



Colegio Oficial de Biólogos
de la Comunidad de Madrid



PhDay Biología

13 octubre 2021

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En memoria de **Carlos Vicente Córdoba**, que nos hizo entender la
fisiología vegetal

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PROGRAMA

- 9:30 Bienvenida y conferencia inicial
9:45 *Homenaje a Carlos Vicente Córdoba*
10:00 *Conferencia plenaria I. Margarita Marqués Martínez* (Universidad de León). Entre dos aguas: de células STEM y otros cantares.

Comunicaciones orales: Sesión I

- 10:30 **Andrea Seral.** Effects of Martonne aridity index and altitude on stomatal traits in two *Asplenium L saxicolous* ferns species.
- 10:45 **Anibal Sánchez.** CB1 receptors deficiency in oligodendrocyte precursors disrupts postnatal oligodendrogenesis and causes hypomyelination in mice.
- 11:00 **Diego López.** Invasion in the city: monitoring the expansion of the Argentine ant, *Linepithema humile* (Mayr, 1868), in the urban environment of Madrid natural.
- 11:15 **Paula Alonso.** In-depth analysis of Cdc14 meiotic behaviour reveals a novel pre-anaphase I role for the phosphatase.
- 11:30 **Eduardo Tranque.** PAT1 proteins differentially regulate abiotic stress response in *Arabidopsis*.
- 11:45 **Irene Picazo.** Effects of ambient alkaline pH on gene expression: a key regulatory role for the cation-homeostasis transcription factor SlTA.
- 12:00 **Elena Alonso.** A Case Report of Chronic Stress in Honey Bee Colonies Induced by Pathogens and Acaricide Residues.

12:15 *Pausa para el café**

* Por razones sanitarias este año el evento no ofrecerá café ni desayuno

Comunicaciones orales: Sesión II

- 12:45 **Elena Requena.** The use of comparative genomics for the identification of *Penicillium rubens* strain 212 genes involved in the control of tomato vascular disease.
- 13:00 **Fernando García.** Unravelling the taxonomy of the genus *Belgrandia Bourguignat*, 1870 (Mollusca: Hydrobiidae) in the Iberian Peninsula through the use of multilocus species delimitation methods.
- 13:15 **Héctor Lorente.** Diversity and phylogeny of membrane intrinsic proteins across eukaryotes.

13:30 **Jorge Peralta.** Diversity patterns and distribution of aquatic Hemiptera in coastal wetlands of Perú.

13:45 **Iván Martín.** Improving protein loop modelling for antibody H3-CDR loops.

14:00 **Jorge García.** The early maternal environment shapes the parental response to offspring UV ornamentation.

14:15 **Julio Sempere.** Treatment of *Staphylococcus aureus* and *Streptococcus pneumoniae* mixed biofilms by antioxidants.

14:30 Comida y sesión de pósteres

15:30 *Conferencia plenaria II.* **Aldo Croquer.** La restauración de arrecifes de coral: logros, limitaciones y retos.

Comunicaciones orales: Sesión III

16:15 **Natasha Tilikj.** How to resist dry soil: transcriptional changes in a Mediterranean earthworm during aestivation.

16:30 **Mariano Rodríguez.** EphB2 and EphB3 in Murine Mesenchymal Stromal Cells Biology.

16:45 **Pablo Recio.** Site selection based on conspecific chemicals in the amphisbaenian *Blanus rufus*

17:00 **Carolina Pascual.** Extraction and characterization of Argentine red shrimp (*Pleoticus muelleri*) phospholipids as raw material for liposome production.

17:15 **Rubén Vázquez.** The genus *Cranfillia* (Blechnaceae, Polypodiopsida): key to natural sections proposed for the genus.

17:30 **Sonia Molino.** Taxonomy and evolution of *Parablechnum*, the most diverse genus of one of the most recent fern families.

18:15 Entrega de premios y ceremonia de clausura

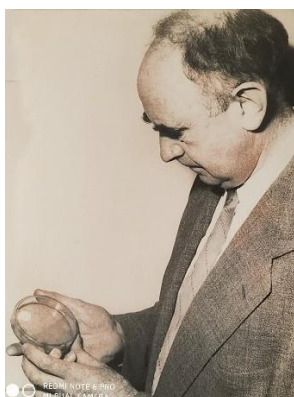
EN MEMORIA DE NUESTRO MAESTRO, PROFESOR CARLOS VICENTE CÓRDOBA

Me dais la oportunidad de escribir unas líneas sobre Carlos y me llena de gozo que queráis dedicarle la 5ª edición del PhDay Biológicas. Gracias a todos los que habéis hecho posible que esto suceda. Lo hago con orgullo e intento resumir su valía. Estoy segura que, como siempre hizo, corregirá mis errores.

Era algún día a mediados de Junio de 1978, mis compañeros de curso Toni y Javier, y yo, decidimos armarnos de valor y subir a la quinta planta del pabellón quinto de la Facultad de Medicina, el "pisito". Queríamos hablar con el Catedrático, le llamábamos Prof. Córdoba porque entonces no sabíamos que Vicente era su primer apellido, e íbamos a decirle que queríamos hacer una Tesina en el Departamento y entrar los tres en bloque. Yo no sabía qué profesor dirigiría a quien, en caso de que aceptaran hacerlo, pero sí sabía que yo solo aceptaría trabajar bajo la dirección del Prof. Vicente. A lo largo de mi extensa carrera en la Facultad de Ciencias Biológicas de la Universidad Complutense, se cumplieron 43 años este junio de 2021, me han pasado muchas cosas, la mayoría buenas, unas cuantas regulares y muy pocas, malas, pero una de ellas, excepcional. La excepcionalidad fue que el Prof. Carlos Vicente se cruzara en mi camino y que decidiera acompañarme desde ese día de Junio en el que aceptó dirigir mi Tesina de Licenciatura.



Prof. Carlos Vicente Córdoba (2017), en el laboratorio, delante de la pizarra que utilizó su Maestro, Prof. Bustinza.



Prof. Florencio Bustinza Lachiondo sosteniendo en sus manos la placa original con el cultivo de *Penicillium notatum* en el que Fleming descubrió la penicilina. St. Mary's Hospital.

El 19 de Junio de 1974 tomó posesión de la Cátedra de Fisiología Vegetal que dejara vacante, por jubilación, D. Florencio Bustinza Lachiondo, que fuera su titular desde 1942. Fue un acto sencillo en el despacho del Rector, D. Ángel González Álvarez, según me comentó. Adoraba a D. Florencio, su Maestro, le tenía un gran respeto y admiración, fue su ejemplo a seguir durante toda su vida. Yo tuve el inmenso honor de que presidiera el tribunal de defensa de mi tesis doctoral, un frío 17 de diciembre de 1981 en el que fuera su último acto académico. D. Florencio falleció unos días después, el 10 de enero de 1982. El Prof. Vicente era un hombre tímido, afable, modesto, cercano, educado, culto, sabio y honesto a carta cabal. Un hombre bueno, muy metido en su mundo, pero de un grandísimo corazón, siempre dispuesto a ayudar a los demás sin reclamar nada a cambio. Gran Maestro, gran Profesor, excelente científico, revolucionario en sus teorías, escritor de

novela, ensayista y profundamente religioso. Podría decir cientos de cualidades de Carlos y aún me quedaría corta, pero sin duda, su mejor cualidad fue la humildad. Nunca presumió de los muchos talentos que Dios le había dado, es más, admiraba el talento de los demás cuando el suyo propio era superior. Quizás eso también era el reflejo de su profunda inteligencia. Doy las gracias a Dios por haberme permitido conocerle y disfrutar de él; esa persona maravillosa que, después de mis padres, me ha enseñado casi todo lo que sé. Mi compañero de vida, mi amigo, mi Maestro, mi refugio.

Mi Maestro me enseñó muchas cosas, aunque no fui capaz de aprenderlas todas. Me enseñó toda la Fisiología Vegetal que podía saberse en aquella época, pero también me enseñó su entusiasmo, su independencia de criterio, su buen hacer, su valor callado y sin alharacas, su hombría de bien, su coherencia y otras muchas cosas más. Me enseñó su amor por la Ciencia y por las cosas bien hechas, para él no había experimento sin valor, se trataba nada más y nada menos que de la búsqueda de la verdad, investigar las causas de las cosas, lo mejor que un ser humano podía hacer en la vida. Hablar de ciencia con mi Maestro era como recibir una invitación para volar, para alejarse del suelo y remontarse a las alturas, era crear de la nada. Todo lo sabía, todo lo entendía, era capaz de conectar todo con todo, de relacionar hechos independientes, de dar vida a sus ideas. Su cerebro nunca estaba en descanso, dormía muy poco y creo que, cuando lo hacía, era de forma ligera. No recuerdo despertar una mañana y encontrarle en la cama, él ya se había levantado hacía mucho rato y escribía o leía o anotaba cosas en sus muchas libretas y cuadernos del despacho. Le encantaban los cuadernos pequeños, de papel grueso y blanco, donde hacía sus anotaciones de todo lo que le “chocaba” al cabo del día. Podía ser una palabramal dicha o un refrán o una anécdota o una simple observación según iba caminando por la calle; seguro que les encontraba sitio en su próxima novela. Ya os he comentado antes, era capaz de conectar ideas vagas y darles un hilo conductor que lo explicara. Por eso, cada vez que un experimento no producía los resultados que debiera, él, lejos de decir que no valía, intentaba buscar una explicación lógica y, de verdad os digo, finalmente la encontraba.

Me enseñó la Ciudad Universitaria de Madrid, sus edificios, sus colegios mayores, sus jardines, sus campos de deportes y su vida universitaria. Y lo mismo que le dijera entonces su Maestro, me dijo a mí: quiero que sepas, añadió, y que no se te olvide, que esto es Universidad, un lugar en el que se genera el conocimiento. Su función no se reduce a ser un mero transmisor del mismo, aquí se crea. Si no haces que la Universidad avance en el conocimiento, en la medida de tus fuerzas, estarás cometiendo un fraude contra tu país y contra sus ciudadanos. Por eso él todos y cada uno de los días que impartía sus clases, explicaba a los alumnos lo que había descubierto hacía unos días.

Este era mi Maestro, este fue el Prof. Vicente, nuestro Maestro. A nosotros, sus alumnos, dedicó su vida. Trabajó incansablemente en seguir formándose, en estudiar todo lo nuevo que se publicaba, su cabeza siempre en ebullición, incluso cuando parecía que se quedaba dormido. Por eso su producción científica fue tan elevada: 342 artículos de investigación, la mayoría de ellos en revistas de alto índice de impacto, 43 capítulos de libros, 10 libros, 270 comunicaciones a congresos científicos. También le quedó tiempo para escribir 4 novelas. Le gustaba llegar cada día al laboratorio y preguntar si había salido el experimento que habían planteado. Cuando le decíamos que sí, que tenía muy buena pinta, él siempre nos respondía lo mismo: “qué grandes sois”. Nuestro trabajo en el laboratorio fue nuestra vida, nos lo pasábamos en grande haciendo experimentos porque no solo era eso, sino muchas cosas más, era tomar el café a primera hora de la mañana, eran las comidas con sus largas sobremesas, eran las fiestas de Navidad, de la primavera, del verano, de lo que fuera. Hemos sido todos tan felices en “el pisito”... Todos le debemos a nuestro Maestro lo que somos científicamente hablando y, hablo en nombre de los que nos hemos formado a su lado. En las 29 Tesis Doctorales que dirigió a lo largo de su vida académica, se aúnan ingenio, trabajo, estudio, investigación científica y formación de nuevos científicos, esa doble función que la Universidad tiene, tarea en la que se esforzó a lo largo de sus 49 años de profesión. Permitidme sólo dos de las últimas dedicatorias de sus doctorandos. La primera dice así:

“GRACIAS (así, con mayúsculas) al Prof. Dr. D. Carlos Vicente Córdoba por cautivar-me como solo pueden hacer los buenos Maestros. Siempre me acordaré de ti para no flaquear y “seguir en la lucha”. Gracias Carlos por confiar en mí, por dar valor a mis ideas, por la infinita humildad (que sólo tienen los más grandes) y por tu ejemplo. Gracias por tu disponibilidad 24 h.

