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SUBPROGRAMA RAMON Y CAJAL

CONVOCATORIA 2011

Nombre: **MATAS ARROYO, ANTONIO JAVIER** **Referencia:** RYC-2011-08839

Area: Agricultura

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Titulo:

Evaluating the Spanish tomato (Solanum lycopersicum) repository diversity for a molecular breeding program based on high throughput sequencing approaches and computational tools

Resumen de la Memoria:

High throughput sequencing approaches, with ever reducing costs, combined with bioinformatics tools loaded with robust statistical analysis methods, is making affordable to study genome-wide patterns of natural variation and to link genomic polymorphism with the phenotype of complex trait variations. In a single sequencing experiment, hundreds to thousands of single nucleotide polymorphism can be characterized from several lines, and used in a genome-wide association (GWA) mapping to identify genes and quantitative trait loci (QTL) underlying complex variation in plants. However, only a small percentage of the genetic diversity available in tomato germplasm collections has been explored. In this regard, Spain counts with a long tradition of tomato breeding and was prolific at generating hundreds of different cultivars due to its diverse geography, climatic variation and cultural practices. Part of this heritage has been preserved in public germplasm repositories, with hundreds of old cultivars representing a source of sequence variability. I intend to develop a project to explore the exceptional diversity of tomato lines in these collections, starting with an extensive phenotypical characterization of those lines with higher potential for exceptional fruit quality and nutritional values, taking into account it phenotype plasticity. Genomic data for the lines will be gathered from databases (solgenomics.net) or generated in collaboration with peer groups by means of high throughput sequencing, providing quantitative information for gene expression, gene mapping and DNA variability. These results will be combined with other sequencing efforts in tomato that have lead to extensive EST resources and the tomato genome sequence, with preliminary assemblies already published. It will use tools from current project that seek the standardization of data collection to ensure future compatibility in GWA studies (GMOD, iPlantcollaborative.org) facilitating the data analysis. This project would increase the value of the Spanish tomato germplasm collection and prepare it for better genotype-phenotype based tomato breeding programs.

Resumen del Curriculum Vitae:

Biology degree (UMA, 2000), undergraduate student at ¿Departamento de Biología Molecular y Bioquímica, UMA¿ (un-official appoinment) and ¿Departamento de Biología Vegetal, UMA¿ (official collaboration fellowship 1999-2000). Doctoral studies in Plant Physiology courses (UMA, 2000-2002) and PhD work studying plant cuticle and its role in tomato fruit cracking at the CSIC-Estación Experimental ¿La Mayora¿, funded by a research contract with a company (2000-2001) and a FPU fellowship (2001-2005) defended the thesis at Universidad de Málaga (2005) and was recognized with Honors (¿premio extraordinario de doctorado). I also received the VIII Award ¿Severo Ochoa¿ of Science and Technology from Ateneo de Málaga/Universidad de Málaga. In this period I was actively involved in outreach activities, including invited technical talks to produces and field technicians. During my Postdoctoral period I was hired to a research project in ¿Departamento de Biología Vegetal, UMA¿ (2005-2006), and then received a MEC/Fulbright (2006-2008) at Cornell University following as Postdoctoral Associate (2008-present). I have three stays in internationally recognized centers, in Cornell University during my PhD for 6 weeks, as a Visiting Fellow, as a Fulbright Visiting Scholar and Postdoctoral Associate in Cornell for 5 years and IVIA-CSIC Valencia for 6 weeks as a Guest Scientist. I have participated in projects related with plant cuticle and waxes structure and composition, plant cell wall water relations and disassembly, tomato quality phenotyping, tomato fruit cracking and gene expression. I have acquire experience in techniques and methodologies ranging from biochemistry and biophysics to histology, fruit production and postharvest biology, genomics, transcriptomics and proteomics. This experience is reflected in the publication of 18 research articles in JCR indexed journals and a invited review for Current Opinion in Biotechnology. This account for a combined impact factor of 68.833 and 170 citations indexed in Web of Science (197 in Google Scholar) that represents a H-index = 8. Twelve of these publication (63%) are among the top 25% of their field by impact factor. I am first author in 8 of them, 2 belongs to my period as undergraduate, 10 to my PhD, and 7 were published as postdoctoral research. I am also author of a book about tomato fruit cracking and coauthor of a book-chapter about tomato transcriptomics. A new publication will be submitted in the following weeks (first author) and 3 more manuscripts will be submitted during this year (co-author) including the publication of the tomato genome. I have contributed to 25 national and international conferences, including 4 guest talks and a Gordon conference. All these publication are the products of my participation in 10 research projects being, 3 in the USA with funding from USDA and NSF, 5 in Spain (Ministerio de Ciencia y Tecnología / Ministerio de Agricultura) and 2 with private companies in Spain. I have invited to review research papers for Plant Physiology and Journal of Experimental Biology and grant proposal for NSF related with tomato biology, gene expression and cuticle biology. Teaching experience during the Ph.D. as teaching assistant in three Plant Physiology courses and also involved in the initiative plantingscience.org both as mentor and content developer/web tester since 2008.

