Expositor	Work Title	Abstract
Dra. María del Carmen García-Rodríguez carmen.garcia@unam.mx Facultad de Estudios Superiores—Zaragoza, Universidad Nacional Autónoma de México (UNAM), Mexico City.	**Protection of hexavalent chromium-induced genotoxic damage in peripheral blood of mice by resveratrol and its relationship to the apoptotic activity**	Resveratrol (3,4',5-trihydroxy-trans-stilbene) it has high antioxidant potential associated with beneficial health effects in the context of neurodegenerative and cardiovascular diseases, as well as some types of cancer, diabetes, and obesity-related disorders. The antioxidant effects of resveratrol have been attributed to its ability to scavenge reactive oxygen species, and notably, resveratrol has been found to prevent DNA damage. Although the effects of resveratrol on toxicity induced by metals (e.g., arsenic and copper) has been studied, there are no studies evaluating the effects of this polyphenol on hexavalent chromium [Cr(VI)] compound-induced genotoxicity. The aim of the present study was to examine the protective effects of resveratrol against Cr(VI)-induced genotoxicity in vivo and the underlying processes of the apoptosis, which may be involved in preventing Cr(VI)-induced DNA damage. Hsd:ICR male mice are divided into groups of the following five individuals each: (a) control 1, distilled water; (b) control 2, ethanol 30%; (c) resveratrol, 50 mg/kg by gavage;(d) CrO3, 20 mg/kg intraperitoneally; (e) resveratrol+CrO3, resveratrol administered 4 h prior to CrO3. The genotoxic damage caused by Cr(VI) was evaluated with the micronuclei (MN) assay in erythrocytes of peripheral blood using acridine orange-coated slides. Apoptotic and necrotic cells were evaluated using differential acridine orange/ethidium bromide staining. The assessment is performed on peripheral blood. Micronuclei kinetics are measured from 0 to 72 h, while apoptosis were quantified at 48 h. In the CrO3 group, an increase of about 7, 10, and 5 MN was observed at 24, 48, and 72 h, respectively, which was significantly higher than the control C1 ($p < 0.001$, $p < 0.0001$, and $p < 0.015$, respectively). The group treated with resveratrol and CrO3 had lower MN frequency than the CrO3 only treatment at all times examined. When comparing the effect of treatments on apoptosis, resveratrol reduced the frequency of total and early apoptotic cells compared to control groups ($p < 0.022$ and $p < 0.015$, respectively), while CrO3 induced an increased number of total, early, late apoptotic, and necrotic cells compared to control groups ($p < 0.0001$). In the resveratrol+CrO3 mice,there were fewer late apoptotic and necrotic cells compared to the CrO3 group ($p < 0.001$ and $p < 0.0001$, respectively) and an increase in total and early apoptotic cells compared to the control group ($p < 0.0001$) and the resveratrol group. The increase in apoptotic cells and the decrease in necrosis further confirmed that resveratrol effectively blocks the actions of Cr(VI). Financial support was obtained from DGAPA-UNAM PAPIIT IN216122.
Omar Franco omarfranco352@gmail.com Instituto Nacional de Medicina Genómica, México.	**Coordinated activity of genes associated to a given function is a more critical factor in determining functional engagement than overall level of expression.**	Our genes direct the development, maintenance and functional complexity of the whole organism. However, any specific cellular function is rarely the result of individual genes acting in isolation, but, Instead, the result of hundreds or thousands of genes acting in concert and close functional coordination. If a particular cellular function results from the activity of a defined set of genes, whether the engagement of that cellular function is more related to either their collective level of expression, or to the overall level of coordinated expression (co-expression), remains unclear. Here we use available expression data to assess whether genes involved in a well defined cellular function (cell cycle), display a concomitantly higher or lower collective level of expression, or coexpression, when comparing between human tissues with a high, medium or low proliferative activity. Our results show that the collective level of correlated expression of cell cycle-associated genes, but not their collective level of expression, is a more robust indicator of proliferative function in human tissues; suggesting that the level of coordinated activity of genes associated to a given function is a more critical factor in determining functional engagement than overall level of expression.

