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2º Ph Day Biológicas

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ABSTRACTS

Comunicaciones orales

Sesión 1

Anthropometric variability in children and adolescents based on food behavior evaluated through kidmed index

María Sánchez Álvarez[1], Roberto Pedrero-Tomé[1], Ana Alaminos-Torres[1], Noemí López-Ejeda[1,2], Maria Dolores Cabañas[1], Marisa González Montero de Espinosa[1], María Dolores Marrodán[1,2]

[1]. EPINUT Research Group. School of Medicine. Complutense University, Madrid
[2]. Spanish Society of Dietetics and Food Sciences (SEDCA)

Childhood and adolescence are stages of opportunity to establish dietary habits. It is interesting to know how nutrition and body composition interact with quality of diet.

The aim of this research is to analyze the relationship between the anthropometric profile and the quality of the diet in schoolchildren of Madrid.

Participants were 467 boys and 549 girls between 9 and 16 years old from educational centers in the Community of Madrid. The following measurements were taken: weight, height, waist circumference (WC), hip and subcutaneous adipose folds. Waist-height index (WHEI), Skin fold Sum (ΣP), Body Mass Index (BMI), Body Fat percentage (%BFat) and waist-hip index (WHII) were calculated. The KIDMED questionnaire was applied and we analyzed its relationship with anthropometric variables.

The prevalence of overweight was 20.6% in women and 24.6% in men and obesity 4.4 and 5.6 respectively. The category of corporal fat < p10 grouped to 6.4% of the girls and no boys; category > p97 grouped 10.7% of the girls and 24.5% of the boys. The KIDMED score for the entire sample was 4.29 ± 1.89, showing a medium-low diet quality. A reduction in WHEI, WHII, WC, ΣP, and %BFat was observed with the increase in KIDMED score.

The quality of diet evaluated through the KIDMED index was low and was closely related to the levels of total and relative adiposity and the body fat distribution. A greater adherence to the Mediterranean diet acts as a protection factor against obesity.

Keywords: KIDMED, WHII, nutritional status, obesity, children

Diversity and specificity of viruses in Neotropical birds

Truchado, Daniel A.[1,2]; Fernández-Correa, Izaskun[1]; Díaz-Piqueras, José Manuel[1]; Cerrada, Belén[1]; Gomez-Lucia, Esperanza[3]; Domenéch, Ana[3]; Pérez-Tris, Javier[2]; Cadar, Daniel[4]; and Benítez, Laura[1]

[1] *Department of Physiology, Genetics and Microbiology. Faculty of Biology. Complutense University of Madrid. José Antonio Novais, 12. 28040, Madrid, Spain*

[2] *Department of Biodiversity, Ecology and Evolution. Faculty of Biology. Complutense University of Madrid. José Antonio Novais, 12. 28040, Madrid, Spain*

[3] *Department of Animal Health. Faculty of Veterinary Medicine. Complutense University of Madrid. Avda. Puerta de Hierro s/n, 28040, Madrid. Spain*

[4] *Bernhard Nocht Institute for Tropical Medicine, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research, National Reference Centre for Tropical Infectious Diseases, Bernhard-Nocht-Strasse 74, 20359, Hamburg, Germany*

In the face of the growing interest of scientific community to know the virome of wild fauna in our planet, deep sequencing has become the main tool to discover novel viruses. Knowing the diversity of viruses and their ecological context in remote areas will provide important information for human population to prevent new emerging viral epidemics. Zoonotic viruses are considered the most probable causative agents of emerging diseases and avian hosts are one of their main reservoirs. In this multidisciplinary study, we carried out a metagenomics analysis of cloacal, blood and oral samples from 50 birds sampled in the Nouragues Natural Reserve (French Guiana). This region is located in the Neotropics, one of the most biodiverse regions on Earth but which remains under-explored. From the viral sequences we obtained, we selected those with a particular pathogenic, zoonotic or economic interest to analyze their genomes, compare them with those already available at genomic databases, study their phylogeny and, in most cases, provide some data related to the prevalence in the analyzed population. At present, we are focusing on viruses from the families *Anelloviridae*, *Astroviridae* and *Hepeviridae.*

Keywords: virome, Neotropics, Neotropical birds, gyrovirus, astrovirus, hepevirus

Systematics of the family Blechnaceae (Polypodiopsida): results regarding the genus *Struthiopteris* Scop.

Sonia Molino de Miguel[1] , José María Gabriel y Galán Moris[1], Carmen Prada del Moral[1], Emily B. Sessa[2], Pawel Wasowicz[3]

[1]*Department of Biodiversity, Ecology and Evolution; Faculty of Biology, Universidad Complutense. Avenida Jose Antonio Nováis, 12. 28040 Madrid, Spain.*

[2]*Department of Biology, University of Florida, Box 118525, Gainesville, Florida 32611, U.S.A*

[3]*Icelandic Institute of Natural History, Borgir vid Nordurslod, 600 Akureyri, Iceland.*

The family Blechnaceae is a fern family with around 250 species mostly distributed in tropical America and Australasia, with some species growing also in temperate zones in the North Hemisphere. This family used to have 8-10 genera, but during last decade evidence has been accumulating about the polyphyletism of its biggest genus *Blechnum* L., which comprised the 80% of the diversity of the family. After morphological and phylogenetical studies a new classification of the family has been published, considering now 24 genera. However, a revision of each of these genera individually is still lacking. Our aim is making a revision of the genus *Parablechnum* C. Presl, that is now the largest in the family with 65 species which occurs in subtropical-tropical America and in Australasia, in order to get a complete monograph, phylogeny and historical biogeography of the genus. To this aim, we will examine morphological and anatomical characters and conduct a molecular phylogenetic study using herbarium specimens and material collected from the field. To understand what kind of result we can get from a study like this, we here present the work what we have already carried out with a smaller Blechnaceae genus, *Struthiopteris* Scop., which comprised 6 species from the North Hemisphere. After revising anatomical and morphological characters, making a complete phylogeny and the historical biogeography of the group, we concluded that it constituted a heterogeneous and paraphyletic genus. Thus, we proposed the separation of three of its species into the resurrected genus *Spicantopsis* Nakai.