Y la segunda reza:

“Gracias por abrirme las puertas de “vuestra casa”, por enseñarme tanto, por tu paciencia y cariño. Porque para mí eres la definición de MAESTRO con mayúsculas. Fuente inagotable de conocimiento que tiene explicación para todo, pero siempre, con una humildad genuina. Gracias por ayudarme y formarme para el mañana. Te admiro como profesor y mucho más como persona, porque (aunque no sé si es políticamente correcto decirlo), YO SOY FAN. Unos cuantos años después, lo único que puedo hacer es repetir aquellas palabras que me dijiste en respuesta a mi e-mail sobre trabajar con vosotros: ... “Mi jefe, que es un hombre sabio, me enseñó a trabajar. Mi jefe, que es un hombre bueno, me trató con afecto, con paciencia y con respeto. Yolo único que hago es imitarlo en la medida de mis posibilidades”

El 3 de junio de 2015 fue uno de sus días más tristes, escribía lo siguiente: *“No ha sido solamente la última clase de este curso, sino la última vez que bajo a clase con pleno derecho. ¿Por qué razón? Muy sencillo, mi ciclo se ha completado y aunque se haya alargado un año más al permanecer como profesor emérito y me esperen dos años más como honorífico, la ley no me permite seguir como docente pleno. El tiempo ha pasado volando”* Carlos siempre hacía alusión a los versos de Alberti que le mostró otro de sus Maestros, D. Ángel Vián Ortuño, Rector Magnífico de la UCM, una tarde de verano paseando por El Paular.

*Haz un milagro, Señor,
Déjame bajar al río,
Volver a ser pescador,
Que es lo mío.*

El último día de cada curso me decía que los repetía para sus adentros, sin mover los labios, deseando que al siguiente curso volvieran otros alumnos a los que enseñar lo que había aprendido. Por eso, el 3 de junio de 2015 fue uno de sus días más tristes porque también como él reflejó de forma magistral en su escrito de despedida como profesor, se lamentaba:

“Este 3 de Junio, por primera vez en 41 años, no he repetido los versos de Alberti al salir de clase. Ya no puedo pedir un nuevo milagro, la Administración no me lo permite. Hoy he omitido mi oración sin tristeza por la despedida, quizá con algo de nostalgia. Vosotros, vuestros compañeros, volveréis a llenar el aula el próximo curso, yo no acudiré esta vez a la cita”

El Profesor Carlos Vicente Córdoba falleció el día 1 de Diciembre de 2020. Se fue de forma callada, sin alboroto, como él era, SIGILOS. Desde entonces no puedo acariciar sus manos ni contemplarle mientras duerme, pero le siento a mi lado, siento que me ayuda como siempre lo ha hecho, que me protege, que me calma, que me sigue amando. Dejé mi alma herida, porque como cantaba Neruda:

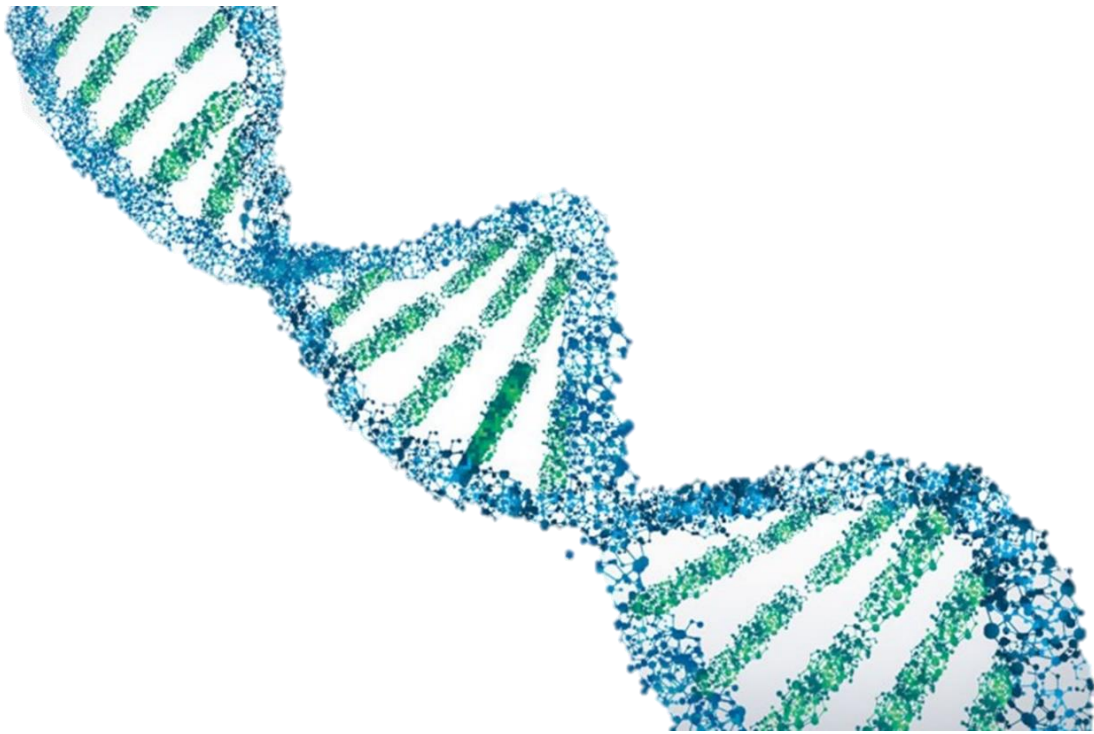
*También eras una pequeña hoja
que temblaba en mi pecho.
El viento de la vida te puso ahí.
Al principio no te vi: no sabía
que ibas a ir conmigo
hasta que tus raíces
atravesaron mi pecho,
unió los hilos de mi sangre,
habló por mi boca,*

Por último, reflejo alguno más de sus méritos y os dejo unas cuantas fotografías de recuerdo.

- Académico correspondiente de la Real Academia de Ciencias, Bellas Letras y Nobles Artes de Córdoba, 5 de Mayo de 2016.
- Fellow of the Linnean Society of London (elected), 1987.
- Miembro de la Academia Paraibana de Ciencia y Tecnología (Brasil), 1991.
- Doctor Honoris Causa, Universidad Federal de Paraíba (Brasil), 1991.
- Título de Profesor Honorario de la Universidad de La Habana, otorgado por el Ministro de Educación Superior de Cuba, 1996.
- Titular de la Cátedra Internacional Álvaro Reynoso, Universidad de La Habana desde 1998.
- Profesor Emérito, Universidad Complutense, 2014-2017.
- Profesor Honorífico, Universidad Complutense, 2017-2020.
- Diploma de la Academia de Ciencias de Cuba a la investigación más distinguida en el periodo 1986-1991
- Dos Diplomas de la Academia de Ciencias de Cuba a la investigación más distinguida en 1997.
- I Premio de Investigación CSIF-educación por toda su trayectoria científica, 2017.
- Referee of the National Science Foundation (Washington) for Developmental Biology, 1984.
- Referee of the International Science Foundation (Washington) for Analytical Sciences, 1993.
- Evaluador de la Zcek Science Foundation, 2011-2014.
- Asesor del Programa de la Ricerca de la Universidad de Padua en 2013.
- Evaluador de la French Research Agency (ANR), Agence nationale de la recherche française, 2017.
- Evaluador de Proyectos de Investigación del Plan Nacional, MEC, MCYT, desde 1988 a 2000.
- Miembro del Patronato del Parque Nacional de las Tablas de Daimiel, 1980-1981.
- Asesor Científico del Programa Antártico Brasileño, 1984-1985.
- Consejero del Patronato del Canal de Isabel II, 1981.
- Editor asociado para Biotecnología de la revista Fragmenta, editada por la Universidade de Tiradentes (Sergipe, Brasil).
- Referee del Boletín de la Real Academia de Ciencias, Bellas Letras y Nobles Artes de Córdoba y de 27 revistas internacionales de su especialidad.
- Director de la colección de libros (17 volúmenes) "Ciencias de la vida", publicado por Editorial Síntesis, Madrid*.
- Vocal de la Agencia de Medio Ambiente, Comunidad Autónoma de Madrid, 1990-1993.
- Miembro fundador de la Sociedad Española de Fisiología Vegetal.
- Miembro fundador de la Sociedad Española de Biotecnología.
- Miembro de la Sociedad Española de Medicina Nuclear y Biología.
- Miembro de la British Lichen Society.
- Miembro de la American Society of Plant Physiologists.
- Miembro de la American Society of Botany.
- Miembro de la International Association of Endocytobiology.
- Miembro de la Sociedad Cubana de Botánica
- Miembro de la Japan Society of Bioscience, Biotechnology and Agrochemistry, Japan.
- Miembro de la Real Sociedad Española de Química (Grupo de Cromatografía y Técnicas Afines).
- Decano de la Facultad de Biología de la Universidad Complutense, electo (1976-1979 y 1979-1982).
- Director de Instituto Universitario de Ciencias Ambientales, UCM, electo (1984-1989 y 1989-1994).
- Director del Departamento de Biología Vegetal I, Facultad de Biología, UCM, electo, 1994-1998.

Madrid, 17 de Septiembre de 2021

María Estrella Legaz González, discípula de Carlos Vicente Córdoba



RESÚMENES:

COMUNICACIONES ORALES

Sesión I

EFFECTS OF MARTONNE ARIDITY INDEX AND ALTITUDE ON STOMATAL TRAITS IN TWO *ASPLENIUM* L SAXICOLOUS FERNS SPECIES

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Summary

Stomata are pores delimited by two occlusive cells that play an important role in the exchange of gases (CO₂ and H₂O) between plants and the environment, which allows them to adapt to changing environmental conditions. Due to this, stomata can respond to environmental changes by adjusting their stomatal traits in order to maximize the photosynthetic rate and water use efficiency. There are three main stomatal traits, density, length y PCI (Potential Conductance Index) that has been broadly used to study how plants are adapted to different environments. Studies focused on analysing the variation of these traits in ferns are scarce. The main objective of this work is to analyse the variation of the three functional traits mentioned in two rupicolous fern species of the *Asplenium* L. genus widely distributed in the Iberian Peninsula (*Asplenium trichomanes* subsp. *quadrivalens* L. and *Asplenium ceterach* L.) and to correlat these traits with IAM (Martonne Aridity Index) and altitude.