Gonzalo Rivera gro.spaider@hotmail.com Facultad de Estudios Superiores Zaragoza, UNAM, México.	**Genes associated to maximum lifespan in mammals are more closely associated to genes involved in post mitotic maintenance than to genes involved in cellular senescence**	Work over the past years has identified distinct gene sets associated to either post mitotic cellular longevity, cellular senescence or maximum lifespan in mammals. However the functional links between these groups of genes so far remains unclear. Using available human gene expression data we use coexpression analysis to assess the possible functional association between these groups of genes. We found that while the collective correlation between genes associated to maximum lifespan in mammals and cellular senescence is no greater than chance expectations in several groups of human tissues, lifespan-associated genes display a stronger level of collective correlation with cellular longevity-associated genes than expected by chance. These results suggest a close functional link between genes associated to maximum lifespan in mammals and genes involved in post-mitotic cellular longevity in human tissues
Arturo Kenzuke arturokenzuke@gmail.com Instituto Nacional de Medicina Genómica, México.	**The network structure of hematopoietic cancers**	Hematopoietic tumors arise from the malignant transformation of blood cells and are classified into three main categories: leukemias, myelomas and lymphomas. Leukemia frequently presents as a "liquid tumor" originating from the malignant transformation of a cell of the lymphoid or myeloid lineage. Notably, the mutated gene landscape of acute myeloid leukemia has shown the lowest mutation levels among adult cancers. Lymphomas are solid tumors that arise within the lymphatic system from the malignant transformation of a B or T lymphocyte. Multiple myeloma is a type of blood cancer in which fully differentiated plasma cells acquire mutations that cause them to divide rapidly, these cells secrete high levels of a monoclonal protein (monoclonal immunoglobulin), which affects the clinical manifestations of the disease. In this work, RNA-Seq data from three types of leukemia, multiple myeloma and normal bone marrow were downloaded from TCGA. The gene expression data was filtered to remove low count genes and normalized to reduced eliminate GC-content and length bias. We used the ARACNe algorithm to calculate co-expression values between the genes and selected the strongest 10,000 values to construct the co-expression networks. We then performed a differential expression analysis for each of our cancer groups to detect which genes are over or under-expressed in comparison to the control group. After constructing the networks, we inferred an intersection network made up from the common interactions of the four cancer networks (using the top 100,000 interactions). We applied the community detection algorithm called HiDeF to detect persistent communities in each network. These communities were used to perform a functional enrichment analysis using clusterProfiler and hence detect biological processes that are represented in the networks. Integrating these results with our differential expression analysis allowed us to infer over- and under-expressed processes present in the cancer phenotypes. In this work, we focus on the analysis of the intersection network communities, which was useful to identify the biological processes that are represented in each cancer network by the same group genes and edges, and at the same time we were able to identify different expression patterns from each hematological cancer. The topological analysis of the cancer networks revealed an elevated proportion of interactions between genes of the same chromosome, which is a phenomenon called loss of inter-chromosomal regulation that has been observed in networks of other types of cancer. Also, we observed another interesting aspect in our networks: the co-expression between pseudogenes is elevated in the cancer networks, which are also mostly over-expressed in every hematological cancer. The community analysis showed that there are several biological processes that are represented in each of the networks, some of them could be related with some clinical characteristics of the diseases (for example, the communities representing the differentiation of erythrocytes are under-expressed which could be related with anemia, a frequent sign of hematological cancers). Our results reasserts that the co-expression networks are useful tools to analyze and obtain information of biological interest through the topological analysis.