Keywords: anatomy, *Blechnum*, morphology, phylogeny, *Spicantopsis*, taxonomy

Mind the gap: Effects of canopy openings on temperate forest bat assemblages

Elena Tena[1*], José Luis Tellería[1], Roberto de la Peña[2], Guillermo Fandos[3], Marisol Redondo[4] and Óscar de Paz[5]

[1] *Departamento de Biodiversidad Ecología y Evolución, Universidad Complutense de Madrid. Madrid. Spain* (e.tena@ucm.es)*
[2] *Calle Treinta y ocho, 5. El Escorial, Madrid. Spain.*
[3] *Department of Geography, Humboldt-Universität zu Berlin. Germany.*
[4] *Organismo Autónomo de Parques Nacionales. Centro Montes y Aserradero de Valsaín. Valsaín, Segovia. Spain.*
[5] *Departamento de Ciencias de la Vida, Universidad de Alcalá. 28871, Alcalá de Henares, Madrid. Spain.*

Gaps in the forest canopy seem to play a major role on forest species biodiversity. In this study, we test if in gaps within a large Scot pine (*Pinus sylvestris*) woodland in central Spain, occur more bats than in the surrounding tree covered control plots. To approach this, we used pairs of bat detectors in 9 gaps and the surrounding control plots. Bat activity in every gap and its nearby control forest was recorded during ten nights between July and August of 2016 and 2017. The results support that bat richness and the activity of some individual species were higher in gaps than in the adjacent control plots. These results support the importance of gaps as feeding areas for the forest bat assemblage and suggest the interest of preserving gaps from a conservation perspective.

This study is a contribution to the Projects of Distribution of bats in Montes de Valsaín of 2016 and 2017 of the Autonomous Authority for National Parks (OAPN).

Keywords: Biodiversity, Chiroptera, forest gaps, forest management, habitat selection, landscape heterogeneity

Pulmonary surfactant and drug delivery: surfing the lungs to vehiculize drugs

Alberto Hidalgo

Department of Biochemistry, Faculty of Biology, and Research Institute "Hospital 12 de Octubre", Complutense University, Madrid, SPAIN. Tel. 91 394 5032

The respiratory system has favorable properties that improve the delivery and pharmacokinetics of drugs intended for both local and systemic therapies. Pulmonary surfactant (PS), a membrane-based lipid-protein material coating the respiratory surface in charge of preventing pulmonary collapse during breathing and minimizing the entrance of undesirable entities, offers greater opportunities for drug delivery. According to our previous biophysical investigations, PS is able to travel interfacially while carrying hydrophobic drugs, such as corticosteroids or Tacrolimus, without affecting its functionality. However, it is essential to evaluate whether this process also happens in the lungs, where different barriers and obstacles, such as mucus, air and liquid flows or the immune system are present. Therefore, we used LPS-induced inflammation mouse models and unique live lung imaging techniques to observe, describe and demonstrate the vehiculizing potential of PS directly on proper lungs.

The in vivo results confirmed our biophysical findings. PS is able to travel over the respiratory surface and share the interfacial trip with an anti-inflammatory drug (Tacrolimus) to reach the alveolar region. Once there, in a process facilitated by breathing cycles, the drug is excluded from the interface to the aqueous alveolar lining layer, where alveolar macrophages uptake it and revert more efficiently the inflammation. This opens the use of pulmonary surfactant to vehiculize different therapeutic agents through the airways (drugs, nanocarriers, siRNA, etc.) and to develop novel strategies in medicine targeting the lungs (tuberculosis, acute lung injury, lung cancer or fibrosis) and peripheral locations.

Keywords: Pulmonary surfactant, respiratory interface, drug delivery, interfacial therapy

Climate change and relict tree species evolutionary potential: understanding the molecular basis of the drought stress response in the southernmost european fir (*Abies pinsapo* Boiss.)

Irene Cobo Simón[1,2]

[1]. *Department of Genetics, Faculty of Biology, Complutense University, Madrid*
[2]. *Department of Physical, Chemical and Natural Systems, University Pablo de Olavide, Sevilla*

Climate change represents one of the main threats for current biodiversity. Trees are particularly concerning due to their theoretically slower evolutionary rate and their ecological importance. Drought stress is among the premier limitations for plants facing this changing climate. Thus, understanding the underlying mechanisms involved in the drought response in trees constitutes one of the most valuable research objectives of evolutionary ecology. Furthermore, relict species are ideal models, since they are able to persist under sub-optimal conditions. Here, we used the Spanish fir (*A. pinsapo*) as a model to carry out a drought experiment and a transcriptomic analysis to the main objective of finding out differences in the gene expression at different stages of drought. Differences in drought sensitiveness were found, as it can be observed in nature, and seedlings were clasified as “tolerant” and “sensitive”. In addition, exclusive differentially expressed genes were found in the “tolerant” seedlings, which can be considered as potential candidate genes of drought resistance. Furthermore, we found out that drought response in this species is an “additive process”. This is the first study in analyzing the molecular basis of the drought response in this species. We propose our novel workflow to be applied in this and other threatened species to help improve the success of conservation management strategies, as well as to shed light to the evolutionary potential of trees facing climate change.

This Project is funded by the Ministry of Economy of Spain. Irene Cobo has a FPI fellowship (Ministry of Economy, Spain).

Keywords: Relict, conifers, climate change, drought, RNA-seq

Comunicaciones orales

Sesión 2

Why only in mammals is there a layered cortex? Implication of Cajal-Retzius cells in evolution.

Sara Jiménez Álvarez

Department of Cell Biology, Faculty of Biology, Complutense University, Madrid

The evolution of the telencephalon in the different vertebrates is currently the center of an intense debate. The highest level of complexity is found in mammals that are the only vertebrates that possess a layered cortex development following an inside-out order. In this process, Cajal-Retzius cells (CRc) are the first subclasses of neurons to be generated in the embryonic telencephalon, and they are playing an important role in cortical development and lamination, generating at signaling centers and migrating over long distances. However, in models with no cortical layered structures, such as sauropsids, it has been described abundant CRc in homologous areas, but its functional implication is under study. On this line, amphibians constitute the only group of anamniote tetrapods, and thus the closest living model to tetrapod antecessor, in addition to be a water to land transition model.

In the present study, we examined the neuronal types in the telencephalon of the amphibian Xenopus laevis. We found that, in comparison to mammals in Xenopus there are at least three different CRc subtypes distribute in telencephalic territories, expressing specific conserved transcription factors like Reelin, Ebf3, ER81 or Zic1/2. In contrast, in Xenopus is lacking the CRc described in the pallial-subpallial boundary, implicated in early neocortical development regionalization through its Dbx1 expression.

