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Daniela Kantor. Médanos, 2018

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Daniela Kantor nació el 23 de marzo de 1970. Es diseñadora gráfica (FADU-UBA), pintora, dibujante, historietista e ilustradora. Autora de la novela gráfica Mujer Primeriza (Ed. Burlesque, 2014) y Aprendiza (2019), Naturalella (con guión de Arekasadaro, 2017) publicada en Dis-Tinta (Ed. Sudamericana, coordinado por Liniers y Martin Pérez). Con guion de Alejandro Farias dibujó Las moradas de Santa Teresa de Jesús en historietas (Ed. Loco rabia + CCEBA Centro Cultural de España en Buenos Aires) y Marilyn (Tren en movimiento, 2019). Es miembro de la revista de historietas “El Tripero” fundada en 1993 junto al grupo de alumnos de Alberto Breccia. En el ámbito de la enseñanza es Jefa de Trabajos Prácticos en la materia Ilustración inicial, y docente en Ilustración Editorial en la Facultad de Arquitectura, Diseño y Urbanismo FADU/ UBA. Dicta talleres sobre pintura e ilustración (C C Recoleta, 2019/ Quinta Trabucco, 2020/ taller particular junto a Daniel Roldan, 2019). Es maestra de niños y niñas en Dibujo e Historieta en Escuelas primarias, talleres (Filbita, Festival de literatura de Buenos Aires, 2018-9/ CCK, 2018/ taller propio desde 2014). Estudió Dibujo de Historieta con Alberto Breccia, Técnicas de Acuarela y Pastel con Carlos Nine, charlas sobre Historieta con José Muñoz, Curso de Color con Carlos Gorriarena, Clínica de Pintura con Mariano Sapia y Tulio de Sagastizábal, y Sumi- e en el Centro Okinawense. Trabaja para editoriales y revistas con ilustraciones e historietas (Ed. Troquel, Abran Cancha, Ed. Norma, Unicef, Barcelona, Crisis, Suplemento Ñ/ Clarín, Borges en la Biblioteca Nacional- Lectores de Borges). Fue invitada a la Feria del libro de los Universitarios de UNAM para presentar el libro “Palabra de ilustrador”, y en 2019 ganó la Beca UBA Internacional en el marco de un programa de intercambio docente con la Universidad Regiomontana, Monterrey, México.

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not show positive selection among all studied phylogenetic groups. These results strengthen the idea that ZPs are proteins that provide a more specific-specificity isolation than IZUMO1R, which is specialized in fusion events.
Altogether, our findings indicate that sperm-oocyte interaction and fusion proteins lack the degree of diversification necessary to fix a prezygotic reproductive isolation barrier in felidae.

37. (498) **PROTEOMIC STUDY OF BREAST CANCER CELL LINE AFTER HEMIN TREATMENT**

Schweitzer K[1], Coló GP[1], Fernandez Chavez L[1], Alonso EG[1], Fässler R[2], Curino AC[1]., Facchinetti MM[1]
1. Laboratorio de Biología del Cáncer – Instituto de Investigaciones Bioquímicas Bahía Blanca (INIBIBB) Universidad Nacional del Sur (UNS-CONICET). Departamento de Biología, Bioquímica y Farmacia.
2. Department of Molecular Medicine Max Planck Institute of Biochemestry (MPI), Martinsried, Germany.

Hemin is a ferriporphyrin (C34H32ClFeN4O4) with antitumoral effects on prostate, breast and colon cancer. It is widely used to increase the expression and activity of hemoxigenase-1 (HO-1). HO-1 is a microsomal enzyme that catalyses the degradation of heme group and can be translocated to subcellular compartments. Our laboratory, among others, has demonstrated that HO-1 regulates several processes related to cancer progression. The aim of this work was to study the protein expression modification due to hemin treatment in a murine breast cancer cell line (LM3). After hemin or vehicle (control) cell treatment, we performed Mass Spectrometry (MS) and Perseus proteome analyses. The proteome analysis showed that 1033 from 7292 proteins detected were modulated after hemin treatment. We observed that 595 proteins were significantly increased, including HO-1, and 353 proteins were significantly decreased in the group treated with hemin respect to their controls ($p<0.05$). ANOVA significant proteins reveal an upregulated group of proteins related with lipid and iron metabolism. In the group of proteins whose expression decreased after hemin treatment, we found cytoskeleton-related proteins. The Perseus-MS-data analysis revealed that hemin treatment regulates adhesion proteins like vimentin and talin, actin and tubulin cytoskeletal proteins and their stabilizing proteins. In addition, from MS data after hemin treatment, we found an increase in some cancer suppressor proteins such as PTEN and SMAD2/3. Finally, we found that proteases involved in HO-1 nuclear translocation were upregulated after hemin treatment. We further corroborated some of the *in-silico* analysis in LM3 cell line by immunofluorescence and Western blot techniques. In addition, we used a syngeneic LM3 mice model to detect by immunohistochemistry some of the regulated protein. These results show the multiple physiological effects that pharmacological modulation with hemin has in a breast cancer cell line.