Paola V. Olguín-Rodríguez. vane23.star@gmail.com Instituto de Ciencias	**Long-covid treatment by Polymerized Type I Collagen: changes on the physiological network.**	The human body is a complex system, patterns emerge as a result of the interactions between multiple physiological systems. These interactions as affected by illnesses such as COVID-19 [1]. A potential treatment of COVID-19 patients is intramuscular administration of polymerised type I collagen (PTIC). However, the underlying mechanism of collagen-induced immunomodulation remains not clear. In this work we evaluate the effect of the intramuscular administration of PTIC and Placebo in the physiological network in patients with long COVID. Furthermore, we investigated sex differences in the correlation between baseline and time evolution of experimental test. Using a data set of eighty-nine participants with a confirmed COVID-19 diagnosis (mild to moderate disease) that were followed for 12 weeks. Patients were randomly assigned to receive either 1.5 ml of PTIC intramuscularly

Nucleares, Universidad Nacional Autónoma de México,		every 12 h for 3 days and then every 24 h for 4 days (n = 45) or a matching placebo (n =44). The blood samples were taken from study subjects at days 1 (baseline), 7 (day 1 posttreatment), 15 (day 8 posttreatment) and 90 (day 90 posttreatment) We considered subjects who completed the experimental test in each group: PTIC group (n=20, female= 8, Male=12), Placebo group (n=17, female= 10, Male=7). In order to study the physiological network in each experimental period we calculated the Spearman correlation between physiological variable and epsilon measure as directional network [3,4]. We found sex-depend on differences in the epsilon and correlation measures for PTIC and Placebo group a long treatment. In summary, we provided numerical evidence that intramuscular PTIC treatment of symptomatic COVID-19 decreases the correlation between baseline and experimental period. In contrast for the placebo group there are correlation between baseline and day 97 in some physiological variables. We found that this result is stronger for the group of women than men.
Russell Abel Morales-Rubio russell.morales@cinvestav.mx Centro de Investigación y de Estudios Avanzados del I.P.N	**Noisy stimulation effect in cardiomyocytes shortening**	Noise is an intrinsic property of physiological systems, affecting the nervous and cardiovascular systems[1]. It has experimentally been shown that noise enhances the homeostatic function of the blood pressure regulatory system. Recently, we demonstrated that noise added in low intensities favors amplitude and raises the rate of calcium dynamics[2]. Here, we investigate whether noise induces changes in contractile response in myocytes when stimulated with periodic electrical signals disturbed by Gaussian white noise. Ventricular cardiomyocytes were isolated from a heart with retrograde perfused in a Langendorff system. For electrical stimulation, pulse trains created from a function generator were used, transmitted by two platinum electrodes, where it is possible to control amplitude (20 V) and frequency (0.2-5Hz), as well as the intensity of additive white noise to the signal by increasing the amplitude of the white noise by 10-30% of the amplitude with respect to the original signal. To obtain the temporal recordings of the contraction, we used a fast camera (IonOptix). The results showed that with a 10% noise level, the contractile response increased the maximum contraction and relaxation speed and a slight increase in the shortening percentage. This project has improved our understanding of variability's role in electrical stimulation in cardiomyocytes. In the future, associate it with clinical data and test new therapeutic alternatives such as the condition of variability in electrical stimulation.
Daniela Mayari del Toro Instituto Nacional de Medicina Genómica, México.	**Changes in regulator expression are poorly associated with changes in target expression in gene regulatory networks.**	Noise is an intrinsic property of physiological systems, affecting the nervous and cardiovascular systems[1]. It has experimentally been shown that noise enhances the homeostatic function of the blood pressure regulatory system. Recently, we demonstrated that noise added in low intensities favors amplitude and raises the rate of calcium dynamics[2]. Here, we investigate whether noise induces changes in contractile response in myocytes when stimulated with periodic electrical signals disturbed by Gaussian white noise. Ventricular cardiomyocytes were isolated from a heart with retrograde perfused in a Langendorff system. For electrical stimulation, pulse trains created from a function generator were used, transmitted by two platinum electrodes, where it is possible to control amplitude (20 V) and frequency (0.2-5Hz), as well as the intensity of additive white noise to the signal by increasing the amplitude of the white noise by 10-30% of the amplitude with respect to the original signal. To obtain the temporal recordings of the contraction, we used a fast camera (IonOptix). The results showed that with a 10% noise level, the contractile response increased the maximum contraction and relaxation speed and a slight increase in the shortening percentage. This project has improved our understanding of variability's role in electrical stimulation in cardiomyocytes. In the future, associate it with clinical data and test new therapeutic alternatives such as the condition of variability in electrical stimulation.