Our hypothesis is although layered cortex vs non-lamination pallium organization observed in different groups has multifactorial causes, the distinct CRc patterning between tetrapods might have been one the reasons that contributed to it.

Keywords: Telencephalon, Evolution, *Xenopus laevis*, Pallium, Cajal-Retzius cells (CRc)

The conotoxin diversity of the magical cone *Pionoconus magus* (Linnaeus, 1758) and the discovery of potential new drugs

José Ramón Pardos Blas

National Museum of Natural Sciences, CSIC, Madrid

Summary Cone snails are renowned among marine gastropods because of their striking method to hunt their preys using an arsenal of peptids (conotoxins) injected by harpoon-like radular teeth. Conotoxins are produced within a specialized venom gland and the composition of the venom cocktails is deeply linked to the type of preys they consume. NGS methods have uncovered an astonishing diversity of conotoxins. Given that their target are voltage-gate channels, cone venoms are sound candidates as source for new drugs oriented to reduce chronic pain. Currently, ziconotide, an omega conotoxin isolated from the cone species *Pionoconus magus*, is the most successful example of drug discovery from cone snails. Here, we performed a RNA-seq approach to assemble the transcriptome of the venom gland and determine the conotoxin diversity of two individuals of *P. magus* from Okinawa island (Japan). Using various assembly strategies, we recovered over 200 different peptids per individual, and assigned them to known and new superfamilies of conotoxins. We compared conotoxin diversity between individuals and against other species of the genus *Pionoconus*. We also determined the relative diversity of each superfamily and levels of expression. By providing an accurate catalogue of *P.magus* conotoxins, we aim at contributing to a better understanding of cone venom diversity and at providing candidates for potential drug discovery. This project is been supported by the Spanish Ministry of Science and Innovation (CGL2016-75255-C2-1-P and BES-2017-081195).

Keywords: cone snail, conotoxins, Pionoconus magus, transcriptome

Acute Δ9-THC administration accelerates oligodendrocyte development and regeneration

Alba Huerga1[1]

[1]*Instituto Ramón y Cajal de Investigación Sanitaria (IRYCIS), Dept. of Biochemistry and Molecular Biology and Instituto Universitario de Investigación Neuroquímica (IUIN), Complutense University, 28040, Madrid, Spain*

Research on demyelinating disorders has consistently demonstrated that cannabinoid agonists have the potential to relieve symptomatology and to control inflammatory-mediated neurodegeneration in Multiple sclerosis (MS). Thus, the contribution of oligodendroglial cannabinoid receptors to the beneficial effects of cannabinoids in MS animal models has mostly focused on their capacity to prevent cell survival of oligodendrocytes (OLs) and their progenitors (OPs) against excitotoxic injury. However, very few attention has been paid to the potential of targeting OPs by cannabis-based compounds to promote OL regeneration and functional recovery in demyelinating disorders. Here, we studied the effect of administering Δ9- Tetrahydrocannabinol (Δ9-THC) in OPs cell cycle dynamics and OL differentiation, both, during the critical periods of postnatal CNS myelination and under demyelination condition. First, we studied the effect of administering Δ9-THC at early postnatal ages in the process of OL development during the critical periods of subcortical white matter (SCWM) myelination. We found that acute Δ9-THC administration induced OPs cell cycle exit and differentiation, accelerating the process of OL maturation, SCWM myelination and motor function development during postnatal ages. Further, we used the Cuprizone animal model of demyelination and remyelination. We administered Δ9- THC following 6 weeks of Cuprizone diet and studied the dynamics of OPs proliferation and differentiation along the process of OL regeneration and SCWM remyelination. We found that acute Δ9-THC administration following demyelination induced OPs cell cycle exit and differentiation, and accelerated the process of SCWM remyelination and motor function recovery. Contrato Empleo Joven de la Comunidad de Madrid como Investigador Predoctoral.

Keywords: Δ9-Tetrahydrocannabinol, Oligodendrocyte progenitors, Multiple Sclerosis

The immune impairment shown by post-traumatic stress disorder mice depends on their anxiety levels.

Ceprian N[1,2], Garrido A[1,2], Díaz del Cerro E[2], Hernández M[2], De la Fuente M[1,2].

[1]. *Institute of Investigation 12 de Octubre (i+12), Madrid, Spain*
[2]. *Dept. Genetics, Physiology, Microbiology (Animal Physiology Unit). Fac. Biology. Complutense University. Madrid. Spain*

Post-traumatic stress disorder (PTSD) is a chronic and disabling stress that represents the long-term consequences of an organism's failure to recover from a traumatic situation and it takes place time after having lived the stressful. This PTSD involves changes in the immune system that predispose to autoimmune disease. In addition, how psychological stress affect the individual is heavily influenced by individual's state, especially the anxiety levels. For all of this, the aim of the present work was to study if an involuntary car accident could generate a PTSD in mice and if its effects on the behavior and immunity depends on the anxiety levels. ICR-CD1 mice who suffered an involuntary traffic accident (n=22, PTSD) at 8±age months and control mice (n=12) of the same age were used. 5 months after the accident, behavioral test (spontaneous exploratory by T-maze and anxiety levels by elevated plus maze) and immune function in peritoneal leukocytes (phagocytic function of macrophages, chemotaxis capacity of macrophages and lymphocytes and the natural killer activity (NK)) were performed. The results shown that PSTD-mice has elevated levels of anxiety and less exploratory capacity, an overactivation in the chemotaxis and phagocytosis of macrophages and a lower chemotaxis of lymphocytes in the PSTD-mice in relation to the controls. These results were remarkable in PSTD-mice with high anxiety. The NK shown a differential effect depended on the anxiety levels of PSTD-mice. In conclusion, the PSTD provokes an impairment of immune function depending on the anxiety levels shown by the individual. Support:FIS-(PI15/01787)-ISCIII-FEDER.

Keywords: Post-traumatic stress disorder, anxiety levels, immune function, behavior

Oxidative stress in blood cells of men and women with Alzheimer disease and mild cognitive impairment

Irene Martínez de Toda[1,2]

[1]. Department of Genetics, Physiology and Microbiology (Unit of Animal Physiology), Faculty of Biology, Complutense University, Madrid.
[2]. Research Institute Hospital 12 de Octubre, Madrid.