We sampled several individuals in different populations of Iberian Peninsula with different IAM and altitude. To analyses the influence of IAM and altitude on stomatal functional traits we fit generalized estimating equations. Analyses showed that IAM does not modulate (in general) the variation of stomatal traits in both species. However, a significant effect of altitude on PCI and Density was found. This strategy would be aimed at increasing photosynthetic rate in response to the decrease in CO₂ pressure with altitude.

Keywords: functional traits, stomata, ferns, saxicolous.

CB1 RECEPTORS DEFICIENCY IN OLIGODENDROCYTE PRECURSORS DISRUPTS POSTNATAL OLIGODENDROGENESIS AND CAUSES HYPOMYELINATION IN MICE

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3. Department of Biochemistry and Molecular Biology, Complutense University, Instituto Universitario de Investigación en Neuroquímica (IUIIN), 28040, Madrid, Spain.
4. Department of Neurosciences, University of the Basque Country UPV/EHU, Spain.
5. Achucarro Basque Center for Neuroscience, 48940, Leioa, Spain.
6. Biocruces, 48903, Bizkaia, Spain.
7. Institute of Physiological Chemistry, University Medical Center Mainz, 55128 Mainz, Germany.

Summary

Exogenous and endogenous cannabinoid molecules have been shown to modulate oligodendrogenesis and developmental CNS myelination. However, the cell-autonomous action of these compounds on oligodendroglial cells in vivo has never been explored.

Here, by using oligodendroglial precursor cell (OPC)-specific genetic mouse models we found that selective CB1 cannabinoid receptor depletion in OPCs prevented cell differentiation and perturbed oligodendrogenesis and postnatal myelination, causing hypomyelination and behavioral alterations. Conversely, CB1 receptors pharmacological activation by inducing RhoA proteasomal degradation promoted oligodendrocyte development and CNS myelination in CB1-wild type but not in OPC-CB1-null mice. Moreover, exogenous ROCK inactivation in vivo overcame the defects in oligodendrogenesis, CNS myelination and behavior of OPC-CB1-null mice. Overall, this study addresses a cell-autonomous role for CB1 receptors modulating oligodendrogenesis in vivo that may help in understanding the complex network of signaling molecules that drive CNS myelination.

This work has been supported by the MINECO Grants SAF2017-83516 and PID2020-112640RB-I00, Comunidad de Madrid Grants 2016-T1/BMD-1060 and 2020-5A/BMD-19728 and Fundación Tatiana Pérez de Guzmán el Bueno.

Keywords: Cannabinoids, CB1 cannabinoid receptors, Oligodendrocyte precursor cell, Oligodendrogenesis, Myelination.

INVASION IN THE CITY: MONITORING THE EXPANSION OF THE ARGENTINE ANT, *LINEPITHEMA HUMILE* (MAYR, 1868), IN THE URBAN ENVIRONMENT OF MADRID

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Summary

The Argentine ant, *Linepithema humile* (Mayr, 1868), stands out for its exotic and invasive character: its biological strategies give it an enormous capacity to colonize new enclaves worldwide and displace native species, thus harming local ecosystems.

In the Iberian Peninsula they present a marked coastal distribution. However, it is found in urban environments in several inland provinces where green areas such as parks or private gardens provide them with suitable conditions for the maintenance of their colonies once they are introduced due to the transport of goods or the green areas management.

Together with sampling data from the last four years in green areas and other enclaves in the city of Madrid, an exhaustive search for records of the Argentine ant has been carried out by terms of bibliographic references, citizen science platforms and through personal communications.

From 1952 to date, twelve locations have been recorded in the urban area of Madrid and four points outside, ten of them after 2018. Many of the colonies have experienced growth associated with their area of influence, revealing a possible gradual entry and a silent expansion in the city in recent years. The features that best explain the presence of the Argentine ant in green areas are related to the level of anthropization. Although no clear effect on the local ant community has been detected, given the possibility of new entrances or movements of the species, applying a monitoring system that involves citizens, researchers and local authorities would be very advantageous.

Keywords: Invasive species, *Linepithema humile*, Madrid, urban green areas.

IN-DEPTH ANALYSIS OF CDC14 MEIOTIC BEHAVIOUR REVEALS A NOVEL PRE-ANAPHASE I ROLE FOR THE PHOSPHATASE

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Summary

Meiosis is a specialized type of cell division, which consist in a single round of DNA replication followed by two consecutive rounds of chromosome segregation. In the budding yeast, *Saccharomyces cerevisiae* cells enter meiosis when they grow in restrictive conditions of nutrients, and they are respiration competent.

Cdc14 is an evolutionarily conserved dual-specificity phosphatase that resides in the nucleolus during most of the cell-cycle, presumably inactive. It is required in both mitosis and meiosis. During meiosis Cdc14 is necessary for the transition between meiosis I and II, the re-duplication of the SPBs and we have recently identified that Cdc14 is crucial for timely nuclear localization and activation of Yen1 as early as in metaphase I (Alonso-Ramos *et al.* IJMS 2021). Little is known about the pre-anaphase I roles of Cdc14, therefore, we performed a detailed characterization of Cdc14 behaviour throughout the meiotic cycle. Analysis using fluorescently labelled proteins and inducible/repressible gene-expression systems in multiple mutant backgrounds, it allowed us to pinpoint the precise timing of early Cdc14 nucleolar release. We found that a subpopulation of Cdc14 was released from the nucleolus before anaphase I took place, which lasted between 30-45 min, these could be seen in ~90% of the wild type cells. We called this early type of release diffusion. This pre-anaphase I diffusion is likely related with our recently described role of Cdc14 in controlling meiotic recombination.

Alonso-Ramos, P.; *et al.*; *Int. J. Mol. Sci.* **2021**, 22, 9811. <https://doi.org/10.3390/ijms22189811>

Keywords: Meiosis, Cdc14, Diffusion

PAT1 PROTEINS DIFFERENTIALLY REGULATE ABIOTIC STRESS RESPONSE IN ARABIDOPSIS

Eduardo Tranque, M. Fernanda Ruíz, Ema Olate, Rafael Catalá and Julio Salinas.

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Centro de Investigaciones Biológicas Margarita Salas-CSIC, Madrid

Summary

Adverse environmental conditions, such as extreme temperatures, drought or soil salinity, negatively affect plant development and reduce crop yields, causing important economic losses. To cope with these conditions, plants have evolved sophisticated adaptive responses, most of them controlled through extensive changes in gene expression. Although many stress-responsive genes have been identified, their functional characterization remains to be studied. Results from our laboratory allowed us to identify PAT1, which encodes an activator of mRNA decapping, as a cold-inducible gene in Arabidopsis. Interestingly, the Arabidopsis genome codes for three PAT1 proteins, named PAT1, PAT1H1 and PAT1H2, but, so far, only PAT1 has been shown to participate in decapping. Moreover, the implication of Arabidopsis PAT1 proteins in plant response to abiotic stress has not yet been addressed. Our data reveal that the expression of PAT1 genes is differentially regulated in response to low temperature and high salt. Furthermore, the characterization of *pat1*, *pat1h1* and *pat1h2* mutants has shown that PAT1 proteins are involved in regulating Arabidopsis tolerance to those abiotic stresses. Finally, RNAseq analyses have uncovered that each PAT1 controls the expression of a set of specific stress-induced genes, depending on the environmental conditions. All these results suggest that PAT1 proteins could differentially regulate Arabidopsis tolerance to abiotic stress conditions by promoting selective mRNA decapping.

Keywords: Arabidopsis, decapping, PAT1, abiotic stress.

EFFECTS OF AMBIENT ALKALINE pH ON GENE EXPRESSION: A KEY REGULATORY ROLE FOR THE CATION-HOMEOSTASIS TRANSCRIPTION FACTOR SltA

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Summary

Aspergillus nidulans is able to tolerate ambient alkalinity up to pH 10. The ability to grow at alkaline pH depends on the effective function of, at least, three regulatory pathways mediated by high hierarchy zinc-finger transcription factors: PacC, which mediates the ambient pH regulatory pathway, the calcineurin-dependent CrzA and the cation-homeostasis responsive factor SltA. Using RNA sequencing, we have determined the effect of external pH alkalinisation on gene expression and compared it to saline stress caused by sodium chloride. Transcriptional data demonstrate that the pattern of gene expression is largely modified under alkaline pH and different to that induced by salt stress. The role of SltA has been also studied by sequencing the transcriptomes of the null mutant under both stress conditions. The transcriptional role of SltA is wider than initially expected and probably implies both inhibitory and positive roles. This includes, for example, the regulation of the PacC-dependent ambient pH regulatory pathway. SltA is positively involved in the expression of *pacC* in response to alkalinity. Our data present a new scenario for understanding the transcriptional response to alkalinity and the cross regulation of major regulatory pathways in Ascomycetes, specifically in the Pezizomycotina subphylum.

This work was carried out through the projects BFU2015-66806R and RTI2018-094263B-I00 whose PI is Espeso.E, being funded by the Ministry of Science, Innovation and Universities, State Research Agency and European Regional Development Fund (FEDER).I. Picazo has a contract funded by the project RTI2018-094263B-I00.

Keywords: *A.nidulans*, pH regulatory systems, Transcription factor, SltA, PacC.

A CASE REPORT OF CHRONIC STRESS IN HONEY BEE COLONIES INDUCED BY PATHOGENS AND ACARICIDE RESIDUES

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Summary

Here we present the possible causes of collapsing honey bee colonies from a professional apiary of *Apis mellifera iberiensis* L. located in Gajanejos (Guadalajara, Spain). To investigate the factors that had possibly provoked this situation, we performed a pathogen screening, pesticide analysis, and foraging flora determination.

The analysis showed the accumulation of acaricides in the beebread and climatic conditions increased the vulnerability to the infection to *Nosema ceranae*, potentially favoring the apiary collapse. The results highlight the importance of evaluating these factors in future monitoring programs in order to adopt adequate preventive measures as part of national and international welfare programs aimed at guaranteeing the health and fitness of honey bee colonies.

Keywords: *Apis mellifera*; *Nosema ceranae*; *Varroa destructor*; beeviruses; acaricides; toxic unit.

RESÚMENES:

COMUNICACIONES ORALES

Sesión II



THE USE OF COMPARATIVE GENOMICS FOR THE IDENTIFICATION OF *PENICILLIUM RUBENS* STRAIN 212 GENES INVOLVED IN THE CONTROL OF TOMATO VASCULAR DISEASE

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Summary

Genome sequencing and comparative genomics is a very useful tool to identify the genetic basis underlying biological processes of interest. *Penicillium rubens* strain 212 (PO212) is a biological control agent (BCA) effective against pathogenic fungi in horticultural crops, such as *Fusarium oxysporum* f.sp. *lycopersici* causing vascular wilt of tomato. *Penicillium rubens* strains have been isolated. Among them, strain S27 highly similar to PO212 but lacking the biocontrol activity making it a suitable candidate for the genomic comparative with PO212.

The main objective of the study was to compare the PO212 genome with the genome of S27 to identify possible genes involved in biological control. Thus, by sequencing the genome of strain S27 and using two independent approaches both genomes were compared. An automatic annotation of genes and proteins was obtained with the AUGUSTUS server, which allowed us to know the genes and regions that accumulated changes between the two genomes.

The comparative studies established high sequence conservation between both strains of different origins and showed the presence of specific changes in the sequence in both coding and non-coding regions. The nucleotide changes that generate modifications in protein sequences that can compromise their functionality will be presented.

