2017

medicina

BUENOS AIRES VOL. 77 Supl. I - 2017

MEDICINA

Volumen 77, Supl. I, págs. 1-620

medicina

BUENOS AIRES, VOL. 77 Supl. I - 2017

La Tapa (Ver p. IV)
Imagen ígnea, 1996.
María Esther Gené

MEDICINA (Buenos Aires) – Revista bimestral – ISSN 1669-9106 (En línea)

REVISTA BIMESTRAL
Registro de la Propiedad Intelectual N° 5324261
Personería Jurídica N° C-7497
Publicación de la Fundación Revista Medicina (Buenos Aires)
Propietario de la publicación: Fundación Revista Medicina
Queda hecho el depósito que establece la Ley 11723

Publicada con el apoyo del Ministerio de Ciencia, Tecnología e Innovación Productiva.
MEDICINA no tiene propósitos comerciales. El objeto de su creación ha sido propender al adelanto de la medicina argentina. Los beneficios que pudieran obtenerse serán aplicados exclusivamente a este fin.
Aparece en *MEDLINE (PubMed), ISI-THOMSON REUTERS (Journal Citation Report, Current Contents, Biological Abstracts, Biosis, Life Sciences), CABI (Global Health), ELSEVIER (Scopus, Embase, Excerpta Medica), SciELO, LATINDEX, BVS* (Biblioteca Virtual en Salud), *DOAJ, Google Scholar y Google Books.*
Incluida en el Núcleo Básico de Revistas Científicas Argentinas del CONICET.

Directores Responsables:
Basilio A. Kotsias, Damasia Becú Villalobos, Isabel Narvaiz Kantor, Guillermo B. Semeniuk

Secretaría de Redacción: Ethel Di Vita, Instituto de Investigaciones Médicas Alfredo Lanari, Combatientes de Malvinas 3150, 1427 Buenos Aires, Argentina
Tel. 5287-3827 Int. 73919 y 4523-6619
e-mail: revmedbuenosaires@gmail.com – http//: www.medicinabuenosaires.com

Vol. 77, N° 5, Noviembre 2017

Edición realizada por
GRAFICA TADDEO – Charrúa 3480 – Buenos Aires – Tel: 4918.6300 l 4918.1675 l 4918.0482
e-mail: ctp@graficataddeo.com.ar – www.graficataddeo.com.ar

medicina
BUENOS AIRES, VOL 77 Supl. I - 2017

REUNIÓN CONJUNTA DE SOCIEDADES DE BIOCIENCIAS

LXII REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INVESTIGACIÓN CLÍNICA (SAIC)

LIII REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INVESTIGACIÓN BIOQUÍMICA Y BIOLOGÍA MOLECULAR (SAIB)

LXV REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INMUNOLOGÍA (SAI)

REUNIÓN DE LA SOCIEDAD ARGENTINA DE ANDROLOGÍA (SAA)

XLVI REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE BIOFÍSICA (SAB)

XIX REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE BIOLOGÍA (SAB)

XLIX REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE FARMACOLOGÍA EXPERIMENTAL (SAFE)

REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE FISIOLOGÍA (SAFIS)

REUNIÓN DE LA SOCIEDAD ARGENTINA DE HEMATOLOGÍA (SAH)

XXIX REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE PROTOZOOLOGÍA (SAP)

13-17 de noviembre de 2017
Palais Rouge– Buenos Aires

inhibitory effect of this polyphenol on membrane bound enzymes.

Keywords: acetylcholinesterase, cholesterol, polyphenols.

(1741) **ROLE OF CHARGED RESIDUES IN THE PROTEIN-MEMBRANE AND PROTEIN-PROTEIN INTERACTION DURING ACTIVATION OF THE MITOCHONDRIAL PATHWAY OF APOPTOSIS.**

Omar Jaure, Juan F Viso, María Julia Amundarain, Fernando Zamarreño, Marcelo Costabel

IFISUR, Universidad Nacional del Sur, CONICET, Departamento de Física, UNS.

The intrinsic pathway of apoptosis is activated by signals of cellular stress and regulated at the mitochondrial level. Such regulation is carried out by members of the Bcl-2 protein family (B leukemia cell lymphoma 2). Protein-protein and membrane-protein interactions allow the exposure of hidden domains in the initial conformation of pro-apoptotic members. Bax and Bid are members of the Bcl-2 family of proteins that promote apoptosis by an external mitochondrial membrane permeabilization mechanism (MOMP). The interaction between Bax, Bid and membrane, triggers a series of events that include; opening of a pore in the external mitochondrial membrane, release of apoptogenic factors from the intermembrane space and activation of caspases, to finally culminate in a process of cell death program by apoptosis. Although there is a broad knowledge at the structural level of proteins belonging to the Bcl-2 family, the mechanisms involved in MOMP require a better understanding of the conformational changes and specific contacts required to trigger apoptosis.

In a previous work we demonstrated the influence of non-specific electrostatic interactions in the first approach between Bax-membrane and between Bax-Bid. In the present work, we computationally model the interaction between Bid and membrane, determine the amino acids important for the interaction between Bax and membrane by in silico mutagenesis, and try to elucidate the mechanism involved in the formation of the apoptogenic pore in the external mitochondrial membrane. Free Electrostatic Energy of Binding, was computed using Finite Difference Poisson Boltzmann Equation (FDPB) method as implemented in software APBS (Adaptive Poisson Boltzmann Solver). This type of calculations provided a starting point for further computational analysis through molecular dynamics simulations (MD). To this end, we used GROMACS simulation package.