38. (501) **ENZYMES INVOLVED IN EXTRACELLULAR MATRIX PROTEOGLYCAN´S SYNTHESIS AS A POTENTIAL THERAPEUTIC TARGET FOR COLORECTAL CANCER STEM CELLS**

Ariadna BIROCCO1, Agustín BLACHMAN 1, Nicole ZLOTOLOW1, Sofia CURCIO1, Graciela C. CALABRESE1,2
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Cancer Stem Cells (CSC) are characterized by self-renewal, differentiation, chemoresistance and phenotypic reversibility, which is associated with worse prognosis in tumors. Interaction with the microenvironment is one of the factors related with stemness. The aim of the present work is to analyze the expression of extracellular matrix proteoglycans in CSC derived from cell lines. CSC were enriched by scaffold free 3D culture (colonospheres) of human colorectal cancer cell line HCT116 in the presence of bFGF and EGF, employing ultra-low attachment plates in serum-free culture conditions. After 14 days of culture, microscopy studies were performed to assess colonosphere formation. Stemness was addressed by the expression of master genes SOX2, Nanog and CD44 by RT-PCR. Decorin and biglycan proteoglycan´s core protein expression was also analyzed by RT-PCR. Moreover, glycosaminoglycan and protein quantification was addressed by ionic exchange chromatography of the culture medium followed by colorimetric determination. RT-PCR was performed for the study of glycosaminoglycan synthesis enzyme expression. Bright light microscopy showed colonospheres around 50-100um. The expression of master genes was heterogeneous among cultures correlated with an heterogeneous expression of decorin (number of experiments, n =3). On the other hand, no biglycan expression was detected among different colonospheres (n=3). No differences were registered in glycosaminoglycan/protein ratio among spheres (0,274 ± 0.127). Nevertheless, Chondroitin-4-O-Sulfotransferase (C4ST) expression was detected in colonospheres while no expression was observed for Dermatan-4-O-Sulfotransferase (D4ST). The heterogeneity presented by 3D cultures represents the heterogeneity reported for CSC within tumors and C4ST and D4ST pattern suggests differences in GAG chain´s quality. Therefore, colonospheres are a suitable model for the study of GAG enzymes as potential therapeutic targets.

39. (522) **A PROTEOMIC STUDY REVEALS NEW MARKERS OF PROLACTIN-MODULATED OVARIAN FUNCTION IN PLAINS VIZCACHAS**

Cortasa, Santiago[1,2], Feehan, Kevin[1], Schmidt, Alejandro[1,2], Vitullo, Alfredo[1,2], Dorfman, Verónica[1,2], Halperin, Julia[1,2]
[1]Centro de Estudios Biomédicos Básicos, Aplicados y Desarrollo (CEBBAD), Universidad Maimónides, Buenos Aires, Argentina
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Prolactin (PRL) modulates the expression of the LH receptor in the ovary and, thus, the cascades of steroidogenic enzymes that synthesize and produce ovarian steroids. When pathological hyperprolactinemia occurs, the pulsatile release of GnRH decreases and alters the pituitary production of FSH and LH. Furthermore, it directly impairs the endocrine activity of ovarian follicles. To analyze which ovarian factors, aside to the aforementioned enzymes, respond to a high PRL environment, an ovarian proteomic study of vizcachas with sulpiride-induced hyperprolactinemia was performed. For this, ovarian protein extracts from hyperprolactinemic (HPRL) and control (CTL) females (n=5 per group) were used. Briefly, equal amounts of protein were analyzed using MALDI-TOF/MS and then, LC-ESI/MS (Orbitrap). The resulting peptides were identified with Proteome Discoverer Software using the Rodentia UniProt Database, and functional enrichment analysis was performed using DAVID, STRING and FunRich softwares. Proteins differentially expressed in each treatment were depicted in a volcano plot (t-test, $p<0.05$). Functional enrichment analysis showed that 24 proteins were differentially expressed in HPRL ovarian tissue compared to that of CTLs. Among those, some cytoskeleton regulation markers such as annexin 2 (ANXA2), Actin related protein 2/3 complex subunit 5 like (Arpc5l), and Myosin regulatory light chain 12A (MYLC12A) prevailed in HPRL-ovaries, while other markers related to mitochondrial function as Dynamin-1-like protein (DNM1L), Succinate-CoA ligase (SUCLG2), and Mitochondrial fission 1 protein (FIS1) were down-regulated. In addition, the interactomes showed different network topology with different nodal peptides in HPRL vs CTL treatments. The present work showed an ovarian expression profile that significantly varies under a hyperprolactinemic environment. Finally, this report provides new markers for future investigations on PRL-dependent modulation of ovarian function.

40. (565) **ANALYSIS OF REGULATORY CIS-ELEMENTS AND FOXA1/GATA2 TRANSCRIPTION FACTORS BINDING BEHIND MRP4/ABCC4 LEVELS IN PANCREATIC CANCER**

Samanta N Gancedo[1], Ana Sahores[1], Natalia Gómez[1], Maximiliano De Sousa-Ferro[1], Carlos Davio[1], and Betina González[1]
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