It is known that oxidative stress in brain plays a fundamental role in the development and progression of Alzheimer´s Disease (AD). In addition, alterations in the redox state of immune cells have been reported in AD patients and also in triple-transgenic mice for AD even before the pathology is established. Therefore, the aim of the study was to investigate the redox status of peripheral blood in AD patients and in individuals suffering from Mild Cognitive Impairment (MCI), which can be considered an early stage of the disease.

Therefore, the activity of the antioxidant enzymes catalase (CAT), glutathione reductase (GR) and peroxidase (GPx); reduced (GSH) and oxidized glutathione (GSSG) and malondialdehyde (MDA) concentration, as a marker of peroxidative damage to lipids, were measured in blood cells of men and women with MCI and AD (n=20; 10 women and 10 men, for each group) compared to a control group of the same age (n=30; 15 women and 15 men).

The results showed that AD subjects have in general lower antioxidants (GPx and GR activities and GSH) and higher oxidants (GSSG, GSSG/GSH and MDA) than age-matched controls. Interestingly, MCI patients also showed lower antioxidants (GPx and GR activities) and higher oxidants (GSSG, GSSG/GSH and MDA) than age-matched controls.

These results suggest that these parameters have potential as prodromal markers of Alzheimer´s Disease in the clinical setting. Since Alzheimer´s pathology starts 15-20 years prior to first clinical symptoms, an early diagnosis of the disease would allow the development of early interventions in these subjects.

Keywords: Oxidative Stress, Mild Cognitive Impairment, Alzheimer's Disease, Parkinson's Disease, Malondialdehyde

Mantellid frog speciation and tricky transcriptomics

Reyes-Moya I.[1], Vieites D.[1]

[1]. Departamento de Biogeografía y Cambio Global, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid.

The Reproductive Isolation Mechanisms (RIMs) are a set of processes that are crucial to speciation, reducing gene flow between taxa. In the presented thesis we study the evolution of genes related to RIMs present in frogs of the Mantellidae family of Madagascar, which originated in a speciation event from a colonizing ancestor. The taxa present in Mantellidae exhibit two markedly different mechanisms of reproduction: In the Mantellinae subfamily there is a unique mating method in which the male rests the ventral surface of his thighs, with overdeveloped femoral glands, in the head of the female, so that the sperm travels along the back of the female towards the clutch. The rest of the taxa present in Mantellidae perform the more common amplexus mating. We hypothesize that genes transcribed in the femoral gland will be under a strong selection in frogs of the Mantellinae subfamily, whereas genes transcribed in the testicles and related to Isolation Mechanisms involving sperm compatibility will have a more attenuated selection, and as such, a slower evolutionary change when compared to those of the other subfamilies. In this presentation we will also discuss the problems derived of working with non-model animals and big data.

Keywords: Speciation, Mantellidae, Reproductive Isolation Mechanisms, differential evolutionary rates, Big data, Non-model species

Comunicaciones orales

Sesión 3

Inferring species ranges from the geographical distribution of SNPs under selection

Alejandro Llanos

Department of Biodiversity, Ecology and Evolution. Faculty of Biology. Complutense University of Madrid. José Antonio Novais, 12. 28040, Madrid, Spain

All across the distribution range of a species, independent individuals have to confront contrasting ecological requirements relying on the genetic variation that evolution supplies. Using as a model the lizard *Psammodromus algirus*, whose range extend over most of the western Mediterranean region, we show that by scanning the genome of only five populations located along an environmental gradient close to the center of the species distribution, we are able to adequately infer its whole distribution range. We characterized the fractions of the genome under selection and we used them as input in a genotype-environment association model. Then we extrapolated this model to unsampled populations constituted by unsampled (but plausible) genotypes. By using this approach, we created a very accurate reconstruction of the geographical locations where the species as a whole could inhabit, given their genotypes: the resulting inferred distributional map showed an 85% overlap with the 'real' one (i.e. the species range according to published sources), and it also adequately predicted its latitudinal boundaries. Assuming that the genome is the ultimate and only determinant of a species' range, we have developed a very simple model that explains the vast majority of a species distribution. So that, given that genomes constitute very specific instructions manuals even at broad levels, we have shown that it is possible to define entire geographical distributions from only a few SNPs under selection detected only in a few populations far away from its distribution boundaries.

Keywords: landscape genomics, species range, local adaptation, lizard

Birds and "junk food"

Javier Pineda-Pampliega[1]

[1]. Department of Biodiversity, Ecology and Evolution, Faculty of Biology, Complutense University of Madrid, 28040 Madrid, Spain

In the mid-twentieth century, White storks (*Ciconia ciconia*) suffered a marked decline along entire Europe due to the destruction of their natural habitat by human activities. Since several decades ago, its populations have been recovered impressively due to the occurrence of a new food source, rubbish dumps. The use of these sites as food resource facilitates breeding, making easier higher numbers of nestlings, with the consequent increase in the population. However, the quality of these resources is very questionable. Food at rubbish dumps consists mostly of manufactured products, which not always contains the nutrients essential for a correct growth. Furthermore, these products are mixed with a wide variety of waste that may contain potentially dangerous substances. In previous studies, we observed that the use of this food resource is not harmful to nestlings, but the study was very located in space and in time. In this study, we tried to evaluate the effect of the use of food from rubbish dumps in nestlings. For this purpose, we checked their health status using biochemical parameters and variables related to oxidative stress, due to many pollutants produce their harmful effect modifying oxidative stress balance. To obtain more general and consistent results, nestlings were sampled in different colonies, distributed by several autonomous communities, and during two different years.