Research supported by grant RTA2013-00060-C05-01 and RTA2017-00019-C03-01 from the Ministry of Science, Innovation and Universities (MCIU, Spain), Agencia Estatal de Investigación (AEI) co-financed with FEDER funds from the European Union. E. Requena received a Ph.D. fellowship from the Ministry of Science, Innovation and Universities (Spain).

Keywords: PO212, biological control agent (BCA), *Penicillium rubens*.

UNRAVELLING THE TAXONOMY OF THE GENUS *BELGRANDIA* BOURGUIGNAT, 1870 (MOLLUSCA: HYDROBIIDAE) IN THE IBERIAN PENINSULA THROUGH THE USE OF MULTILOCUS SPECIES DELIMITATION METHODS

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Summary

The genus *Belgrandia* Bourguignat, 1870 includes 30 extant species of freshwater snails distributed in continental Europe. Most species have been described essentially based on conchological characters, since their small size challenges the study through anatomical data. Here we re-assess the taxonomic identity of the seven nominal species occurring on the Atlantic and Mediterranean slopes of the Iberian Peninsula through the use of molecular tools. Mitochondrial (mtCOI and 16S) and nuclear (28S, 18S and H3) sequences of 22 specimens collected from nine Iberian localities were phylogenetically analysed by Bayesian Inference (BI) and Maximum Likelihood (ML). In addition, populations of the type species *B. gibba* and other two species from southern France were included in this study. For species delimitations, we used the methods: ABGD, bPTP, mPTP and GMYC. The ML and BI analyses showed strong phylogenetic support for the most of morphologically recognised species, but the mean sequence divergence (measured as uncorrected pairwise distances) among them was low (from 0.2 to 4.1% for COI). Besides, both inferences grouped the Iberian species according to their Mediterranean and Atlantic distributions. The species delimitation methods suggested three (GMYC) to ten (ABGD) species-groups, being the ABGD the one that best fits the number of described taxonomic species (match ratio = 0.70). In conclusion, the diversity scheme suggested by our novel phylogenetic results needs to be verified and compared with anatomical data to correctly identify the Iberian species of *Belgrandia*.

Acknowledgements: To financial support of Fauna Ibérica Projects: PGC2018-095851-B-C61, CGL2014-53332-C5-1-P and 202030E213 CSIC Intramural Project.

Keywords: Taxonomy, freshwater gastropods, ABGD, PTP, GMYC.

DIVERSITY AND PHYLOGENY OF MEMBRANE INTRINSIC PROTEINS ACROSS EUKARYOTES

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Summary

The membrane intrinsic proteins (MIPs) are transmembrane channels that allow the transport of water and other small uncharged solutes. MIP represent a widespread and highly diverse protein family. In eukaryotes, land plants and animal MIPs are well described and categorised, but the diversity in other eukaryotic groups, particularly unicellular protists, remain largely understudied.

Here we take advantage of a database containing a comprehensive representation of genome and transcriptome sequences for all major eukaryotic supergroups, as well as orphan taxa. Using BLAST and HMMER, we searched for MIP homologs and built a large and taxonomically comprehensive phylogeny of MIPs. We recovered all main known main MIPs groups, including s.s. aquaporins (AQPs) mainly involved in water transport and aquaglyceroporins (GLPs) able to transport glycerol. The large phylogenetic diversity of our tree allows to better define the evolutionary origin of MIP groups, most of them previously defined exclusively in plants and vertebrates. Interestingly, unicellular eukaryotes display a high diversity of MIP homologs despite they should be able to exchange water and small solutes by simple diffusion due their small size. Finally, we observe some cases of possible horizontal gene transfer involving bacteria and eukaryotes.

This research is funded by Complutense University of Madrid and Banco Santander financing program (PIFUC) and by Erasmus + Internship program.

Keywords: Aquaporins, Eukaryotes, Evolutionary relationship, Membrane intrinsic proteins, Molecular Phylogeny.

DIVERSITY PATTERNS AND DISTRIBUTION OF AQUATIC HEMIPTERA IN COASTAL WETLANDS OF PERÚ

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Summary

Coastal wetlands have important ecological functions; however, anthropogenic pressure has been responsible for its deterioration and loss biodiversity worldwide, and Peru is no stranger to this reality. Considering this context, the aims is to provide information about the biodiversity patterns and geographic distribution of aquatic hemipterans that inhabit Peruvian coastal wetlands, due they are an aquatic insects group widely represented in lentic habitats and poor studied in Peru. The study area comprised seven coastal wetlands, three in the northern region of Peru: Vice (Piura), Eten (Lambayeque) and Huanchaco (La Libertad), three in the central region (Lima): Santa Rosa, Ventanilla and Villa; and one in the southern region: Mejía (Arequipa). The data were obtained from the review of samples from collections carried out in the wetlands of Vice, Eten and Villa; in addition to bibliographic references of the wetlands of Eten, Huanchaco, Santa Rosa, Ventanilla, Villa and Mejía. The diversity of aquatic hemipterans was represented by 14 species, grouped in 13 genera and 11 families. *Limnogonus profugus* (Gerridae) and *Buenoa absidata* (Notonectidae) presented the wider latitudinal distribution (from north to south); while eight species have been reported only in central region wetlands (Lima). The wetlands of Santa Rosa and Villa, in central region, presented the higher diversity with 14 species. Aquatic hemipterans are widely represented in the coastal wetlands of Peru, with the higher diversity in the central region. The project was financed by Investigation and Postgrade Vicerrectorado of National University of San Marcos (Code B20100071).

Keywords: lentic habitats, fragile ecosystem, Nepomorpha, Gerromorpha, richness.

IMPROVING PROTEIN LOOP MODELLING FOR ANTIBODY H3-CDR LOOPS

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Summary

Prediction of protein loop structures is crucial for protein structure modelling, structural refinement, antibody design, or ion channels modelling. We present an improved version of our loop modelling package: Random Coordinate Descent (RCD+ <http://rcd.chaconlab.org>). This method combines an ab initio loop closure algorithm with a Rosetta full-atom refinement. We include a novel knowledge-based pairwise potential (KORP) which takes into account information of the relative position and orientation per residue. The extensive parameter optimization of KORP significantly improve the prediction accuracy of the server. We validate and quantify the enhancements with standard loop benchmarks.

Interestingly, we have obtained promising results in one of the most interesting and challenging applications scenarios: the H3 loop of the antibody Complementarity Determining Region (CDR). H3 loop gives the major antibody specificity in ligand binding and is the most variable CDR loop. In this particular case, we apply a soft constraint for the last N-terminal and C-terminal residues based on the distributions observed in crystal structures, since such regions adopt a characteristic kink conformation. This kink constraint leads to an enrichment in near-native models, especially for the more challenging longer loops. The new method can generate sub-angstrom loop predictions for short and medium-length loops (yellow ribbon in the figure) and 1.0–2.0 Å RMSD up to 19 residues long.

Keywords: Protein structure prediction, CDR, H3 antibody loops, RCD, KORP.

THE EARLY MATERNAL ENVIRONMENT SHAPES THE PARENTAL RESPONSE TO OFFSPRING UV ORNAMENTATION

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Summary

Parents allocate resources to offspring to increase their survival and to maximize their own fitness, while this investment implies costs to their condition and future reproduction. Parents are hence expected to optimally allocate their resources. They should invest equally in all their offspring under good conditions, but when parental capacity is limited, parents should invest in the offspring with the highest probability of survival. Such parental favouritism is facilitated by the fact that offspring have evolved condition-dependent traits to signal their quality to parents. In this study we explore whether the parental response to an offspring quality signal depends on the intrinsic capacity of the parents, here the female. We first manipulated the intrinsic capacity of blue tit (*Cyanistes caeruleus*) females through lutein-supplementation during egg laying, and we subsequently blocked the UV/yellow reflectance of breast feathers on half of the nestlings in each brood. We did not find evidence that the female intrinsic capacity shaped parental feeding or sibling competition according to offspring UV/yellow colouration. However, nestling UV/yellow colour affected costly behavioural interactions in the form of prey-testings (when a parent places a prey item into a nestling's gape but removes it again). In lutein-supplemented nests, fathers but not mothers favoured UV-blocked chicks by testing them less often, supporting previous results. Accordingly, in lutein-supplemented nests, UV-blocked nestlings gained more mass than their siblings, while in control nests we found the opposite effect and UV-blocked nestlings gained less. Our results emphasize that the prenatal environment shaped the role of offspring UV/yellow colour during certain family interactions and are indicative for sex-specific parental care strategies.

Keywords: parental care, parental favouritism, parent-offspring conflict, sibling conflict, life-history trade-offs, prey-testings, UV colouration.

TREATMENT OF *STAPHYLOCOCCUS AUREUS* AND *STREPTOCOCCUS PNEUMONIAE* MIXED BIOFILMS BY ANTIOXIDANTS

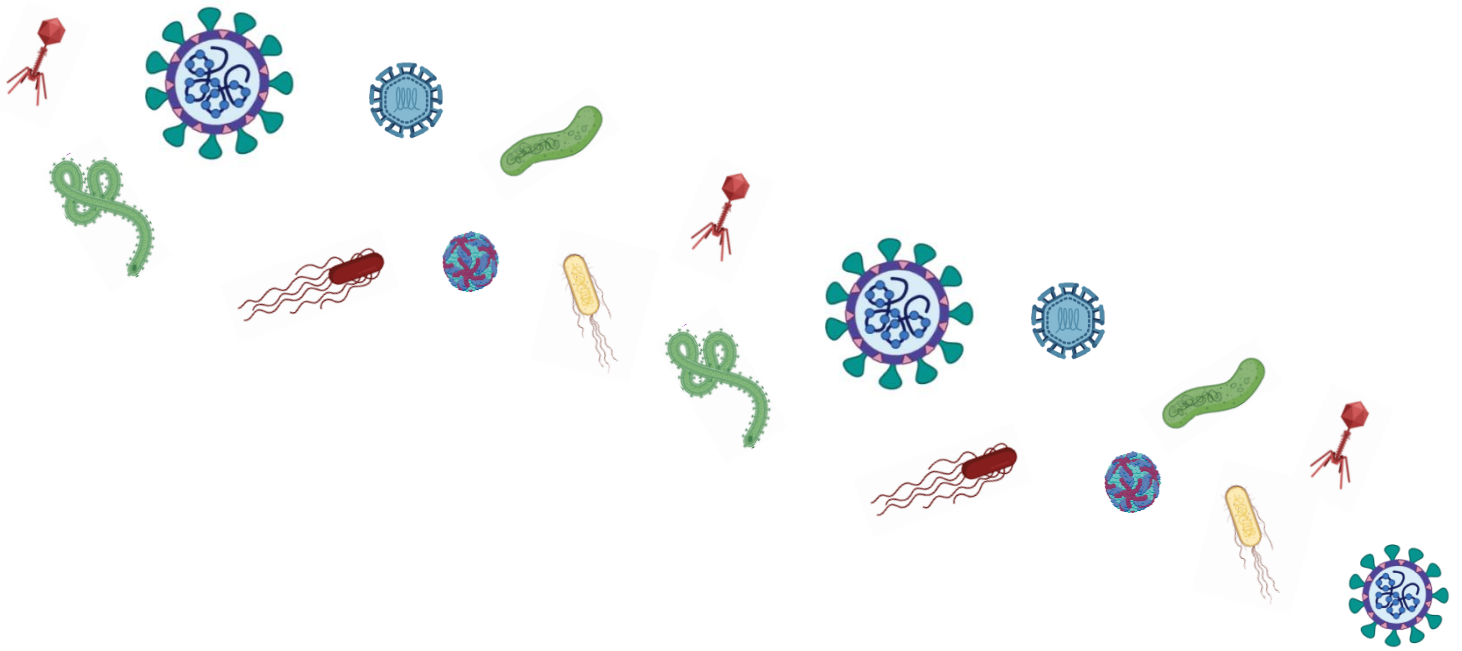
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Summary