Esbeidy García-Flores
esbeidy.garciaflores@gmail.com

Escuela Superior de Medicina del Instituto Politécnico Nacional

"DNA methylation levels of the TBX20 gene promoter in paediatric Mexican patients with congenital septal defects"

Introduction: Congenital heart defects (CHDs) are defined as defects in the structure of the human heart during embryonic development. Recent studies have shown that the genetic and environmental components have an impact on the presentation of these diseases. In particular, the *TBX20* gene encode to an important cardiac transcription factor that has a key role during the cardiogenesis. Up today, there are no studies evaluating DNA methylation of the *TBX20* gene in septal defects paediatric patients. **Objective:** The aim of this research was to evaluate the association of DNA methylation levels of the *TBX20* gene with the risk of development CHDs; specifically, septal defects. In addition, we performed an in silico analysis through bioinformatic tools in the *TBX20* gene promoter region. **Methodology:** Using a pyrosequencing analysis, a region of a CpG island in the promoter region of the *TBX20* gene was quantified, which included 7 CpG sites in 48 patients with septal defects and 104 control individuals. Also, an in silico analysis was performed with bioinformatic online tools to identify potential binding sites for transcription factors in the sequence evaluated. Finally, we assessed a protein-protein interaction (PPI) network. **Results:** We found statistically significant differences in the average of all sites of the DNA methylation levels of the *TBX20* gene promoter between septal defects patients and controls (18.46, IQR= 16.85-20.39 vs 20.64, IQR=18.85-22.92, respectively, $p< 0.001$). Then, we classified the methylation levels of the *TBX20* gene into quartiles and we identify the association of the highest quartile of average of all CpG sites with a significant increased risk of developing septal defects (OR= 4.73, 95% CI= 1.69-13.27), $p= 0.003$). Regarding the in silico analysis showed binding sites for Hey-like basic Helix-Loop- Helix (bHLH) and Specificity protein 1 (Sp1) transcription factors. Moreover, the analysis of PPI network reported the interaction between several proteins implicated with CHDs, where *TBX20* gene participates in the cardiac chamber and atrial septum formation, and a marked association with atrial septal and ventricular septal defect. **Conclusion:** Our preliminary results suggest that high levels of DNA methylation of the *TBX20* gene promoter could be considered as an epigenetic marker for early detection of these types of congenital heart malformation. However, it is suggested to carry out additional studies in other populations and increase the number of participants to confirm our findings.

Antonio Barajas Martinez antonio.barajas@c3.unam.mx UNAM, México.	**Physiological network to assess achalasia**	Achalasia is a disorder of the motility of the gastrointestinal tract that occurs in the esophagus. Here, a series of inhibitory and motor neurons work together to control swallowing, which is a mechanism that involves the orderly contraction of the three muscular layers that make up the esophagus. While vagal stimulation is primarily responsible for controlling esophageal skeletal muscle, a gradient of cholinergic to non-cholinergic innervation is responsible for controlling the esophageal smooth muscle locally. The arrangement of the muscle fibers in each of the three layers of the esophagus, in conjunction with the neurons that are affected by achalasia, gives rise to various motility patterns. Through the use of high-resolution esophageal manometry, it is possible to distinguish between three distinct motility patterns. The pattern of dysfunction varies depending on which neurons are damaged, although all three forms share a lack of normal peristalsis. Despite the thorough clinical description of this disease, there is currently insufficient information to pinpoint its causes or developing prevention strategies. Currently, treatment focuses on alleviating disease symptoms without addressing their underlying cause. Recent research on multiple sclerosis has focused on the possibility that a viral infection may trigger an autoimmune response. It has been speculated that this could be true for achalasia patients as well. However, the viral infection responsible for triggering autoimmunity towards these neuronal populations has not been identified. Here, we describe a method that employs a physiological network approach to address the probability landscape behind this disease's occurrence. Before undergoing surgical treatment at a facility in Mexico City, cross-sectional data from 189 patients was collected. Using clinical history, immunological, and tissular biomarkers, an extensive database was elaborated. Due to the role of gender in immune system illnesses, this study evaluated both males and females separately. Correlation matrices were constructed using bivariate relationships in order to generate complex inferential networks. Then, these matrices were filtered based on statistical significance to determine the most pertinent relationships between variables. Network topology description and variable's centrality were obtained using tools available for R programming language. We identified that previous history of chicken pox, measles and mumps may be risk factors for this disorder, especially in females. Principal components analysis identifies serum Il-22, and Th2 and regulatory B lymphocytes as variables that contribute most to this disease. The clinical presentation and systemic consequences of a local disease could be predicted based on changes in network topology. While immunological involvement appears to be localized in men, who have a highly modular physiological network, it is systemic in women, who have a robust network with more inter-cluster linkages.