Keywords: White stork, rubbish dumps, oxidative stress, nestlings, junk food

Experimental evidence of time compaction in human cognition

Sergio Díez-Hermano[1]

[1] *Biomathematics Unit, BEE Department, School of Biology, Complutense University, Madrid*

The time-changing nature of our world demands processing of huge amounts of information in fast and reliable way to generate successful behaviors. Significant brain resources are devoted to the processing of spatiotemporal information. Neural bases and their cognitive correlates are well established for processing of static environments, while in time-changing situations the challenge persists. In dynamic environments the brain exploits specific processing mechanisms based on prediction and anticipation, as time compression during visual perception and mental navigation. The alternative hypothesis of time compaction integrates these findings, postulating that dynamic situations are internally represented as static spatial maps, where temporal information is removed by predicting and structuring the relevant interactions of the subject and the environment. Nevertheless, empirical evidence tackling the biological soundness of time compaction is lacking. Here we show that human performance in a discrimination learning task involving dynamic situations can be either favored or hampered via previous exposition to interfering static scenes. Our results also reveal a gender difference: men are more prone to exploit time compaction over other cognitive strategies, contrary to women, who rely on a broader range of approaches. We then further corroborated time compaction mechanism through mathematical modelling. Our results suggest that static internal representations of dynamic situations are involved in decision-making and strategy planning at cognitive level. The existence of time compaction in the human brain could provide a functional framework unifying essential aspects of cognition demanded for active interaction with our world, introducing a new venue to embed human skills in robots.

Keywords: dynamic situations, internal representations, static maps, spatiotemporal cognition

Evidence of positive selection suggests possible role of aquaporins in the water-to-land transition of mudskippers

Héctor Lorente-Martínez[1], Ainhoa Agorreta[1], María Torres-Sánchez[1,2], Diego San Mauro[1]

1 Department of Biodiversity, Ecology, and Evolution, Complutense University of Madrid, José Antonio Novais 12, 28040Madrid, Spain
2 Present address: Department of Neuroscience, Spinal Cord and Brain Injury Research Center & Ambystoma Genetic Stock Center, University of Kentucky, Lexington, KY 40536, USA

Aquaporins are integral membrane proteins that exchange water and small solutes. They played an important role in the colonisation of terrestrial environments by tetrapod ancestors via the appearance of three exclusive paralogs. Like early tetrapods, mudskippers represent an independent case of amphibious lifestyle evolution that is unparalleled by other extant fish groups. Given this lifestyle parallelism and that aquaporins were relevant for tetrapod terrestrialisation, this study examines the aquaporins in mudskippers to investigate whether similar changes in aquaporins could have possibly occurred during their water-to-land transition. We have catalogued aquaporin genes in four mudskipper genomes and studied their diversity and molecular evolution (including detection of positive selection) in a broad phylogenetic context of vertebrates. Our genomic screening returned 55 aquaporin genes for mudskippers (none of them constituting novel paralogs) that can be assigned to 10 different known classes. We detected signatures of positive selection in AQP10a and AQP11b in mudskippers (both the entire clade and the clade containing the most terrestrial species, implying different evolutionary times). This suggests possible alteration of the molecular function of such paralogs caused by changes at specific protein sequence positions, some of them located in relatively close proximity to parts of the molecule involved in pore formation and substrate selectivity. Given the importance of aquaporins for osmotic regulation in fishes, it might be possible that these selective changes (perhaps allowing permeability to new solutes) could have played a role during the adaptation of mudskippers to an amphibious lifestyle.

Keywords: amphibious lifestyle, aquaporin, molecular evolution, mudskipper, positive selection

Appraising the “entourage effect”: antitumor action of a pure cannabinoid versus a botanical drug preparation in preclinical models of breast cancer

Marta Seijo-Vila [1,2]

[1] *Complutense University, Madrid, Spain*
[2] *Instituto de Investigación Hospital 12 de Octubre, Madrid, Spain*

Breast cancer is the second leading cause of death among women. Although early diagnosis and development of new treatments have improved their prognosis, many patients present innate or acquired resistance to current therapies. New therapeutic approaches are therefore warranted for the management of this disease.

Extensive preclinical research has demonstrated that cannabinoids, the active ingredients of *Cannabis sativa*, trigger antitumor responses in different models of cancer. Most of these studies have been conducted with pure compounds, mainly Δ^9-tetrahydrocannabinol (THC). The cannabis plant, however, produces hundreds of other compounds with their own therapeutic potential and the capability to induce synergic responses when combined, the so-called “entourage effect”. Here, we compared the antitumor efficacy of pure THC with that of a botanical drug preparation (BDP).

The BDP was more potent than pure THC in producing antitumor responses in cell culture and animal models of ER+/PR+, HER2+ and triple-negative breast cancer. This increased potency was not due to the presence of the 5 most abundant terpenes in the preparation. While pure THC acted by activating cannabinoid CB_2 receptors and generating reactive oxygen species, the BDP modulated different targets and mechanisms of action. The combination of cannabinoids with estrogen receptor- or HER2-targeted therapies (tamoxifen and lapatinib, respectively) or with cisplatin, produced additive antiproliferative responses in cell cultures. Combinations of these treatments *in vivo* showed no interactions, either positive or negative.

Together, our results suggest that standardized cannabis drug preparations, rather than pure cannabinoids, could be considered as part of the therapeutic armamentarium to manage breast cancer.

Keywords: Breast cancer, antitumor actions, entourage effect

Pósters

Range-wide genomic patterns and adaptive potential of Scots pine (*Pinus sylvestris* L.) to climate change

Belén Méndez-Cea [1], Irene Cobo-Simón [1,2], Francisco Javier Gallego Rodríguez [1] and Juan Carlos Linares [2]

[1]*Departamento de Genética, Microbiología y Fisiología, Facultad de Biología, Universidad Complutense de Madrid, Calle José Antonio Novais, 12, 28040 Madrid, Spain.*

[2]*Departamento de Sistemas Físicos, Químicos y Naturales, Universidad Pablo de Olavide, Carretera de Utrera, Km 1, 41013 Sevilla, Spain.*

Pinus is a genus of conifers with a wide range of distribution, accounting for more than one hundred species. Among them, *Pinus sylvestris* L. is the most widely distributed pine, with more than 14,000 km from the Iberian Peninsula to the Siberian plain. Nowadays Scots pine has persisted in the Mediterranean region as relict populations, where it is able to grow under contrasting conditions.

Many studies have reported that Climate Change is a real threat for forests, and specifically for Scots pine. The distribution of this species seems to be shifting due to global warming, and specifically as regards increasing drought. Then, it is mandatory to understand the adaptive potential of this tree species to cope with Climate Change. Here we attempt to investigate the range-wide genomic patterns of *P. sylvestris* linking the genotypes variability and the population-level responses to Climate Change.