Biofilm associated infections are of great concern because they are associated with antibiotic resistance and immune evasion. Co-colonization by *Staphylococcus aureus* and *Streptococcus pneumoniae* is possible and suppose a threat in clinical practice. Here, we investigate the interaction between *S. aureus* and *S. pneumoniae* in mixed biofilms and we test new antibiofilm therapies with antioxidants cysteamine (Cys) and N-acetyl-L-cysteine (NAC). We developed two *in vitro* *S. aureus*-*S. pneumoniae* mixed biofilms in 96-well polystyrene microtiter plates. We treated *in vitro* biofilms with Cys and NAC and analyzed the effect of the antioxidants by crystal violet staining, viable plate counting and confocal microscopy. We observed that *S. pneumoniae* needs a higher proportion of cells in the inoculum and planktonic culture to reach a similar population rate in the mixed biofilm. We demonstrated the effect of Cys and NAC in preventing *S. aureus* biofilms and *S. aureus*-*S. pneumoniae* mixed biofilms. In the two mixed biofilms, Cys practically eradicated *S. pneumoniae* but only showed a 50% reduction in the *S. aureus* populations. Administration of 5 mg/ml of NAC nearly eradicated the *S. pneumoniae* population and killed nearly 94% of MSSA cells and 99% of MRSA cells in the mixed biofilms. The methicillin resistance background did not change the antioxidants effect in *S. aureus*. These results identify NAC and Cys as promising repurposed drug candidates for the prevention and treatment of individual *S. aureus* biofilms and mixed biofilms by *S. pneumoniae* and *S. aureus*, independently of the methicillin resistance background.

Keywords: *S. pneumoniae*, MRSA, MSSA, biofilm, treatment.



RESÚMENES:

COMUNICACIONES ORALES

Sesión III

HOW TO RESIST DRY SOIL: TRANSCRIPTIONAL CHANGES IN A MEDITERRANEAN EARTHWORM DURING AESTIVATION

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Summary

Earthworms have a central role in ministering the terrestrial ecosystems and are proving to have an important role in modulating the effects climate change has on soil. Aestivation is a form of dormancy employed by the organisms living in deserts and arid environments, when confronted with prolonged periods of drought. Understanding global metabolic adjustments required for withstanding the harsh conditions of the ever more severe Iberian drought, we performed a global transcriptomic exploration of the endogeic earthworm *Carpetania matritensis* during aestivation. There were a total of 6,352 differentially expressed transcripts in the aestivating group, with 65% being downregulated. Based on GO and KEGG enrichment analyses, downregulated genes seem to be indicative of an overall metabolic depression during aestivation. Indeed we noted a reduction of protein turnover and macromolecule metabolism coupled with suppression of genes involved in digestion. Upregulated genes, namely antioxidant genes and DNA repair genes showed clear signs of abiotic stress caused by ROS generation. Abiotic stress led to transcriptomic changes of genes involved in immune response, mostly affecting the NF- κ B signaling pathway as well as changes in apoptotic genes indicating the necessity of investigating these processes in a tissue specific manner. Lastly we uncovered a possible mechanism for water retention by nitrogenous waste accumulation. This study provides the first ever transcriptomic investigation done on aestivating earthworms and as such serves as a general framework for investigation on other earthworm species and other soil invertebrates, which is becoming increasingly important with the current scenario of climate change.

Keywords: soil desiccation, RNA-seq, paradiapause, adaptation, invertebrates.

EPHB2 AND EPHB3 IN MURINE MESENCHYMAL STROMAL CELLS BIOLOGY

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Summary

The differentiation potential to mesodermal lineages of mesenchymal stromal cells (MSC) and its immunomodulatory properties have caused that these cells are being studied extensively with the objective of developing cell therapies. These functions generally require cell-cell contact, where various cell membrane receptors intervene. Eph receptors, the larger family of tyrosine kinase receptors known, and their ligands, ephrins regulate these interactions and many processes as adhesion, survival, proliferation, differentiation, and others. Our group has previously described their relevance in different organs as thymus and, more recently, in bone marrow, where MSC are an essential part of its cellular niches. Therefore, this project aims to determine the role of EphB2 and EphB3 in the biology of murine MSC. We first demonstrate that murine MSC express EphB2, EphB3 and other molecules of the EphA and B families, as well as their ligands. Then, using mice that lacks these receptors, we showed that both molecules are involved in osteogenic and adipogenic differentiation, because the lack of EphB3 increases the osteogenic differentiation, while the lack of EphB2 promotes adipogenic differentiation, hence repressing the osteogenic one. Also, challenging the mice bone remodeling process with two osteoporosis models (dexamethasone and ovariectomized), we determine that, in both cases, mice lacking EphB3 do not developed osteoporosis as WT mice do. In conclusion, we propose that EphB2 and EphB3 receptors have a regulatory role in MSC differentiation *in vitro* and on the behavior of these cells in an osteoporosis condition *in vivo*.

Keywords: Mesenchymal Stromal Cells, osteoporosis, osteogenesis, Eph.

SITE SELECTION BASED ON CONSPECIFIC CHEMICALS IN THE AMPHISBAENIAN *Blanus rufus*

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Summary

An animal's survival and reproductive success are strongly dependent on its ability to locate the necessary resources. Many vertebrates use conspecific chemical signals to assess the quality of and orient towards them. In reptiles, the use of chemoreception for conspecific recognition and mate location is widely spread. Here, we tested whether conspecific chemical cues influence the selection of novel substrates by an underground-living reptile, the amphisbaenian *Blanus rufus*. We first performed a selection test with two substrates that contained chemical cues from different classes of conspecifics, and secondly, we carried out a T-maze test to examine preferences inside subterranean galleries scent-marked by conspecifics. Preliminary analyses showed no significant differences between chemical treatments in both experiments. However, there is a trend for both females and males to select sites with chemical cues of other males, especially when these males are smaller than the focal individual. Our results provide new information on behavioural responses towards the odour of conspecifics in a poor-studied group of reptiles.

Keywords: amphisbaenians, fossorial reptiles, chemical ecology, behavioural ecology.

EXTRACTION AND CHARACTERIZATION OF ARGENTINE RED SHRIMP (*PLEOTICUS MUELLERI*) PHOSPHOLIPIDS AS RAW MATERIAL FOR LIPOSOME PRODUCTION

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Summary

Production of Argentine red shrimp consisted of 256 thousand tons in 2018. Approximately 50% of the shrimp is cephalothorax, which is considered a waste despite its great content in important fatty acids such as EPA and DHA as well as other important nutrients such as astaxanthin, tocopherol and cholesterol. These important molecules, otherwise wasted, could be incorporated into the diet as liposomes, vesicles composed of a bilayer of phospholipids capable of carrying payloads that are non-toxic to the human body and as such perfect for drug delivery, cosmetic use or nutritional supplements.

Liposomes made with synthetic phospholipids are common, however, we attempt to use and characterize liposomes made with phospholipids extracted directly from *P. muelleri* cephalothoraxes. For this, an extraction method was designed that allowed us to obtain separated lipid fractions, which then we evaluated for its suitability as liposome-forming substances. Liposomes were ultimately carried out and submitted to several assays to identify its appropriateness as a potential food additive with nutritional value.

This research was funded by the Agencia Estatal de Investigación (AEI) and Fondo Europeo de Desarrollo Regional (FEDER), through Project NANOALIVAL AGL2017-84161, and by the CSIC through project 202070E218.

Keywords: Shrimp waste, phospholipids, liposomes, omega-3 fatty acids, extraction, morphology.

THE GENUS *CRANFILLIA* (BLECHNACEAE, POLYPODIOPSIDA): KEY TO NATURAL SECTIONS PROPOSED FOR THE GENUS

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Summary

Cranfillia Gasper & V.A.O. Dittrich is a fern genus in the family Blechnaceae which was firstly described by Gasper in 2016. Originally, including 12 species which were mainly framed by phylogenetic support, the different *Cranfillia* species has been subject of several taxonomic reviews, nomenclatural recombinations and even new species have been described last years, reaching up to 22-23 species. These systematic changes are probably because of the few diagnostic characters that have been initially given to segregate *Cranfillia* from other phylogenetically related genera. Other systematic difficulties are the great morphological heterogeneity among its species, which points to the need of a better morpho-anatomical revision of the genus.

We show here our results working from the traditional taxonomic point of view with *Cranfillia* species, which has led to new diagnostic characters which support it, as well as a key to the species of *Cranfillia* which has been successfully segregated in natural groups.

Keywords: botany, taxonomy, ferns, Blechnaceae, *Cranfillia*, phylogenies.

TAXONOMY AND EVOLUTION OF PARABLECHNUM, THE MOST DIVERSE GENUS OF ONE OF THE MOST RECENT FERN FAMILIES

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Summary

Blechnaceae is globally distributed and amongst the youngest fern families, making it an excellent case study for exploring rapid radiations in ferns. Within this family, Parablechnum is the most diverse genus (ca. 65 species), distributed in the tropics and subtropics. Although a historic Gondwanan vicariance could explain this distribution, the available dating support that the distribution is driven by long-distance dispersal. However, reaching a conclusion on the has been hindered by the lack of resolution of previous phylogenetic studies as well as unclear taxonomic delimitation.

We are undertaking an integrative approach that combines morphoanatomical studies with molecular phylogenetics. We have analysed macro- and micromorphological characters via optical and electronic microscopy. We are also sequencing five chloroplast markers for phylogenetic inferences, dating and reconstruction of biogeographic history.

Our first results have shown that the most interesting morphoanatomical characters at the taxonomic level are the anatomy of the fertile pinna and the macro- and microornamentation of the spores. Likewise, the preliminary phylogenetic reconstructions show an evolutionary landscape that is more complex than previously expected. While the phylogenetic signal supports, to a certain degree, the existence of a Neotropical clade, it is doubtful that vicariance alone can explain the current distribution. In turn, these results are compatible with the occurrence of infrequent LDD events.

Far from being a static lineage fitting a simple paradigm, the Parablechnum case study reinforces that events associated with evolutionary dynamism in land plants, such as rapid radiations and diverse biogeographic divers, also occur in ferns.

Keywords: anatomy, biogeography, morphology, phylogeny, systematics.

RESÚMENES:

Pósteres



EVALUATION OF MYCOTOXIN DETOXIFICATION CAPACITY BY PROBIOTIC MICROORGANISMS OR GRAPE ISOLATES

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Summary

The presence of aflatoxin B₁ (AFB₁), fumonisin B₁ (FB₁) and ochratoxin A (OTA) in food and feed is a major threat to human and animal health, in addition to high economic losses. Biological detoxification and the use of probiotics and other QPS microorganisms, is positioned as one of the most promising strategies to reduce the concentration of these mycotoxins in food and feed.

