR ligands and pro-inflammatory factors. By developing and simulating mathematical models, the biological consequences of microenvironmental perturbation due to temporal TLR signaling on crucial interactive networks between HSPC and mesenchymal stromal cells (MSC) have been investigated. Furthermore, the transcriptome of leukemic microenvironments suggests two types of BM niches: an inductive niche enriched in inflammation signaling pathway components and chemokines, and a potentially repressive/retention niche with high content of extracellular matrix proteins. Retention niches provide the bone marrow with sanctuaries for drug resistant leukemia-initiating cells capable of long-term invasion.

Overall, our findings suggest that the driving force from a restrictive-repressive niche to a permissive niche is the inflammation. Inflammation-derived signals provide a mechanism for leukemic cells to survive and prompt niche edition. Intervening the oncopromotion ability from the microenvironment is a scientific challenge to control leukemic progression.

Nathan Weinstein: Modeling microvascular endothelial cell behaviour and plasticity

IE and C3, UNAM

During development and throughout the life of an individual, vascular networks need to adapt to the changes in oxygen and nutrient requirements that result from growth, wounds, and aging. Vasculogenesis allows endothelial cells to aggregate and to form tubular structures that become vessel segments. Sprouting and intussusceptive angiogenesis allow the formation of new capillaries as well as the pruning of unnecessary capillaries. Arteriogenesis allows vessels to increase in diameter and efficiently augment tissue irrigation, as well as the formation of natural bypasses. Defective vascular network development or adaptation is involved is several cardiovascular diseases including retinal vascular disorders, micro-vascular cerebral diseases, arteriovenous malformations, aneurysms, cerebral cavernous malformations, defective wound healing, and arteriosclerosis.

To gain an insight into vascular development and adaptation, we are modeling and simulating the dynamic behavior of molecular regulatory networks involved in regulating endothelial cell behavior and plasticity. Our first model includes molecules associated to the ANG/TIE, HIF, AMPK/mTOR, VEGF, IGF, FGF, PLC /Calcium, PI3K/AKT, NO, NOTCH, and WNT signaling pathways, as well as the mechanosensory components of the cytoskeleton that are involved in the control of endothelial cell behavior during sprouting angiogenesis. After

formalizing our model as a Boolean network and analyzing its dynamic behavior, we where able to associate the presence of ligands in the extracellular micro-environment surrounding an endothelial cell with Phalanx, Stalk, and Tip behaviors, as well as mapping the pattern of ligand presence to the activity of the cell cycle within the endothelial cell, and with mural cell recruitment. After simulating the microenvironmental conditions and mutations associated with the retinal vascular disorder, tumor vascularization, and arteriovenous malformations, we were able to reproduce in-silico the endothelial behavior associated with the diseases.

In addition to changes in endothelial cell behavior, blood vessel development, adaptation, and stability require endothelial cell differentiation. Specifically, endothelial cells can differentiate into mural cells in a process mediated by the endothelial-to-mesenchymal transition (EndMT). Moreover, endothelial cells can also differentiate first into hematopoietic stem cells and then into macrophages through the endothelial-to-hematopoietic transition (EHT). We are currently studying, modeling and simulating the molecular regulatory networks involved in EndMT and EHT.

Alfredo Rodríguez Gómez: WIP1 contributes to the adaptation of Fanconi anemia cells to DNA damage as determined by the regulatory network of the Fanconi anemia and checkpoint recovery pathways

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DNA damage adaptation (DDA) is a process that allows the progression into the cell cycle of cells with unrepaired DNA damage. Cells with DNA repair deficiencies might take advantage of DDA to survive; however, this cellular outcome promotes carcinogenesis. The Fanconi anemia (FA) pathway is committed to the repair of DNA interstrand crosslinks (ICLs), deficiencies in this pathway cause a fraction of breast and ovarian cancers as well as FA, a chromosome instability syndrome (CIS) characterized by congenital malformations, bone marrow failure and cancer predisposition. Although FA pathway deficient cells are hypersensitive to ICL inducing agents such as Mitomycin C, or intracellular produced aldehydes, DDA seems to be a mechanism allowing their survival.

We present the FA-CHKREC Boolean Network Model (BNM), which explores how FA cells might recur to DDA. This BNM integrates the FA pathway with the G2 checkpoint and the checkpoint recovery (CHKREC) processes. While the first mediates cell-cycle arrest (CCA), the later mediates cell-cycle progression (CCP) after resolution of DNA damage. The analysis of the FA-CHKREC network connectivity and its dynamics indicates that the CHKREC has multiple layers of regulation in the DDA of FA cells, including inactivation of DNA damage repair and checkpoint proteins. In addition, the CHKREC might ignore the presence of unrepaired DSBs and allow cell division despite unrepaired DNA damage. The later hypothesis was tested experimentally by inhibiting WIP1, a critical CHKREC component, in FA pathway deficient lymphoblast and cancer cell lines, which confirmed that its inhibition prevents the entrance of FA cells into mitosis.