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CONVOCATORIA 2011

Nombre: **GONZALEZ BLANCO, MIGUEL** **Referencia:** RYC-2011-07781

Area: Biología Fundamental y de Sistemas

Correo electrónico: miguel.blanco@cancer.org.uk

Titulo:

Regulación de nucleasas específicas de estructura en eucariotas

Resumen de la Memoria:

Background In eukaryotes, multiple DNA repair pathways are in place to eliminate specific types of DNA lesions and preserve genome stability. The removal of such lesions frequently involves the cleavage of the DNA backbone by structure-specific nucleases. Our recent studies in both mitotic and meiotic yeast cells have unveiled a strong regulatory mechanism mediated by cell cycle-dependent phosphorylation that keeps the structure-specific nucleases Yen1 and Mus81-Mms4 in an inactive state until their action is required. Tight control of these nucleases is probably crucial to avoid the unscheduled or inaccurate cleavage of DNA, which could lead to genomic instability, a hallmark feature of cancer cells. The characterization of these regulatory mechanisms is therefore essential to understand how cells balance the introduction of defined breaks in the DNA as part of the process to repair toxic DNA lesions. I intend to further develop this research line in the following aspects: Aim 1: Identification of new cell cycle-regulated structure-specific nucleases and helicases in S. cerevisiae. Currently, we have evidence for the cell-cycle dependent regulation of the Yen1 and Mus81-Mms4 nucleases. My goal is to apply the same methodology employed for these enzymes to a number of candidate structure-specific nucleases and helicases that are involved in DNA repair. This will involve the biochemical analysis of immobilized proteins, protein-protein interactions, identification of potential post-translation modifications, sub-cellular localization, etc. Aim 2: Study of the consequences of the misregulation of structure-specific nucleases. For the relevant enzymes, I will generate mutants that are refractory to the endogenous mechanisms of regulation and introduce them in cells to study their phenotype. This will include analyzing potential defects in cell-cycle progression or chromosome segregation, hypersensitivity to DNA damaging agents, hyper-recombination, etc. Aim 3: Identification of similar regulatory mechanisms in human cells. I will study the human homologs of the yeast proteins described above, using bacmid expression constructs to determine the evolutionary conservation of these regulatory mechanisms and their relevance in the maintenance of genome stability in human cells. In parallel, these constructs will also be used for protein purification and biochemical analysis of the candidate enzymes.

Resumen del Curriculum Vitae:

PERSONAL INFORMATION Name: Miguel González Blanco Nationality: Spanish Date of Birth: 16 August 1978 Work address:Cancer Research UK, London Research Institute. Clare Hall laboratories. Blanche Lane, South Mimms. Potters Bar, EN6 3LD. United Kingdom. E-mail: miguel.blanco@cancer.org.uk Phone: 44 1707625772 Fax: 44 1707625801 EDUCATION 2005 Ph.D. in Biology. Universidade de Santiago de Compostela (USC), Spain. 2003 M.Sc. in Biology. USC. 2001 B.S. in Biology. USC. RESEARCH EXPERIENCE Present-2006 Postdoctoral research fellow. Genetic Recombination Laboratory, Clare Hall, London Research Institute, Cancer Research UK. 2006-2005 Postdoctoral collaborator. Department of Biochemistry and Molecular Biology, USC. 2005-2001 Ph.D. student. Department of Biochemistry and Molecular Biology, USC. Short-term research stays during Ph.D. as a visiting fellow: ¿ 4 months at Memorial Sloan-Kettering Cancer Center (New York, USA). Research adviser: Dr. Jerard Hurwitz. (2005). ¿ 5 months at Instituto de Investigaciones Biomédicas ¿Alberto Sols¿ (Madrid, Spain). Research adviser: Dr. José González Castaño. (2004). 2001-2000 Undergraduate student. Department of Biochemistry and Molecular Biology, USC. AWARDS AND FELLOWSHIPS 2009 Hardiman-Redon Prize to the best scientific publication from the London Research Insitute in 2008. London Research Institute. Cancer Research UK. 2006 Extraordinary Ph.D. award to the best Doctoral Thesis in Biology at USC in 2005. USC. Spain. 2010-2008 Angeles Alvariño Postdoctoral Fellowship. Xunta de Galicia (Regional Government). 2007 Postdoctoral Fellowship. Spanish Ministry of Science and Education 2006 London Research Institute Postdoctoral Fellowship. Cancer Research UK 2005-2003 Ph.D. Fellowship for the Formation of University Professors. Spanish Ministry of Science and Education. 2002-2001 Ph.D. Fellowship. Xunta de Galicia (Regional Government). PUBLICATIONS 1. Rass U. et al. Genes Dev. 2010; 24: 1559-69. 2. Blanco M.G. et al. DNA Repair 2010; 9: 394-402 3. Barros P. et al FEBS J. 2009; 276: 2983-93. 4. Ip S.C.*et al. Nature 2008; 456: 357-61 5. Barros, P.* et al. Mol. Phylogenet. Evol. 2008; 49: 488-94. 6. Boán, F.* et al. Biol. Chem. 2006; 387: 263-267. 7. Barros, P. et al. Electrophoresis 2005; 26: 4304-4309. 8. Blanco, M.G.* et al. J. Mol. Biol. 2005; 351: 995-1006. 9. Boán, F.* et al. FEBS Lett. 2004; 571: 112-118. 10. Blanco, M.G.*. J. Biol. Chem. 2004; 279: 26797-26801. 11. Boán, F. et al. Mol. Biol. Evol. 2004; 21: 228-235. 12. Boán, F., et al. Biochemistry 2002; 41: 2166-2176. (* Co-first author) CONTRIBUTIONS TO SCIENTIFIC MEETINGS 2010 London Research Institute Retreat. Oxford. Poster. 2010 Maintenance of Genome Stability, Abcam Conferences. Antigua. Poster. 2009 International Symposium on DNA Damage Response and Repair Mechanisms. Crete, Greece. Poster. 2008 Il Ciocco, Italy. Invited oral presentation