Keywords: apoptosis, Bcl-2, molecular dynamics.

(1057) **STUDIES ON THE STRUCTURE OF FQS SPECIES PRESENT AT DIFFERENT pH´s AND THEIR INTERACTIONS WITH LYSOZYME PROTEIN**

Hugo Alejanro Pérez (1), Ana Estela Ledesma (2), Maria de los Angeles Frias (1)

(1) Centro de Investigación y Transferencia de Santiago del Estero, (2) Facultad de Ciencias Exactas y Tecnologias-UNSE

Fluoroquinolones (FQs) are synthetic antimicrobial agents with a broad spectrum of antibiotic activity against Gram-positive and Gram-negative bacteria. They play an important role in the treatment and prevention of disease in both humans and animals. On the other hand, patients often take antibiotics with foods or dairy products such as milk to help swallow easier and to decrease their gastrointestinal side effects. Therefore FQs may be in contact with proteins present in milk as lysozyme (Lyz). It is known, that food–drug interactions may occur by many mechanisms, and they can result in changes both in the rate and the extent of absorption. The pH of the gastric milieu may also be an important determinant of the magnitude of the interaction.

In this context the purpose of this work is to study the structure of Ciprofloxacin (Cpx) and Levofloxacin (Lev) species present at basic, acid and neutral pH´s and their interactions with Lyz structure by Fourier transform infrared spectroscopy (FTIR) and Theoretical Calculations.

Theoretical calculations using DFT/B3LYP/Lanld2z methodology with gaussian09 program calculate that the more stable structure in solution is the neutral ones for both FQs. Docking Molecular analysis predict that the main forces involved in the interaction between FQs species and Lyz protein are Van der Waals forces and hydrogen bond. These results are in agreement with FTIR in solid phase and buffered solution. The spectra show significant changes in the quinolone carboxylic group and the piperazine amine group. When Lyz is present, it is observed that the FQs modify the secondary structure of Lyz. These theoretical and spectroscopic studies give a deeper understanding of the structural changes occurring between Cpx and Lev molecules with Lyz protein.

Keywords: Fluoroquinolones, Lysozyme, DFT calculation, FTIR, Molecular Docking.

(882) **FIBRIL LIKE STRUCTURES CAN BE INDUCED IN LIPID/PEPTIDE (BETA-AMYLOID AND MELITTIN) LANGMUIR MONOLAYERS**

Alain Bolaño Alvarez (1), Benjamin Caruso (2), Gerardo Daniel Fidelio (1)

(1) Departamento de Química Biológica Ranwel Caputto, Facultad de Ciencias Químicas y Centro de Investigaciones en Quimica Biológica de Córdoba, CIQUIBIC, CONICET, Universidad Nacional de Córdoba, (2) Instituto de Investigaciones Biológicas y Tecnológicas IIBYT, CONICET, Universidad Nacional de Córdoba.

Langmuir monolayers at air-water interface is a proper technique to study the interfacial properties of film forming peptides mixed with lipids. It allows manipulating the lipid/peptide mole ratio, the amount the **P**eptide **C**overed **A**rea (**PCA)**, the physical state of the lipid and the degree of lateral compactness in a confined environment, mimicking a biological membrane interface. Using lipid/peptide monolayers we studied the surface properties of AB1-40 **A**myloid **P**eptide (**AP**) mixed with different proportions of lipid that differs in their physical state. As AP form beta-sheet conformation, we also include the amphiphilic alfa-helix Melittin peptide (**Mel**) for comparison. Both AP and Mel form homogeneous monolayers with reproducible Pi-Area isotherms and maximal stability in between 15-25 mN/m. Their rheological properties were related to their secondary structures.

In a liquid-condensed environment (DSPC/peptide mixed systems), we observed immiscible behavior at all proportions with a first collapsing point close to that detected for pure peptide. In a liquid expanded lipid environment (POPC/peptide systems) both miscibility and stability of the film depend on the peptide used. For POPC/Mel at low PCA a mixed film exhibit composition-dependent stability, whereas at high PCA the lateral stability corresponds to that of pure peptide, which together with BAM images indicates lateral segregation induced by compression of the film. For AP/POPC, lateral segregation was observed (BAM images) at all proportions. However we found an unexpectedly complex stability behavior, corresponding to pure peptide at high PCA but composition-dependent at low PCA; interestingly at PCA 5-10% fibrils like structures are clearly observed and the film exhibit a pronounced compression hysteresis. Surprisingly, fibrils could also be observed for DSPC/Mel at certain proportions. We discuss on the conditions and kinetic aspects affecting fibrils formation.

Keywords: beta amyloid, melittin, lipid-peptide interaction, Langmuir films, peptide monolayers.

(65) **EFFECT OF AMYLOID OLIGOMERIZATION ON ALPHA-SYNUCLEIN CURVATURE-MEMBRANE SENSITIVITY**

J. Ignacio Gallea (1), Carlos Mas (1), Ernesto E. Ambroggio (1), Nicholas James (2), David Jameson (2), M. Soledad Celej (1)

(1) Dto. Química Biológica Ranwel Caputto-CIQUIBIC, Fac. Ciencias Químicas, Universidad Nacional de Córdoba. (2) Dept. Cell and Molecular Biology, John A. Burns School of Medicine, University of Hawaii at Manoa, Hawaii, USA.

Abstract: The protein α-synuclein (AS) is as a critical regulator of synaptic vesicle dynamics in dopaminergic neurons. The amyloid aggregation of AS is pathognomonic of Parkinson's disease, a movement disorder associated with axon degeneration of dopaminergic nigral neurons. In this context, prefibrillar oligomeric species