Carlos Espinoza-Soto: Phenotypic plasticity and evolution of genetic regulatory networks

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Many developmental processes depend on the coordinated change in gene expression driven by gene regulatory networks. Modifications in such networks have produced many evolutionary novelties in a wide range of lineages. Different researchers have postulated that phenotypic plasticity, a genotype's ability to produce phenotypic variants in response to non-genetic perturbations, may have an important role in the evolution of new beneficial traits through a mechanism called genetic assimilation. We used a model to study the dynamics and evolution of gene regulatory networks to assess whether genetic assimilation can be a frequent means of producing new gene expression patterns. Our results support that mutation, recombination and plasticity frequently collaborate in the evolution of new adaptive phenotypes.

Claudia Rangel Escareño: Modeling gene expression dynamics using a convoluted approach of feature selection and a hidden markov model

Alejandro Cárdenas-Ovando, Edith Fernández-Figueroa & Claudia Rangel-Escareño*

A variety of methods for the analysis of gene expression with longitudinal measurements have been proposed. In all cases, we deal with noisy data, small number of time points, limited replication and questionable dependencies. In this talk, I present a novel algorithm that integrates a probabilistic graphical approach using Hidden Markov Models (HMMs) ideal for

modeling sequential data, convoluted with feature selection (FS) for gene classification. Its novel contribution or major innovation resides in how the method handles limited data points and low replication. This innovation is relevant because most genome-based studies face this same challenge, particularly longitudinal designs for which, sample size is a combination of time measurements and biological replicates. The proposed method is intended for almost any longitudinal study where we deal with thousands of variables, few time points, and sometimes even fewer replicates. The mathematical and graphical nature of the HMM allows adding structure to model design. That structure represents both gene-to-gene interactions and system dynamics. The strategy involves an embedded FS with HMM (FSHMM) that models the possible states for a gene at each time point. This sequence of such states describing a path of change/no-change across time then goes into the FS algorithm for classification ranking genes according to three criteria: Magnitude of the change between consecutive time points; frequency of changes across the time series; and replication quality. The method is adapted to work for either one or multiple conditions. The main contribution of our approach is that the ranking identifies genes with differential profile across time and between one or multiple conditions simultaneously. Its importance resides in that it models expression values without discretizing it works well with really small sample sizes due to the way data is arranged for the HMM. The algorithm has been coded as an R-package and is also available at GitHub (https://github.com/robalecarova/fshmm).

Flash talks

Carlos Muñoz, Instituto de Ecología, UNAM (poster #1): Boolean vs Continuous, an analysis of the behaviour of Boolean and continuous models of small genetic regulatory motifs.

Genetic regulatory networks (GRNs) are usually modelled using Boolean algebra and/or continuous equations. This project aims to explore the behaviours present in each model using a small GRN motif. This will be useful for deciding which type of model (Boolean or continuous) will be more useful for analysing certain properties of GRNs.

Antonio Barajas Martínez, UNAM (poster # 2): Metabolic Syndrome as a Network.

We performed a transversal, community-based study of an ethnically and educationally diverse sample comprehending 1076 adults. Each participant answered a questionnaire and underwent anthropometric measurement along with blood tests for biomarkers of metabolic syndrome. Using correlation matrices, we modelled metabolic syndrome in two scenarios, as a continuous or as a dichotomic association. The sample was stratified by age and education and networks were assembled from the correlation matrices. Centrality measures show how some variables drive the metabolic syndrome while others work as metabolic intermediaries. This model suggests possible targets for intervention within each group.

Mathieu Hautefeuille, UNAM (poster # 3): Standardizing the development of on-demand cell culture scaffolds and organ-on-chip technology at LaNSBioDyT: from microfabrication to mechanobiology

We will demonstrate that our solution-oriented design and validation strategy allowed to fabricate solutions that perform similarly to other published works and that our fabrication methods offer an excellent control over cellular behaviours and functions within our scaffolds, such as adhesion and spreading. Thanks to the recent progress in our lab, it is now possible to start developing platforms with on-demand features for mechanobiology applications.

Carlos Villarreal, UNAM (poster # 4): Complex network characterisation of type 2 diabetes progression.

We propose a regulatory network for components of pancreatic-beta cells playing an essential role in type 2 diabetes. The network dynamics characterises the disease progression as a transit between steady states associated to health, metabolic syndrome, and diabetes. Progression from health to diabetes is precipitated by alteration of characteristic expression times or exhaustion of key cellular components. By merging the present approach with former models that describe the dynamic balance of beta cells, glucose, and insulin in the disease, we provide an accurate description of patient data for the long-term progression of beta cell mass, insulinemia, glycemia, and glycosylated haemoglobin.