Mildred Alejandra López Olaiz milyolaiz@gmail.com Universidad del Valle de Atemajac, Jalisco, México	**"Nutritional Genomics in Type 2 Diabetes: Exploring Genetic Variants Related to Absorption and Metabolism of Nutrients"**	Introduction :Type 2 diabetes mellitus (T2DM) is one of the most studied polygenic diseases today and is determined by genetic and environmental factors. Genetic factors generate various pathophysiological defects such as insulin resistance, inadequate insulin secretion, decrease in the effect of incretins, among others, and the environment plays a very important role in their prevention or control, which includes lifestyle (diet, smoking, alcoholism and physical activity). For this reason, in recent years a new area has emerged: nutritional genomics. She is in charge of applying bioinformatics in nutrition research that helps to design personalized diets, in order to prevent and control genetic diseases.Objective: Identify the genetic variants involved in the absorption and metabolism of nutrients present in the Mexican population with T2D. Material and method: An observational, cross-sectional, descriptive, retrospective study was designed using the GWAS Sigma project database of Mexicans with type 2 diabetes, with 3,848 patients diagnosed with the disease and 4,366 control cases. The sampling method was non-probabilistic by quota. Results: Genes related to nutrient absorption and metabolism were found: INS, TCF7L2, SLC30A8, TRPM6, PPARGC1A, FTO, ARNTL and PLIN with variants that were not present in the control cases of the study population, in addition to being associated in the literature predisposition to develop T2DM. Conclusion: This research provides information on the relationship between nutrients and genes, as well as their role within the pathophysiology of T2DM. In addition, there is a relationship between the individual genetic load that Mexicans have and the importance of environmental factors to influence gene expression and define the individual risk of T2DM. This is only a small part of what can be done with this information for future research in nutritional genomics to reach its practical application.

Camila García Camilajimenez000@gmail.com Universidad de Guadalajara, CUT Tonalá, México	**MITOCHONDRIAL SINGLE NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH TYPE 2 DIABETES IN A MULTIETHNIC POPULATION**	Background. Type 2 Diabetes (T2D) is a chronic-degenerative systemic disease. Within etiopathogenesis, mitochondrial dysfunction has been reported in several tissues of patients with T2D. However, it is not clear if mitochondrial dysfunction is a primary cause, or if there is any relationship with polymorphisms in the mitochondrial genome sequence. Therefore, the purpose of this project was to identify the frequency of polymorphisms of mitochondrial DNA (mtDNA) in patients with and without T2D, as well as their potential association with the disease. Methodology.We performed a secondary data analysis, using complete mtDNA sequences from patients with and without T2D, which were obtained from the NCBI NUCLEOTIDE DATABASE. Subsequently, we aligned the sequences using UCSC BLAT tool (GRCh38/hg38 Assembly) using the revised Cambridge Reference Sequence as reference, and identified the polymorphisms present in the mtDNA sequences. Results. We analyzed polymorphisms in the mtDNAs of 1261 individuals with T2D and 1105 control individuals. We found 80 different polymorphisms, of which five were identified in the scientific literature as relevant for T2D. According to our data, m.1438A>G (72.4%%), m.14766C>T (63.1%), m.16519T>C(56.6%), m.10398A>G (53.1%) and m.16189T>C (53.0%) polymorphisms were more frequent in T2D patients compared to controls. Finally, in the logistic regression analysis we evidenced that the presence of m.1438A>G (OR:2.46;95%CI:1.64-3.78; p<0.001), m.16519T>C (OR:1.24; 95%CI:1.05-1.47;p=0.012),m.14766 C>T (OR:2.57;95%CI:2.18-3.04;p<0.001) were significantly associated with a higher probability of presenting T2D. Conclusion. The mechanisms underlying the hereditary predisposition to T2D are largely unknown. Our results suggest that there is a relationship between the presence of mtDNA polymorphisms and the probability of presenting T2D. Whether the presence of these polymorphisms is the cause or consequence of said pathology remains in question. Finally, we hypothesize that the early identification of mtDNA polymorphisms could be an important predictive marker of future disease.