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La Tapa (Ver pág. 4)
Atardecer en la tarde
Antonella Ricagni

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REUNIÓN ANUAL DE SOCIEDADES DE BIOCIENCIA 2019

**LXIV Reunión Anual de la
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**IX Reunión Anual de la
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**VI Reunión Científica Regional de la Asociación Argentina
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**con la participación de
The Histochemical Society**

13 - 16 de noviembre de 2019
Hotel 13 de Julio - Mar del Plata

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**Dra. Mónica Costas
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with HFD and P1 (interaction diet probiotic $p= 0.06$, $n= 4$). We conclude that probiotic treatment improved metabolic parameters that were altered during HFD treatment. These data suggest the importance of gut microbiota as a therapeutic target in the treatment of obesity complications.

Bioinformática, genoma, proteoma y nuevas tecnologías / Bioinformatic II

Chairs: David Brudke/ Alberto Penas Steinhardt

0117 - CYTOTOXICITY OF METHYL VANILLATE AND METHYL DIVANILLATE IN BREAST CANCER CELLS

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Breast cancer is the most common cancer among women worldwide, with over 1.3 million new cases per year resulting in about half a million deaths. Current treatment strategies are based on surgical removal of the tumor and/or radiotherapy followed by chemotherapy, which are usually associated to harmful side effects. Regarding this, there is a constant search for new selective and low toxicity drugs. Phytochemicals and their chemically modified derivatives are potential candidates in this scenario. Recently, some studies have evaluated the antioxidant properties of vanillic acid and its esters in which methyl vanillate has been found to have higher antioxidant activity than vanillic acid itself and vanillin. This effect was related to their higher lipophilicity and self-dimerization that occurs when they react with free radicals, as vanillin. Considering previous studies with vanillin and vanillic acid and the fact that there are no reports in the literature about the effects of methyl vanillate and its dimer methyl divanillate on human breast cancer cells, the aim of this work was to study the cytotoxic and antitumor effects of these compounds on MCF-7 and MDA-MB-231 cancer cell line, estrogen dependent and triple negative, respectively. For cytotoxicity assays, MTT reduction viability assay, flow cytometry cell apoptosis, and Hematoxylin/Eosin and DAPI/Phalloidin stains were performed. The MTT reduction assay showed that divanillate was 15-fold more cytotoxic than vanillate for MCF-7 and 9-fold higher for MDA-MB-231 cell lines ($p<0.05$). The cells incubated with the average of IC50 and IC25 values were stained and showed lower cell damage for IC25. This concentration was chosen for the apoptosis assay, which showed higher cytotoxicity for the MCF-7 than MDA-MB-231. In conclusion, divanillate presents higher cytotoxicity than vanillate and the MCF-7 strain is more sensitive to both compounds.

Financed by The São Paulo Research Foundation-FAPESP, n. 2017/26309-9.

0318 - GENETIC DIAGNOSIS OF CONGENITAL HYPOPHYSECTOMY BY MOLECULAR INVERSION PROBES SEQUENCING: NOVEL PATHOGENIC VARIANTS

Maria Andrea CAMILLETI (1) | Maria Florencia MERCOGLIANO(1) | Sebastian VISHNOPOLSKA(1) | Debora BRASLAVSKY(2) | Ana KESELMAN(2) | Ignacio BERGADA(2) | Roxana MARINO(3) | Pablo RAMIREZ(3) | Natalia PEREZ GARRIDO(3) | Marta CIACCIO(3) | Maria Isabel DI PALMA(3) | Alicia BELGOROSKY(3) | Marcelo Adrian MARTI(4) | Jacob KITZMAN(5) | Sally CAMPER(5) | Maria Ines PEREZ-MILLAN(1)

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Congenital hypopituitarism (CH) is a life-long and threatening disease, associated with an abnormal pituitary development. CH is highly variable comprising a spectrum of disorders that range from isolated growth hormone deficiency (IGHD) to combined pituitary hormone deficiency (CPHD). Mutations in at least 30 genes have been implicated in CH, but at present, precise diagnosis remains a challenge. In the present study, we report variants found in pediatric patients with CPHD ($n= 116$) or IGH ($n= 55$) from Argentina using the molecular inversion probes sequencing (MIPS) method and our own custom designed gene panel. We identified pathogenic, likely pathogenic or variants with uncertain significance but predicated to be damaging for at least 3 independent software in about 23 % of the cases. We have identified a number of phenotypes associated with mutations in known genes that cause hypopituitarism (HESX1, LHX3, LHX4, GLI2); in less frequently reported genes (BMP4, FGFR1, GLI3, TGIF1, FOXA2) and in genes that require additional evidence about causality (ARNT2, ZSWIM6, GPR161, PNPLA6, CDH2). We have identified de novo heterozygous variants in LHX3 and LHX4, transcription factors involved in the development of the pituitary. Two variants on LHX3 (p.L220S and p.P187S) were found in a patient with IGH and a patient with CPHD, micrognathia, chiasm hypoplasia and bilateral cryptorchidism. LHX4 variants (p.Q100H, p.W204L and p.R84H) were found in a child with septo optic dysplasia, a child with CPHD and a third patient with GH and TSH deficiency, respectively. Transient transfection of HEK293T cells with human wild-type or mutant hLHX3/ hLHX4 showed an impairment in transcriptional reporter activity by the mutant variants, except for variant LHX4 p.R84H. Collectively, using the first screening panel for known genes and candidate genes for CH, we identified a significant number of variants in a large cohort of patients associated with the complex phenotype. Our studies will facilitate early diagnosis and prognosis, assessing the risk of future affected individuals. Furthermore, understanding the mechanisms behind new genes involved in CH would lead us to develop new tailor-made therapies that could benefit the patients. This work was supported by the Agencia Nacional de Promoción Científica y Técnica, Buenos Aires, Argentina (grant PICT 2016-2913 y PICT 2017-0002).

0591 - EXPRESSION OF RECOMBINANT FATTY ACID DESATURASE IN A BOVINE MAMMARY GLAND CELL LINE INDUCES CHANGES IN LIPID PROFILES

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Vertebrates are unable to synthesize a subset of polyunsaturated fatty acids (PUFA) known as omega 3 and omega 6. The nematode *C. elegans* is able to synthesize them thanks to a family of lipid desaturases (delta desaturases, i.e., FAT2). Our hypothesis proposes that heterologous expression of a FAT2 in a bovine mammary gland cell line (MAC-T) will induce synthesis of PUFA. The aim of the present work was to transduce the *C. elegans* fat2 gene into the genome MAC-T and to study the resulting PUFA profile. Cotransfections of MAC-T with the Sleeping Beauty (SB) transposon system were performed. Two transposons, one carrying a cassette for the expression of a GFP, and a second one for expression of the FAT2 enzyme and neomycin resistance were used. For transfection