In this work, the detoxification capacity of AFB₁, FB₁ and OTA by various microorganisms isolated from probiotic products and grapes was evaluated. The results indicate that most of the bacteria and yeasts tested show a high capacity to reduce the initial concentration of AFB₁, OTA and FB₁ with values up to 87%, 81% and 82%, respectively. *Hanseniaspora uvarum* U1 was able to significantly reduce the three toxins evaluated, both FB₁ (79.4%), AFB₁ (79.5%) and OTA (71.6%). To find out the mechanism involved in the detoxification of *H. uvarum* U1, the same assay as above was performed, but with thermally inactivated cells. The results of this study seem to indicate that *H. uvarum* U1 detoxifies mycotoxins by adsorption to the cell wall and by an active mechanism.

In conclusion, these results describe the great potential of the microorganisms analyzed in this study as biological detoxification agents of mycotoxins, which would allow reducing the problems associated with their exposure.

Work supported by Spanish Ministry of Science and Innovation (RTI 2018-097593-B-C21). C. Gómez-Albarrán is supported by a FPI fellowship by the Spanish Ministry of Science and Innovation (PRE 2019-087768).

Keywords: ochratoxin A, fumonisin B, aflatoxin B, biological detoxification, *Hanseniaspora uvarum* U1.

MAIN ACTORS INVOLVED IN THE TECHNOLOGY TRANSFER OF BIOMEDICAL PROJECTS IN SPAIN AND INDICATORS USED FOR PROJECTS VALUATION

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Summary

In the field of biomedicine, the actors involved in the transference of research results to society are diverse and multidisciplinary.

The research and development (R&D) of biomedical projects are carried out not only in universities or research centers, but also in hospitals, and in Spain, the successful exploitation of results necessarily involves the National Health System (NHS).

Now, there are 202 entities registered as Technology Transfer Offices (TTO) in the Spanish Science Ministry, that belong to universities, hospitals, medical institutes, research centers and other organizations.

We have classified these entities according to their nature (kind of organization, dependence from national or regional government, etc.) to understand the technology transfer network in Spain.

The indicators currently used to evaluate the technology transfer in universities, established by the RedOTRI platform, are general to all the knowledge areas, and they do not reflect the actual value of health projects, as the pathways to reach patients' and users' needs are varied.

The Innovation Platform in Medical and Healthcare Technologies (ITEMAS) uses specific indicators for the assessment of health projects, but they are not adequate to projects developed out of the NHS. Therefore, it is necessary to select a pool of indicators that reflect the real potential of health projects independently of the nature of the center of origin.

We have analyzed the most used indicators and a selection of them will be quantified through an online form by the TTOs technicians to agree in a weighted group of indicators to evaluate health projects exploitation.

Keywords: technology transfer, indicators, biomedicine, health.

GENOME-WIDE METHYLATION ANALYSIS IN *Abies alba* (MILL.): OUTCOMES OF A DROUGHT-SENSITIVE TREE UNDER A CLIMATE CHANGE SCENARIO

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Summary

A climate change-induced decline has been reported in several silver fir (*Abies alba* Mill.) populations across Europe over the last decades. Forest tree species, being sessile organisms with long generation times, are highly vulnerable to climatic fluctuations such as prolonged droughts or heat waves. Hence, their adaptation to a local changing environment may rely on epigenetic modifications when genetic frequencies are not able to shift fast enough. Nonetheless, our current knowledge about climate change-induced shifts in the epigenomes of forest trees is scarce, even though these modifications are likely to be of great importance for their survival. The current lack of knowledge on this field is mainly related to the difficulties that arise when working with these species, such as huge genome sizes, often poorly annotated, and a limited availability of bioinformatic tools to analyse the resulting data. In spite of this challenging framework, we report here the preliminary results obtained from natural populations of *A. alba* showing signs of decline. By analysing whole-genome bisulfite sequencing (WGBS) data, we were able to identify differentially methylated regions (DMR) between healthy and declining trees in forests affected by drought-induced dieback.

Isabel García-García is recipient of a predoctoral fellowship (FPU18/01153) and this work is supported by MICINN RTI2018-096884-B-C33.

Keywords: epigenomics, methylation, WGBS, bioinformatics, *Abies alba*.

TESTING INDUCIBLE AND TARGETED DEGRADATION OF PROTEINS IN *Synechococcus* sp. PCC 11901

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Summary

Cyanobacteria are attractive microbes for biotechnology applications as they derive their energy from light and their intracellular carbon from CO₂, two cheap and plentiful substrates. One application of cyanobacteria is as photosynthetic “cell factories”, where the metabolism is engineered so that the cell converts CO₂ into a compound of interest. In cell factory engineering, most of the current methods rely on the manipulation of target gene expression within a metabolic pathway. However, sometimes target enzymes remain in the cell long time until they are degraded, so tools that enable control of protein stability are highly important.

In this work, we have developed a tool for inducible degradation of target proteins in the fast-growing cyanobacteria *Synechococcus* sp. PCC 11901. The system uses two components: 1) an inducible expression of the protease from the tobacco etch virus (TEVp) and 2) a short tag added to the N terminus of the target protein. This tag includes the known consensus sequence and cleavage site of the TEVp and several aminoacids that are known to destabilize proteins and make them more susceptible to degradation, called degrons. In this system, the protein degradation is triggered via the addition of an inducer, which activates the expression of TEVp. After the protease excises part of the N-tag, the destabilizing degrons directly promote protein degradation by the protease complex in the cell. To develop this system in cyanobacteria, we tested a controlled degradation of the yellow fluorescent protein.

Supported by a FEBS Summer Fellowship.

Keywords: Synthetic biology, cyanobacteria, control of proteins levels, proteolysis.

EFFECT OF HOUSEHOLD AEROSOLS IN THE STRUCTURE AND ACTIVITY OF PULMONARY SURFACTANT FILMS

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Summary

Throughout the day, we are in contact with a large amount of aerosolized products that can enter the body via inhalation. These aerosols include deodorants, air fresheners or those coming from electronic cigarettes.

In order to study a possible toxic effect of these aerosols at the level of phospholipid membranes, we have investigated their impact on monolayers of the model lipid dipalmitoylphosphatidylcholine (DPPC) using the Langmuir trough. DPPC monolayers were exposed to these aerosolized products using different methodologies, and subsequently transferred onto solid supports to be observed by epifluorescence microscopy. We could observe marked alterations on the lateral structure of the interfacial monolayers of DPPC as a consequence of the exposure to the different products tested.

DPPC is also the main component of the pulmonary surfactant system, in charge of forming a thin surface-active film lining the respiratory surface to reduce the work of breathing. This surfactant film is the first biological barrier that aerosolized substances find after inhalation. To study the effect of these products in the functional properties of a native pulmonary surfactant isolated from porcine lungs we used the Captive Bubble Surfactometer device, in which an air bubble coated with pulmonary surfactant is subjected to compression-expansion cycles, mimicking breathing dynamics. Our results suggest a relationship between the structural effect generated by these products in DPPC monolayers and the alteration of the functional properties observed in pulmonary surfactant.

Keywords: pulmonary surfactant, aerosols, membranes, monolayers.

UNRAVELLING THE MYSTERY OF THE ARABIDOPSIS MEIOTIC MUTANT *DSY1*: A NOVEL MUTANT ALLELE OF *MSH5*

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Summary

The desynaptic mutant *dsy1* was isolated in a screen of T-DNA transformed Arabidopsis lines with reduced fertility more than 20 years ago. Desynaptic mutants, by definition, typically show full synapsis at pachynema, but many univalents at metaphase I. Despite the interesting phenotype of this mutant, with the lowest mean chiasma frequency known for a mutant with full synapsis, the responsible gene has not been identified. Preliminary analyses conducted in our lab, indicated the presence of several T-DNA copies in *dsy1*. For this reason, we decided to attempt whole-genome massive sequencing (WGS) to map these insertions in order to identify the gene responsible for the observed phenotype in *dsy1*. By mapping the reads against the Arabidopsis genome, it was possible to locate a homozygous insertion in locus At3g20475, encoding AtMSH5, a homologue of the MutS-homolog family involved in meiotic recombination. Given that no other insertions could be found, it is possible that multiple copies of the T-DNA were inserted in this location. In addition, a complementation test has allowed us to further confirm that *AtMSH5* is the causal gene in *dsy1*. All *AtMSH5* mutants described so far are in the Columbia (Col) accession, while *dsy1* was obtained in the Wassileskija (Ws) accession. This finding provides a valuable tool, since it allows taking advantage of having the mutation in two different genetic backgrounds for measuring meiotic recombination rates by performing fine mapping of recombinant chromosomes using SNP markers.

Keywords: *Arabidopsis thaliana*, meiosis, cytogenetics, crossing over.

PHYSICAL CONTACT BETWEEN PREMATURELY AND NON-PREMATURELY AGING MICE WHILE THEY COHABIT IS CRUCIAL TO IMPROVE THEIR BEHAVIOR, IMMUNITY, OXIDATIVE STATE AND LONGEVITY

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Summary

Aging is associated with chronic oxidative stress, which contributes to a deterioration of the nervous and immune systems and, consequently, to a greater morbidity and mortality. Positive social environment is essential for maintaining health and slowing down aging. Adult prematurely aging mice (PAM), characterized by an inadequate response to stress, show premature immunosenescence, high oxidative stress and shorter longevity compared to exceptionally non-PAM (ENPAM) with the same chronological age. Improvements in immune function and oxidative stress in PAM leukocytes and organs were recently shown after living with ENPAM for 2 months continuously, but ENPAM showed some functions deteriorated. Therefore, the objectives of the present study were to verify if living for only 15min/day for 2 months allows maintaining these positive effects and avoids the negative ones in ENPAM and find out the influence of physical contact on these effects. For this, female mice ICR-CD1 cohabited in a ratio of 2 PAM and 5 ENPAM 15min/day for 2 months in contact or physically separated. Then, several behavioral responses, immune function and oxidative stress parameters of peritoneal leukocytes, and longevity of animals were studied. The results showed improvements in the behavior, immunity, redox state, and a greater longevity in PAM without the deterioration of these parameters in ENPAM. The physical contact was essential for obtaining these effects. In conclusion, this kind of short coexistence of PAM with ENPAM improves the aging process of PAM, without deteriorating that in ENPAMs, increasing their longevity, and physical contact is a crucial mechanism in these effects.

Keywords: Prematurely aging mice (PAM), social environment, behavior, immunosenescence, oxidative stress, physical contact, longevity.

SERUM MicroRNAs CATALOG ASTHMATIC PATIENTS BY PHENOTYPE

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Summary

Background

Asthma is a chronic inflammatory condition of the airways with a complex pathophysiology. Stratification of asthma subtypes into phenotypes and endotypes should move the field forward, making treatment more effective and personalized. Due to the health threat posed by eosinophilic asthma, there is a need for reliable biomarkers to identify patients and treat them properly with novel biologics. A promising tool for this matter are miRNAs.

Objective

The main aim of this study was to find serum miRNAs that can phenotype asthmatic patients.

Methods

Serum miRNAs of eosinophilic (N=40) and non-eosinophilic (N=36) asthmatic individuals were evaluated by NGS, specifically miRNAs-seq, and selected miRNAs were validated by RT-qPCR. Statistical analysis and pathways enrichment analysis of deregulated miRNAs was performed.