Ecological genomic approaches coupled with next-generation sequencing might be a reliable way to quantify local adaptations and the underlying genetic basis where they rely. We report results from a study on Scots pine, using genotyping by sequencing (GBS), accounting for contrasting habitats within the latitudinal range in Europe. Our preliminary results suggest that loci under local selection might be related to environmental–functional traits in response to Climate Change.

Keywords: *Pinus sylvestris,* Climate Change, GBS, Selection footprint

Bones and funerary goods in Catalina Huanca. the importance of physical anthropology in the archaeological research

Micaela Álvarez Calmet[1], Gonzalo J. Trancho[2]

[1]. Huaca Pucllana Site Museum (Lima, Perú)
[2]. School of Biology, Complutense University, Madrid

Catalina Huanca was an important settlement of the late Lima society (500-650 AD), located in the current district of Ate-Vitarte, in Lima, Peru. After its abandonment, one of its buildings was used as a cemetery with contexts that, due to their formal characteristics, can be affiliated with what is recognized as Wari, the first great Andean empire whose origin goes back to the seventh century AD. The cemetery was excavated between 2008 and 2009, as part of an archaeological rescue project. Of the 91 graves registered, only 54 had human remains in different conditions of integrity, the remaining 37 had been completely looted. A total of 89 individuals were exhumed, which were analyzed by breaking up their biological and cultural variables.

The sex of 32 adult individuals was determined (15 female and 17 male) and the age group of 73 was estimated, registering an expected distribution for an archaeological population. The pathological lesions recorded were: artificial cranial deformation, degenerative joint disease, cribra orbitalia, porotic cranial hyperostosis, sacralization of L5, trauma ante and peri-mortem in the skull and post-skull, caries, abscesses, hypoplasia and paradontolysis. The most frequent body position was the flexed sitting, inside the most recurrent funerary supports, a funerary bundle. These were in all cases conformed at least by cloths of cotton, thin ropes and botanical conglomerates. A preference of gender and age was observed in the presence of some biological and cultural characteristics at the individual level.

Keywords: Wari empire, funerary bundles, Middle Horizon, prehispanic cemetery

Climate change-related shifts in the genetic diversity of relict tree species: understanding the patterns of molecular markers in *Abies pinsapo*

Irene Cobo Simón[1,2], Francisco Javier Gallego[1], Juan Carlos Linares[2]

[1]. Department of Genetics, Faculty of Biology, Complutense University, Madrid
[2]. Department of Physical, Chemical and Natural Systems, University Pablo de Olavide, Sevilla

The Spanish fir (*Abies pinsapo* Boiss.) is a drought-sensitive conifer, endemic from southern Iberian Peninsula. This relict tree has showed widespread mortality and growth decline over the last decades, which have been related to land-use and recent climate change. It is known that relict species constitute reliable models to shed light on adaptation process to rapid environmental changes. Here we attempt to place population genetic structure in a climate change context, using as experimental system the drought-sensitive fir *A. pinsapo*. We investigated the pattern of nuclear microsatellites (nSSR), chroloplast microsatellites (cpSSR), intermicrosatellites (ISSR) and single nucleotide polymorphisms (SNP) of two drought resistance-related candidate genes to the main hypothesis that selective pressure of climate change is related to molecular markers structure of *A. pinsapo* populations along a climate gradient. Our results aim of (1) obtaining information about its current status in order to design appropriate conservation strategies and (2) testing a possible effect of the recent climate change on its genetic structure. Low genetic diversity and high inbreeding were found for this species, which are characteristic of small and relict populations. In addition, a weak but significant differentiation among populations was obtained, together with evidences of past bottlenecks. Moreover, weak but significant differences were found related to altitude and age in some populations, as well as between dead and alive individuals belonging to the lower stands, where climate change-related selective pressure is stronger. These results point to a possible effect of recent climate change on the genetic structure of these populations.

Keywords: Climate Change, relict, conifers, molecular markers

Identification of CD8 T cell epitopes in VP2 and NS1 proteins of African horse sickness virus in IFNAR(-/-) mice.

de la Poza F[1], Marín-López A[1], Castillo-Olivares J[2], Calvo-Pinilla E[2], Ortego J[1].

[1]. Centro de Investigación en Sanidad Animal, INIA-CISA, Valdeolmos, 28130 Madrid, Spain.

[2]. The Pirbright Institute, Ash Road, Pirbright, Surrey GU24 0NF, UK.

African horse sickness virus (AHSV) is an Orbivirus of the family Reoviridae that causes severe pathology in equids. Previous work in our laboratory showed the presence of AHSV-specific CD8(+) T cells in mice immunized with recombinant Modified Vaccinia Ankara (rMVA) expressing VP2 and NS1 proteins. In the present work, we selected potential CD8 T cell epitopes (MHC-class I binding peptides) for the 129 mouse strain from the VP2 and NS1 proteins of AHSV-4, using a combination of four epitope prediction algorithms (SYFPEITHI, BYMAS, NetMHC I and NetMHCpan). ELISPOT and Intracellular Cytokine Staining (ICS) analysis showed that the VP2-1044 (YTFGNKFLL), and NS1-83 (CVIKNADYV) peptides elicited IFN-γ production in splenocytes of MVA-VP2 and MVA-NS1 immunized mice and were identified as CD8(+) T cell epitopes. In addition, these three MHC-class I-binding peptides induced the expression of CD107a in CD8(+) T cells, an indirect marker of cytotoxic activity. Importantly, VP2-1044 and NS1-83 epitopes are conserved among all nine AHSV serotypes. These data demonstrate the activation of AHSV specific T-cell epitopes during vaccination with rMVAs expressing VP2 and NS1. Furthermore, the characterization of these CD8(+) T-cell epitopes provides information useful for the design of novel marker multiserotype vaccines against AHSV.