Dalia Ortiz, Facultad de Ciencias, UNAM. (poster # 5): Early warning signals in biological systems.

Many catastrophic events exhibit critical transitions, for this reason, it would be important to study how to prevent those abrupt shifts in the system state. In addition, as biological systems have not deterministic behaviour, it is necessary to study its stochastic version. Signals of increase or decline in variance, decrease in autocorrelation and critical slowing down could be detected when a system is reaching its tipping point; these indicators are called early warning signals. These signals have demonstrated their potential to prevent catastrophes; however, there are some cases where those trends do not avert those shifts.

Josué Héctor Azcona Trejo, UVM (poster # 6): A new theory about Alzheimer's disease

At present, dementias are chronic degenerative diseases, which generate disability and dependence on third parties. Alzheimer's disease (AD) is one of the most frequent dementias, with a prevalence of 7.3%. The global prevalence of dependence in older adults is 13% and it is estimated that between 2010 and 2015 the total number of dependents in different parts worldwide will almost double, passing more than 349 million to 613 million, and One third of this estimated population (101 to 227 million) will be older adults. Currently there are 13 million adults over 60 in Mexico. The first national study on Health and Aging in Mexico (ENASEM) in 2001 showed that 7% of the Mexican population had a lower cognitive impairment, and 3.3% had a greater cognitive impairment, with functional dependence. Being the highest prevalence in women and older1. The purpose of this article is to know the biochemistry of amiolide precursor protein and its association with the aetiology of dementia.

Jorge Gomez Tejeda Zanudo, Broad Institute (poster # 7): Network modeling of drug resistance mechanisms and drug combinations in breast cancer.

We present a comprehensive mechanistic network model of signal transduction in ER+ PIK3CA-mutant breast cancer. Focusing on PI3K inhibitors, the model recapitulates known resistance mechanisms and predicts other possibilities: loss of RB1, FOXO3, or P27. We test, verify, and falsify some of the model predictions using genome-wide CRISPR screens and by generating breast cancer cell lines with a stable CRISPR KO. The model also reveals known and novel combinatorial interventions that are more effective than PI3K inhibition alone. In particular, the model predicts that the combination of PI3K inhibitors with inhibitors of anti-apoptotic BH3 proteins (e.g. MCL1) would be effective.

Diana García, INMEGEN (poster # 8): Gene co-expression is distance dependent in breast cancer.

Prognosis in breast cancer can be traced to the transcriptome level. Aberrant gene co-regulatory programs lead to different breast cancer manifestations: the molecular subtypes. We have observed previously that in healthy tissue co-expression takes place between genes from different chromosomes, but in breast cancer, interactions are lost in trans-. To evaluate this effect in molecular subtypes, we characterize the global co-regulatory program in terms of physical distance. We analyze the strength of cis- interactions using Mutual Information, describing the Distance Dependent Gene Co-expression phenomenon in breast cancer and how this loss correlates with loss of specificity and function.

Eliezer Alejandro Flores Garza, UNAM ((poster # 9): Systems biology for the study of the physiopathological progression of tuberculosis: Towards an improvement of prevention strategies

This work aims to study tuberculosis, a deadly world persistent chronic infectious disease caused by bacteria Mycobacterium tuberculosis, from a systemic point of view using mathematical models. We propose a hybrid model, integrated with experimental data from our clinical collaborators, composed by a system of ODEs that describe the host-pathogen dynamics and a Boolean network of macrophage differentiation describing the regulatory interplay between functional macrophage phenotypes and the inflammatory microenvironments that change as the disease progresses. This model will elucidate

mechanisms that regulate the dynamics of host-pathogen interactions and will contribute towards the efforts to improve the strategies of treatment and prevention of the disease.

Posters

María de la Soledad Ochoa Méndez, INMEGEN (poster # 11)

Breast cancer subtypes rest on differences of gene expression that reflect clinical differences. However, the path from a DNA coded piece of information to a phenotype is highly regulated and may be altered at several molecular levels. Given the differences on gene expression, we expect to find characteristic differences on gene expression regulation, that let us build mechanistic hypotheses of what makes breast cancer subtypes different. Linking the PAM50 gene expression signature and its most studied levels of regulation trough elastic net variable selection, we search for mechanistic differences between subtypes in a systematic manner with omics broadness

Raúl Cuauhtémoc Baptista Rosas, Universidad de Guadalajara (poster # 12)

Breast cancer has a predominant prevalence in Caucasian women. Although alterations of mitochondrial genome probably play an important role in carcinogenesis, the actual evidence is inconclusive. The purpose of this work was to explore mitochondria sequences of breast cancer cases by biology system approach. We identified 85 mtDNA sequences from breast cancer cases and 25 sequences used as controls. A repetitive pattern in D310 was found with statistical significance. Although most of these polymorphisms are commonly associated with specific haplogroups, we identified the 315.1C and C309CCT-T310C, evolutionarily related to caucasian origin, in 99% of sequences of non-European origin with breast cancer.