Results

NGS analysis revealed 15 differentially expressed miRNAs between eosinophilic and non-eosinophilic asthmatic patients. Of the 15 differentially expressed miRNAs, hsa-miR-26a-1-3p and hsa-miR-376a-3p were validated by RT-qPCR. Expression levels of these 2 miRNAs were higher in eosinophilic than in non-eosinophilic asthmatics. Furthermore, expression values of hsa-miR-26a-1-3p inversely correlated with peripheral blood eosinophil count and hsa-miR-376a-3p expression values with FeNO values and exacerbations number. Additionally, *in silico* pathway enrichment analysis

revealed that these 2 miRNAs regulate signaling pathways related with asthma pathogenesis.

Conclusion

Hsa-miR-26a-1-3p and hsa-miR-376a-3p could be used to distinguish eosinophilic and non-eosinophilic asthmatic patients.

Funding

This study was supported by FIS and FEDER [PI18/00044]; for CIBERES, ISCIII. M.G.-M. was supported by a PFIS contract (FI19/00067) from the FIS.

Keywords: asthmatic patients; eosinophilic asthma; microRNA-seq; phenotypes/endotypes; serum microRNAs.

COULD THE IGF-1 MODIFY CLOCK GENES EXPRESSION IN NEURAL OSCILLATORS OF GOLDFISH (*Carassius auratus*)?

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Summary

The circadian system determines the temporal organization of physiological processes. The non-hierarchical organization of the circadian system in fish makes necessary the communication among biological clocks. This work investigates the role of the IGF-1 as an output signal from the hepatic oscillator that might synchronize brain clocks in goldfish (*Carassius auratus*). For that purpose, we study the effects of IGF-1 addition (10 nM) on clock genes expression at two different times of daily photocycle, at the light period (ZT4) and at the darkness (ZT14), in organotypic cultures of brain oscillators (vagal lobe, cerebellum, hypothalamus, pituitary and optic tectum). In the vagal lobe, the IGF-1 reduces the expression of *rev-erba* during daytime, meanwhile increases the amount of transcripts of *per1b* (at 2 and 4 h), *rev-erba* and *bmalla* (2 h), but reduces *per2* (4h) during nighttime. In the cerebellum, the IGF-1 reduces the expression of both, *rev-erb-α* (2 h) during daytime, and *bmalla* when is present in the culture medium for 8 hours during nighttime. In hypothalamus, the addition of IGF-1 during light period for 2 hours increases the expression of *per2* and *bmalla*; meanwhile this peptide does not modify clock genes expression in the pituitary and optic tectum. Sumarizing, this study demonstrates, for the first time in fish, the effect of the IGF-1 on clock genes expression in brain areas, supporting the possible role of this peptide as a rhythmic output of the hepatic oscillator that might entrain neural oscillators in fish.

Keywords: Circadian system, Clock genes, IGF-1, Neural clocks, Organotypic cultures.

UNDERSTANDING DROUGHT-INDUCED PROCESSES OF GENETIC SELECTION IN DECLINING Atlas cedar POPULATIONS.

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Summary

The Atlas cedar, *Cedrus atlantica* (Endl.) Manetti ex Carrière, is an endangered endemic conifer species naturally located in Morocco and Algeria and presented in several reforested areas, including the South of Spain. Soil water availability is key for its survival, a requirement that is being threatened by climate change. Indeed, drought-induced dieback and mortality have been recently reported for several Atlas cedar forests. Understanding the genetic bases that underlay the response of *C. atlantica* to this changing environment could be key to guide the conservation of this drought-sensitive endangered tree. Hence, genotyping by sequencing (GBS) may provide a useful way to study large genome size species, such as conifers, and when a reference genome is not available. Here we present the results of an extensive GBS analysis of Atlas cedar, including natural and reforested populations. The analysis of the population structure provides valuable clues to know the origin and drought adaptive capacity of some Spanish reforestations. Moreover, the genome-environment association study (GEA) has shown significant relationships among bioclimatic variables and the genetic variables. For instance, our results showed a main effect of annual mean temperature and annual precipitation, suggesting drought-induced processes of genetic selection in declining Atlas cedar populations.

Belén Méndez-Cea is a recipient of a predoctoral fellowship (Universidad Complutense de Madrid-Banco Santander, CT42/18-CT43/18) and this work was supported by MICINN, CGL2013-48843-C2-2-R.

Keywords: Atlas cedar, GBS, GEA, SNP, climate change.

TEMPERATURE AND FASTING: TWO SYNCHRONIZERS OF NOCTURNIN EXPRESSION IN GOLDFISH?

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Summary

Nocturnin (NOC) is a phosphatase involved in the transformation of NADP(H) to NAD(H). A relationship among nocturnin, circadian system and environmental temperature has been suggested in mice, but none is known in poikilotherms. Our aim is to investigate the effect of thermal acclimation and food availability on the expression of all *noc* paralogs (*noc-a1*, *noc-a2* and *noc-b1*) expressed in goldfish (*Carassius auratus*). For this purpose, fish under 12L:12D photoperiod were acclimated at 3 temperatures (17, 22 and 27°C) and fed 4 times daily at ZT1, ZT4, ZT7, ZT10 for 30 days and then half of them were kept unfed for another 10 days. After the 40 days, liver, adipose tissue, muscle, hypothalamus and retina were sampled and *noc* expression was analyzed by RT-qPCR. In liver, while *noc-a2* and *noc-b1* were induced by low temperature, *noc-a1* was induced by cold and warm. In fish fasted the last 10 days acclimation *noc-a2* expression is repressed at all temperatures studied. In adipose tissue, temperature and fasting effects on *noc-a1* matched the ones observed in liver, while neither temperature nor fasting modified *noc-a2* or *noc-b1* expression. In muscle, warm induce *noc-a1* expression in fed fish and represses *noc-a2* levels in fasting conditions. *Noc-b1* is cold-induced when fish were fed and shows a biphasic compensation in fasted group. Hypothalamus and retina exhibit lower or absent *noc* variations, respectively. These results suggest a possible functional specialization of *noc* paralogs in different tissues, and aim to investigate its possible role as an energy metabolism regulator in poikilotherms.

Keywords: Fasting, goldfish, metabolism, *nocturnin*, temperature.

ASSOCIATION BETWEEN ULTRA-PROCESSED FOOD INTAKE AND ALL-CAUSE MORTALITY

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Summary

Dietary habits have changed in recent decades. One of the most important changes is the increase in the ultra-processed foods consumption all around the world. The purpose of this study is to determine the association between ultra-processed food intake and all-cause mortality in a representative sample of Spanish population.

This prospective cohort study includes 4,679 subjects from the DRECE study. Follow-up lasted from baseline (1991) to December 31, 2017. Dietary information was collected using a validated frequency questionnaire and categorized following the NOVA classification. The association between consumption of ultra-processed food and mortality was analysed using Cox models. Isocaloric substitution models were constructed to compare the health effects of the NOVA groups.

Average consumption of ultra-processed food was 370.8 grams/day (24.4% of energy intake). After a median follow-up of 27 years, 450 deaths occurred. Those who consumed the highest amount of ultra-processed foods had higher risk of mortality. For every 10% of the energy intake from ultra-processed foods consumption, an increase of 15% in the hazard of all-cause mortality was observed (HR, 1.15; 95%CI, 1.03-1.27; p-value=0.012). Substitution of ultra-processed foods with minimally processed foods was significantly associated with a decreased risk of mortality.

An increase in ultra-processed foods consumption was associated with higher risk of all-cause mortality in a representative sample of the Spanish population. Moreover, the theoretical substitution of ultra-processed food with unprocessed or minimally processed foods leads to a decrease in mortality. These results support the need to promote diets based on unprocessed or minimally processed foods.

Keywords: ultra-processed food, NOVA classification, all-cause mortality, isocaloric substitution.

GENETIC DIVERSITY IN THE WESTERN MEDITERRANEAN. α - AND β - THALASSEMIA AS ANTHROPOLOGICAL MARKERS.

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Summary

The α - and β -Thalassemia are hemoglobinopathies characterized by a reduced or absent synthesis of α - or β -globin chains, which are in turn part of the hemoglobin molecule that plays a fundamental physiological role in the organism. Thalassemias represent a large and heterogeneous group of recessive hereditary diseases.

In the present research, a total of 56 DNA sequences of the β -globin locus belonging to patients diagnosed with β -thalassemic trait and family origins in western Andalusia have been genotyped. The results obtained show a high prevalence of the *IVSI-1* mutation (> 50%). Population genetic structure analyses highlight an appreciable genetic heterogeneity within the Mediterranean area. The spatial autocorrelation values (Moran's I index) found from some selected mutations, such as *CD39* and *IVSI-110*, show a clear gradient distributions or "clines" in their patterns of spatial variation. This particular genetic geography seems to be linked to the possible origin of mutations and its subsequent dispersal by migration and gene flow events. Within the Iberian Peninsula, the genetic differentiation with respect to northwestern Africa was shown to be non-significant, although that affinity is closer when southern Iberian populations were considered. This scenario can be interpreted as a consequence of long and sustained history of population relationships between the northern and southern coasts of the westernmost extreme of the Mediterranean basin.

Keywords: β -Globin locus, β -Thalassemic Mutations, Human Genetic Diversity, Epidemiology, Iberian Peninsula.

ON THE ESTIMATION OF ADDITIVE GENETIC VARIANCE WHEN THE ENVIRONMENT HAS A GENETIC BASIS

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Summary

Estimation of relative importance of genotype and environment in expression of a phenotypic trait is key to understand and predict its evolution. *Animal models* are a statistical tool that allows to quantify the genotypic and environmental variance of a phenotypic trait. The aim of this study is to verify what occurs when these models are used when environments and organisms are not independent and there is phenotype-environment genetic correlation. This happens, for example, when there is genetic variation in the preference for an environment (direct genetic preference) or when a phenotypic trait with a genetic basis affects the preference for a given environment. To test it, we created different biological scenarios where we simulated: genetic basis for the phenotypic trait and the environment, phenotypic plasticity (effect of the environment on the phenotype) and/or environmental plasticity (effect of the phenotype on the environment) and we applied *animal models* with different structures. First, we demonstrated that it is possible to quantify the genetic variance of the environment (genetic preference) by treating the environment as a dependent variable, as an extended phenotype. Second, we found that the genetic variance of the phenotypic character is increased by pleiotropic effect, via phenotypic plasticity, if there is genetic preference for the environment that affects the phenotype. Finally, we determined that if the model structure does not reflect the biological reality and it is wrongly assumed that there is no genetic basis for the environment or environmental plasticity, the estimates are numerically and conceptually wrong.

Keywords: Animal models, genetic variance, phenotypic plasticity, environmental plasticity, extended phenotype.