Effects of urbanization on nestling condition in the tree sparrow (*Passer montanus*)

Iraida Redondo García[1], Jaime Muriel Redondo[1], Lucía Arregui Almendral[1], Lorenzo Pérez-Rodríguez[2], Diego Gil Pérez[1]

[1]. Departament of Evolutionary Ecology, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain).
[2] Instituto de Investigación en Recursos Cinegéticos, IREC (CSIC, UCLM, JCCM)

Birds that live in cities must cope with different threats imposed by drastic transformations from the urbanization process. Among these modifications, we find habitat loss and fragmentation, quantity and quality variation in trophic resources as well as several types of pollution (such as air, light and noise pollution) which affect behaviour, breeding performance and success and physiological state. In this work, we studied how the degree of urbanization influences body and physiological condition of tree sparrow (*Passer montanus*) nestlings in three different localities of the Community of Madrid: one control zone, a second rural zone characterized by high noise levels originated by aircraft noise at the Adolfo Suárez Barajas airport and finally an urban area located nearby Madrid downtown. Our study design aimed to detect differential negative effects of noise pollution (airport area) and full urban pollution (Madrid), over the rural control area. We predicted that noise would increase physiological stress levels (corticosterone) but not necessarily the reductions in growth and oxidative stress that are expected in urban areas. We took different morphological (weight, wing length) and physiological (oxidative stress, feather corticosterone) measures to assess nestling condition, as well as breeding parameters (size and number of clutches). The results will be analyzed with respect to the hypothesis that urbanization and airport noise affect reproductive performance in tree sparrows.

Keywords: urban birds; urbanization; aircraft noise; oxidative stress; *Passer montanus*

Abundance and diversity of wild pollinators in corn and sunflower crops and variation in the community composition throughout the crop

Cabezas, G.[1]; Arranz, N.[1]; Benavent-Celma, C.[1]; Ornosa, C.[2]; Castañera, P.[1]; Farinós, G.P.[1]

[1] Biological Research Center, Madrid.
[2] Faculty of Biology, Complutense University, Madrid.

Pollination is an essential ecosystem service in which the honey bee *Apis mellifera* is particularly important, although wild pollinators also play a key role in both the maintenance of wild plant communities and agricultural production. In the last decades a general decrease in pollinators has been reported worldwide. One of the different factors identified as a cause of this decline is the exposure to neonicotinoid insecticides, widely used in seed treatments of corn and sunflower crops. An additional stressor could be Bt corn pollen, since there is some evidence that the insecticidal Cry1Ab toxin expressed in this maize can alter foraging behavior in bees and other pollinators.

The aim of this study is to characterize the pollinator community present in Bt maize and sunflower crops and that therefore, would be exposed to the potential harmful agents mentioned above. To this end, samplings were carried out in experimental fields in Madrid during the summer months of two consecutive years using two different trapping methods: Moericke traps of three colors (blue, white and yellow) and yellow sticky traps, where insects get trapped when they come into contact.

The preliminary results show that bees of the genera *Halictus* and *Lasioglossum* (Hymenoptera: Halictidae) were the most abundant in both crops (76.40% and 77.96% of the catches in sunflower and corn, respectively). However, their abundance peaks did not coincide with the flowering period of the crops. Yellow was the most effective color, since around half of the hymenopterans were captured by Moericke yellow traps.

Keywords: Apoidea, wild bees, sunflower, Bt corn, phenology, trapping methods.

Insuline-like growth factor-1 as rhythmic output signal of goldfish circadian system

Aitana Alonso-Gómez, Diego Madera, Ángel Luis Alonso-Gómez, Ana Isabel Valenciano, María Jesús Delgado

[1]. *School of Biology, Complutense University, Madrid*

Recently, the relevance of the circadian system in the functionality of many different physiological processes has been widely evidenced. The key elements of this circadian system are the biological clocks, their output signals, and the environmental and endogenous synchronizers that adjust the circadian rhythmicity of the oscillators. Non-hierarchical organization of biological clocks has been described in fish, which display a variety of coordinated oscillators widely expressed in the organism. The aim of this work was to investigate the possible role of IGF-1 as an output signal of biological clocks in the liver/pancreas, the retina, and the hypothalamus, using goldfish (*Carassius auratus*) as a teleost model. Firstly, it has been identified the peripheral and encephalic regions that express *igf-1* and its two receptor subtypes, *igf-1ra* and *igf-1rb*. These transcripts show a daily rhythmicity in the retina by RT-qPCR, which are dependent on light/dark cycle. Secondly, our experimental approaches indicate that both synchronizers (light/dark cycle and feeding time) were necessary for the entrainment of daily rhythms in the liver/pancreas and the hypothalamus. Finally, although no periprandial changes have been observed, an increase of *igf-1* and *igf-1ra* expression was found when animals were maintained on fasting conditions for seven days. Taking all together, these results support a possible autocrine and paracrine signalling of IGF-1 in goldfish liver/pancreas, which seems to be related with feeding. This hypothetical role of IGF-1 as an endocrine signal that could mediate the functional communication among the hepatic oscillator, the retina and the hypothalamus requires further investigation.

Keywords: Biological clocks, Circadian system, feeding, goldfish, IGF-1, IGF-1 receptors

Experimental evidence of time compaction in human cognition

Sergio Díez-Hermano[1], Abel Sánchez-Jiménez[1,2], Carlos Calvo-Tapia[2], Sergey Lobov[3], Nadia Krilova[3], Antonio Murciano[1], Gabriela López-Tolsa[4], Ricardo Pellón[4], Valeri Makarov[2,3], José Antonio Villacorta-Atienza[1,2]

[1.] *Biomathematics Unit (BEE Department), School of Biology, Complutense University, Madrid, Spain.*
[2.] *Institute of Interdisciplinary Mathematics (IMI), Faculty of Mathematics, Complutense University, Madrid, Spain.*
[3.] *Lobachevsky State University of Nizhny Novgorod, Russia.*
[4.] *Department of Basic Psychology, Distance Education University (UNED), Spain.*

The time-changing nature of our world demands processing of huge amounts of information in fast and reliable way to generate successful behaviors. Significant brain resources are devoted to the processing of spatiotemporal information. Neural bases and their cognitive correlates are well established for processing of static environments, while in time-changing situations the challenge persists. In dynamic environments the brain exploits specific processing mechanisms based on prediction and anticipation, as time compression during visual perception and mental navigation. The alternative hypothesis of time compaction integrates these findings, postulating that dynamic situations are internally represented as static spatial maps, where temporal information is removed by predicting and structuring the relevant interactions of the subject and the environment. Nevertheless, empirical evidence tackling the biological soundness of time compaction is lacking. Here we show that human performance in a discrimination learning task involving dynamic situations can be either favored or hampered via previous exposition to interfering static scenes. Our results also reveal a gender difference: men are more prone to exploit time compaction over other cognitive strategies, contrary to women, who rely on a broader range of approaches. We then further corroborated time compaction mechanism through mathematical modelling. Our results suggest that static internal representations of dynamic situations are involved in decision-making and strategy planning at cognitive level. The existence of time compaction in the human brain could provide a functional framework unifying essential aspects of cognition demanded for active interaction with our world, introducing a new venue to embed human skills in robots.