Maria Fernanda Robledo Carrasco, UNAM (poster # 12)

Importancia de la microbiota intestinal en la protección ante patógenos.

El objetivo del cartel es describir los componentes principales y las variaciones de la microbiota intestinal en humanos y los mecanismos mediados por el sistema inmune para conferir protección ante patógenos. Así como el análisis de las diferentes moléculas producidas por los comensales que evitan el desarrollo de las infecciones como la colitis

pseudomembranosa o gastroenteritis por diferentes agentes. Es importante mencionar el panorama terapéutico en el campo de la microbiología y la microbiota en la actualidad.

Fredy Omar Beltrán Anaya, INMEGEN (poster # 13)

Expression of long non-coding RNA LncKLHDC7B is enriched in the immunomodulatory triple-negative breast cancer subtype and its alteration promotes cell migration, invasion, and resistance to cell death.

TNBC is a heterogeneous disease, and gene expression analysis has identified seven molecular subtypes. Accumulating evidence demonstrates that long non-coding RNA (lncRNA) are involved in regulation of gene expression and cancer biology, contributing to essential cancer cell functions. In this study, we analyzed the expression profile of lncRNA in TNBC subtypes from 156 TNBC samples, and then characterized the functional role of LncKLHDC7B. Additionally, in silico analysis confirmed for the first time that the low expression of KLHDC7B and LncKLHDC7B is associated with poor prognosis in patients with breast cancer.

Sierra Romero, Hospital General "Dr. Manuel Gea González" (poster # 14)

Jorge Velázquez-Castro, BUAP (poster # 15)

Inhibition of inter-cellular calcium diffusion in photodynamic therapy.

We investigate the causes of inhibition of calcium diffusion in carcinogenic cells. This can lead to new ways of improving the accuracy and scope of photodynamic therapy.

Erick Eduardo Martínez Acosta, CISESE (poster # 16)

Modelado booleano de metástasis ósea de cáncer de mama (poster # 17)

Pese a los esfuerzos por reducir los casos nuevos de cáncer de mama y su diseminación a otros sitios como el hueso, no se ha podido detener la tendencia. Esto sugiere que nos falta mucho por saber de esta enfermedad, pero ¿necesitamos más estudios o estudiar mejor los datos ya obtenidos? Este trabajo busca condensar datos experimentales en un modelo cualitativo, con el fin de analizar la dinámica molecular de esta enfermedad y realizar inferencias sobre interacciones que se desconocen.

José Guillermo Buendía. IPN (poster # 18)

Relación de los polimorfismos en el gen de la colágena tipo II en el desarrollo de l enfermedad de Legg-Calve-Perthes.

a ELCP es una osteonecrosis idiopática de la cabeza femoral en pacientes pediátricos que se ha asociado últimamente a mutaciones en el gen de la colágena tipo II, lo que causa un arresto en la vascularización de la cabeza femoral, causando la patología clínica característica de esta enfermedad.

German Alonso Bernate Obando. Instituto de Fisiología celular (poster # 19)

Glucose stimulated insulin secretion (GSIS) depends on the activity of different ion channels, including the Kv2 voltage-dependent potassium channels. In order to know which genes regulate Kv2 channels expression, we constructed a gene coexpression network based on a previous transcriptome analysis made in our lab from pd20 and adult rat pancreatic beta cells. Additionally, we used probabilistic inference algorithms (Bayesian network) and mutual information algorithm (ARACNE) to come up with candidate regulatory genes. We found that Kcnb1 gene (Kv2.1) is regulated directly by Foxo1, Cacnb2, Vegfa and Gna12, while Kcnb2 (Kv2.2) is regulated by Bad, Pik3ca, Rab11a and Lamp5. The candidate regulatory genes of both channels participate in GSIS.

Jonathan O Connor, Universidad de Guadalajara (poster # 20)

Acute lymphoblastic leukemia interactome and their relationship with mtDNA polymorphisms

Jonathan Alejandro O'Connor Miranda, Luis Enrique Hernández , Arieh Roldán Mercado-Sesma, Raúl C. Baptista Rosas .
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Acute lymphoblastic leukemia is the most common cancer diagnosed in children. It has been demonstrated that various polymorphisms in mitochondrial genome are relates. This mutational changes in the mtDNA could be used as a biomarkers for early diagnosis and as a potential goal in the development of new therapeutic approaches. In this research we explored the frequency of polymorphisms in the mitochondrial genome and their potential interactions with key proteins related with carcinogenesis in leukemic patients.