GENOMIC MAPPING OF SPLICING-RELATED GENES IDENTIFY AMPLIFICATIONS IN LSM1, CLNS1A, AND ILF2 IN LUMINAL BREAST CANCER

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Summary

The alternative splicing (AS) process is highly relevant, affecting most of the hallmarks of cancer, such as proliferation, angiogenesis, and metastasis. Our study evaluated alterations in 304 splicing-related genes and their prognosis value in breast cancer patients. Amplifications in CLNS1A, LSM1, and ILF2 genes in luminal patients were significantly associated with poor outcome. Downregulation of these genes in luminal cell lines showed an antiproliferative effect. Pharmacological modulation of transcription and RNA regulation is key for the optimal development of therapeutic strategies against key proteins. Administration of a BET inhibitor and BET-PROTAC reduced the expression of these identified genes and displayed a significant antiproliferative effect on these cell models. In conclusion, we describe novel splicing genes amplified in luminal breast tumors that are associated with detrimental prognosis and can be modulated pharmacologically. It opens the door for further studies confirming the effect of these genes in patients treated with BET inhibitors.

Keywords: splicing pathway; luminal breast cancer; BET inhibitors, RNA expression.

MODULATION OF THE ACTIVITY OF IYO AND RIMA TO UNDERSTAND THE SELF-RENEWAL AND DIFFERENTIATION OF STEM CELLS IN PLANTS

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Summary

Cell differentiation includes two sequential decisions by the precursor stem cells. The first one common to every differentiation event is whether the cell has to self-renew or change fate and differentiate. The second one, and specific of each process, is what cell identity to attain. These cell fate transitions involve global transcriptional reprogramming and is tightly regulated by cellular factors.

IYO and RIMA are two key factors involved in activating stem cell differentiation in plant meristems. Our results suggest that they regulate transcription of target genes by directly binding and modulating the activity of RNA polymerase II. Through RNA-seq analyses in knockdown mutants and Chip-seq analyses of the IYO and RIMA chromatin distribution, we have identified their potential transcriptional targets. To confirm which of those are bona fine direct transcriptional targets of IYO and RIMA, we have generated dexamethasone-inducible RNAi lines. After incubation in dexamethasone-containing media for several days, the RNAi lines phenocopy the defective differentiation phenotypes of *oyo* and *rima* knockdown mutants, indicating that inducible silencing of *IYO* and *RIMA* is effective. We will use these lines to study the time course of *IYO* and *RIMA* inducible-silencing and then determine by RNAseq what transcriptome alterations occur shortly after their silencing.

Keywords: stem cell, differentiation, transcriptome alterations.

ARE THERE COMPARABLE AREAS IN THE BRAIN OF VERTEBRATES?

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The cortex is part of the pallium, the brain region that possess the greatest functional and organizational complexity during the evolution. Understanding how this structure originates provides valuable information for deciphering the operation of current brains. Amniote vertebrates present different pallium architectonics: layered organization is present in mammals and reptiles, whereas in birds the pallium is a collection of nuclei. The comparison of different pallial cell types is necessary to understand pallial evolution, and additional tetrapod models such as anamniotes (amphibians) provide additional perspectives.

We have compared gene expression patterns of specific pallial markers in the amphibian *Xenopus laevis* and the turtle *Trachemys scripta* by immunohistochemical and *in situ* hybridization analysis. We have identified different amphibian pallial regions, where neither layered nor nuclear structures are formed. Two different domains have been identified in the *Xenopus* medial pallium based on the Prox1/Er81 expressions, which could be homologous to the turtle medial cortices. The dorsal pallium of *Xenopus* shows the same gene expression pattern (Er81, Lmo4 and Ctip2) than *Trachemys* dorsal cortex. In addition, the lateral pallium derivatives have been identified rostrocaudally by the expressions of Satb2 and Reln in both models. Furthermore, the ventral pallium of amphibians and turtles can be subdivided in rostral and caudal levels by its Tbr1, FeZ2 and Lhx2/9 expressions.

These observed comparable pallial areas suggest that in the common ancestor of vertebrates these pallial subdivisions would already be present and that the differences could be evolutionary divergences and adaptations.

Keywords: Pallium, cortex, anamniote, amniote, evolution.

DO BIRDS SELF-MEDICATE WHEN THEY ARE SICK?

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Summary

Birds are common hosts of haemosporidian parasites (genera *Plasmodium*, *Haemoproteus* and *Leucocytozoon*), which develop inside red blood cells. These parasites cause oxidative damage to their host through the activation of the immune system and the breakage of the red blood cells. Then, infections with these organisms originate oxidative stress that must be dealt with either activating their internal antioxidant defences or adjusting their antioxidant intake. We tested whether birds can adaptatively alter their food choice to cope with oxidative stress caused by blood parasites during migration, when they are exposed to high energetic requirements.

During October of 2019 and 2020, we mist-netted young male blackcaps (*Sylvia atricapilla*) stopping over in central Spain. Thirty minutes after capture, we placed the birds in individual cages where they were offered two pieces of melon, one soaked in olive oil (fat-enriched) and another one in blueberry juice (antioxidant-enriched). We recorded their behaviour, took a blood sample, weighed, measured and released them unharmed. Breath rate was used as a measure of individuals' capacity to manage stress. We tested their infection status with PCR techniques, resulting in 7 birds that were not infected and 42 infected (14 of them with several parasite lineages). During the trial, 18 ate and among them, 13 consumed fat-enriched and 8 antioxidant-enriched food (3 ate both choices). If birds can self-medicate, we expect that (co-)infected birds will choose antioxidant-enrich food while healthy birds would choose fat-enriched to put on fats, essential for migration.

Funded: Agencia Estatal de Investigación (CGL2017-082117-P).

Keywords: blackcap, haemosporidian parasites, antioxidants, diet.

EVAR RISK FACTORS PREDICTION: FROM MULTIVARIATE STATISTICS TO ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING TECHNIQUES

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Summary

We are developing techniques to compare the prediction of risk factors in EVAR (Abdominal Endovascular Aneurysm Repair) procedures.

The traditional risk factors evaluations are based on Multivariate Linear Regression and/or Multivariate Logistic Regression. Despite both MRL and MLR are fast and precise techniques they have some limitations that we propose may be outperformed using artificial intelligence methods and machine learning algorithms.

Our main goal is to develop procedures that allow an earlier, more reliable and complex risk factor calculation for patients that are going to follow an EVAR surgical intervention, providing the vascular surgeons a complete decision making tool for designing the best approach to the surgical procedure.

Keywords: EVAR; risk factors; multivariate statistics; machine learning; artificial intelligence; decision making.

FAT: QUALITY, OR QUANTITY? WHAT MATTERS MOST FOR THE PROGRESSION OF METABOLIC ASSOCIATED FATTY LIVER DISEASE (MAFLD)

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Summary

Since a considerable number of countries recently restricted or even banned Trans fats, palm oil has become a preferred replacement for food manufacturers. Whether palm oil is potentially unhealthy food mainly due to its high content of saturated Palmitic Acid (PA), is a matter of debate.

The aim of this study was to test if qualitative aspects of diet, such as levels of PA and the fat source, are risk factors for Metabolic Syndrome (MS) and Metabolic Associated Fatty Liver Disease (MAFLD).

In our study, we used three types of Western diet (WD): 1. LP-WD - low concentration of PA (main fat source - corn and soybean oils); 2. HP-WD - high concentration of PA (main fat source- palm oil); 3. HP-Trans-WD - high concentration of PA (mainly Trans fat). C57BL/6 male mice were fed with all types of diet for 14 weeks. Normal chow diet was used as control.

Feeding with all three types of WD caused significant weight gain, adipocytes enlargement, hepatomegaly, lipid metabolism alterations and steatohepatitis. Feeding with HP groups demonstrated more prominent obesity, hypercholesterolemia, stronger hepatic injury, fibrosis.

Only the feeding with HP-Trans-WD resulted in glucose intolerance and elevation of serum transaminases. Brief diet withdrawal totally ameliorated MS and corresponding symptoms of MAFLD in all treated animals. However, mild hepatic inflammation was still detectable in HP withdrawal groups relative to the controls.

Conclusion: Diets enriched in HP and/or Trans-fat play a crucial role in the genesis of MS and progression of advanced forms of MAFLD.

Keywords: Obesity, Metabolic associated fatty liver disease (MAFLD), Steatohepatitis, Fibrosis, Palmitic acid.

MYELOMA DOUBLE HIT PATIENT

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Summary

Advances in therapies have changed the course of the disease in patients with multiple myeloma (MM). It has evolved to a chronicity characterized by remissions and relapses that, sometimes, require multiple lines of treatment. This implies an increased risk of developing second primary neoplasms. Mainly cases of myelodysplastic syndrome (MDS) or acute myeloid leukemia (AML) have been described. We used next generation sequencing (NGS) to detect the presence of any genetic alterations in the bone marrow (BM), positive/negative BM fraction, total BM cells and cell free DNA (cfDNA) of one interesting patient with MM enrolled in the PETHEMA/GEM2017FIT trial (# NCT03742297) at different time points from diagnosis. Loss of heterozygosity has been observed by NGS, specifically, deletion in the short arm of chromosome 17 where TP53 gene is affected. Same result as those obtained by cytogenetics. In addition, the analysis of variants has also reflected the presence of mutation in TP53 mainly in the two follow-up samples, both in total BM cells and in cfDNA. It could be a double hit patient when detecting biallelic inactivation of TP53 (deletion confirmed by copy number variations in one allele and mutation in the other). This differs from negative minimal residual disease (MRD) observed by multidimensional flow cytometry data (MFC), gold standard technique. The patient has not been diagnosed with any myelodysplasia that could explain the escape of pathological plasma cells from myeloma and it is not yet clear why an alteration in TP53 is observed by NGS and not by MFC.

Keywords: double hit, loss of heterozygosity, deletion, mutation.

MOLECULAR PHYLOGENETICS REVEAL TWO DISTINCT GENERA WITHIN THE BASALLUMBRICIDS ZOPHOSCOLEX (MEGADRILI, ANNELIDA)

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Summary:

The genus *Zophoscolex* (Qiu & Bouché, 1998a) comprises 22 species grouped into four subgenera (*Zophoscolex*, *Aquilonibericus*, *Castillodrillus* and *Euibericus*). This genus is distributed throughout the Iberian Peninsula and Southwestern France. Several authors have related it (on the basis of morphological characters) to some basal lumbricid genera from the Iberian Peninsula. There are hardly any molecular studies that include this genus, and the few that have been done have used the species *Zophoscolex Cyanea*. No molecular study to date has included the type species of the genus, *Zophoscolex atlanticus*. To solve this gap in the knowledge of the most diverse Palearctic earthworm family, 13 species of

Zophoscolex were chosen as representatives (including the type species *Zophoscolex atlanticus*) and sequenced for mitochondrial (cytochrome C oxidase I -COI-, ribosomal RNA 16S, NADH dehydrogenase subunit 1 -ND1-) and nuclear (ribosomal RNA 28S) molecular markers. Maximum likelihood and Bayesian inference of the phylogenetic tree recovered a non-monophyletic *Zophoscolex*. The type species is found in a clade along with the rest of the French species of the *Zophoscolex* genus used in this study and belong to *Zophoscolex* subgenus (*Z. graffi* and *Z. micellus*), and it is separated from another clade that contains most of the Iberian species (*Z. chitae*, *Z. ibericus*, *Z. pulvinus*, *Z. hongae*, *Z. alavanensis*, *Z. opisthoporus* and *Z. eurythricos*). This second clade of Iberian species seems to form a new genus that has been called *Castillodrillus* and it includes all the studied species belonging to the subgenera *Aquilonibericus*, *Castillodrillus* and *Euibericus*.

Keywords: earthworm, *Zophoscolex*, Lumbricidae, basal genus.