Keywords: dynamic situations, internal representations, static maps, spatiotemporal cognition

Bat conservation in the Sistema Central: richness and distribution patterns

Elena Tena[1*], José Luis Tellería[1], Óscar de Paz[2]

[1] Departamento de Biodiversidad Ecología y Evolución, Universidad Complutense de Madrid. Madrid. Spain (e.tena@ucm.es)*

[2] Departamento de Ciencias de la Vida, Universidad de Alcalá. 28871, Alcalá de Henares, Madrid. Spain.

We studied the use of urban parks by bats in the city of Madrid and compared it with bat occupancy in the surrounding countryside to see the effects of a fragmented landscape in species biodiversity. We address: 1) If the occupancy of individual species in the study parks is positively related to their regional occupancy. 2) Which factors (geographical and environmental traits) are shaping the species richness and nested species distribution of bat assemblages occurring in urban parks. We analyzed urban parks varying in area, distance to the regional pool of species, and vegetation structure. During two years, a series of 10-minute samples were taken using ultrasound detectors. A similar sampling method was carried out for four years in the countryside around the city to detect the regional pool of species. The occupancy of individual species in parks was lower and positively related to the regional distribution of individual species in the countryside. Within the species occurring in urban parks, park area was the main determinant of species richness. In addition, bat richness distribution reported a nested pattern of species loss as park area decreases. An indirect sampling of the bats using urban parks can be interpreted where the presence of individual species is strongly related to park area and bat abundance at a regional scale. A proactive approach to species conservation by improving the attractiveness of urban landscapes and urban planning would be required.

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Keywords: area effect, Chiroptera, habitat fragmentation, habitat selection, nested species distribution, species richness

Evidence of positive selection suggests possible role of aquaporins in the water-to-land transition of mudskippers

Héctor Lorente-Martínez[1], Ainhoa Agorreta[1], María Torres-Sánchez[1,2], Diego San Mauro[1]

1 Department of Biodiversity, Ecology, and Evolution, Complutense University of Madrid, José Antonio Novais 12, 28040Madrid, Spain
2 Present address: Department of Neuroscience, Spinal Cord and Brain Injury Research Center & Ambystoma Genetic Stock Center, University of Kentucky, Lexington, KY 40536, USA

Aquaporins are integral membrane proteins that exchange water and small solutes. They played an important role in the colonisation of terrestrial environments by tetrapod ancestors via the appearance of three exclusive paralogs. Like early tetrapods, mudskippers represent an independent case of amphibious lifestyle evolution that is unparalleled by other extant fish groups. Given this lifestyle parallelism and that aquaporins were relevant for tetrapod terrestrialisation, this study examines the aquaporins in mudskippers to investigate whether similar changes in aquaporins could have possibly occurred during their water-to-land transition. We have catalogued aquaporin genes in four mudskipper genomes and studied their diversity and molecular evolution (including detection of positive selection) in a broad phylogenetic context of vertebrates. Our genomic screening returned 55 aquaporin genes for mudskippers (none of them constituting novel paralogs) that can be assigned to 10 different known classes. We detected signatures of positive selection in AQP10a and AQP11b in mudskippers (both the entire clade and the clade containing the most terrestrial species, implying different evolutionary times). This suggests possible alteration of the molecular function of such paralogs caused by changes at specific protein sequence positions, some of them located in relatively close proximity to parts of the molecule involved in pore formation and substrate selectivity. Given the importance of aquaporins for osmotic regulation in fishes, it might be possible that these selective changes (perhaps allowing permeability to new solutes) could have played a role during the adaptation of mudskippers to an amphibious lifestyle.

Keywords: amphibious lifestyle, aquaporin, molecular evolution, mudskipper, positive selection

LISTADO DE PARTICIPANTES

Nombre	Afiliación	Email
Alonso Gómez, Aitana	Universidad Complutense de Madrid	aitanaalonsogomez@gmail.com/ aitaalon@ucm.es
Alvarez Calmet, Micaela	Universidad Nacional Mayor de San Marcos	micaelaa@ucm.es
Cabezas Torrero, Guillermo	Centro de Investigaciones Biológicas	guillermo.cabezas@cib.csic.es
Ceprián Costoso, Noemí	Universidad Complutense de Madrid	nceprian@ucm.es
Cobo Simón, Irene	Universidad Complutense de Madrid	irenecobo88@gmail.com/ irenocob@ucm.es
de la Poza García, Francisco	CISA-INIA	fdlpoza@gmail.com
Díez Hermano, Sergio	Universidad Complutense de Madrid	sergidie@ucm.es
Hidalgo Román, Alberto	Universidad Complutense de Madrid	albertohidalgo@ucm.es
Huerga Gómez, Alba	Universidad Complutense de Madrid	alhuerga@ucm.es
Jiménez Álvarez, Sara	Universidad Complutense de Madrid	sajime01@ucm.es
Llanos Garrido, Alejandro	Universidad Complutense de Madrid	a.llanos@ucm.es
Lorente Martínez, Héctor	Universidad Complutense de Madrid	hlorente@ucm.es
Martínez de Toda Cabeza, Irene	Universidad Complutense de Madrid	Irene_mc90@hotmail.com
Méndez Cea, Belén	Universidad Complutense de Madrid	belenmen@ucm.es
Molino de Miguel, Sonia	Universidad Complutense de Madrid	sonimoli@ucm.es
Pardos Blas, José Ramón	Museo Nacional de Ciencias Naturales	jpardos@ucm.es
Pineda Pampliega, Javier	Universidad Complutense de Madrid	jpineda@ucm.es
Redondo García, Iraida	Museo Nacional de Ciencias Naturales	iraidare@ucm.es
Reyes Moya, Ismael	Museo Nacional de Ciencias Naturales	Ismaelrymy@gmail.com
Sánchez Álvarez, María	Universidad Complutense de Madrid	marisa06@ucm.es
Seijo Vila, Marta	Universidad Complutense de Madrid	marseijo@ucm.es
Téna López, Elena	Universidad Complutense de Madrid	etenalopez@gmail.com
Truchado Martín, Daniel	Universidad Complutense de Madrid	danieltr@ucm.es