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CONVOCATORIA 2011

Nombre: **ISERN MARIN, JOAN** **Referencia:** RYC-2011-09209

Area: Biomedicina

Correo electrónico: jisrnIII@gmail.com

Titulo:

Maduración de las células eritroides en el embrión murino

Resumen de la Memoria:

Los glóbulos rojos desempeñan un papel esencial en la vida de todos los vertebrados. El estudio de la eritropoiesis ha sido un área de actividad científica muy intensa durante años, debido a que defectos en la producción de las células rojas sanguíneas desemboca en anemias, una de las enfermedades genéticas mas comunes en humanos. Las células rojas de la sangre ¿primitivas¿ son las primeras células especializadas que se forman en el embrión de mamífero; sin embargo, se conoce muy poco acerca de cómo se especifica su identidad o cómo transcurre su posterior maduración. Recientemente se ha observado que dichas células primitivas también pierden sus núcleos al igual que los correspondientes eritrocitos ¿adultos¿. Este proceso ocurre algunos días después de que puedan ser detectadas circulando en el embrión. Durante mi labor investigadora, y con el fin de estudiar el proceso de diferenciación de dicho linaje primitivo, he utilizado ratones manipulados genéticamente y comprobado que las células rojas primitivas y definitivas (o adultas) se asemejan más de lo que se pensaba previamente. Asimismo, he observado que dichas células primitivas también están presentes en el hígado fetal, disponiendo de evidencias de que es en este órgano donde posiblemente pierden sus núcleos. En el futuro, me propongo estudiar y desarrollar estas observaciones de forma más detallada e investigar si las interacciones entre las células rojas (primitivas y definitivas) con otros tipos celulares también detectables en el hígado del embrión, como los macrófagos, son importantes para su desarrollo normal. Mi proyecto propone el uso de la eritropoyesis en el hígado fetal, tejido más fácilmente manipulable que la médula ósea, como modelo de estudio de la ontogenia de células rojas, mediante el aislamiento y cultivo de eritroblastos inmaduros derivados de embriones transgénicos. Estos estudios, en combinación con experimentos de diferenciación in vitro de células madre, aportarán nuevos conocimientos acerca del desarrollo y maduración terminal de las células rojas, pudiendo ser útiles en el diseño de nuevas estrategias para la terapia de las enfermedades humanas de la sangre.

Resumen del Curriculum Vitae:

Recientemente me he incorporado al laboratorio de Simón Méndez, del Centro Nacional de Investigaciones Cardiovasculares Carlos III (CNIC), en Madrid. Previamente, he desarrollado mi labor investigadora en Estados Unidos, en el Hospital ¿Mount Sinai¿ de Nueva York, en calidad de becario posdoctoral, primero, y como Profesor Asistente, después. Mi trabajo de estos años se ha centrado en el terreno de la hematopoyesis durante el desarrollo de mamífero, y especialmente, en el estudio del linaje celular de los glóbulos rojos embrionarios. Me incorporé al laboratorio de la Dra. Margaret Baron, en el Centro Médico Monte Sinai de Nueva York, donde he adquirido una formación específica en los campos de la Embriología y la Biología de las células madre (ES cells). Después de un periodo inicial posdoctoral, La estancia en dicho laboratorio me ha permitido aprender y familiarizarme con técnicas de citometría de flujo y cell sorting, desarrollar el uso de modelos de ratón transgénicos y marcadores fluorescentes para imaging, así como los métodos de crecimiento y diferenciación in vitro de ES cells, sobretodo enfocados al estudio a los procesos de especificación y maduración de los eritrocitos primitivos. Como Profesor Asistente, seguí profundizando en el estudio del desarrollo hematopoyético temprano, implementando técnicas de microscopia e imagen, y realizando el análisis transcripcional global de la maduración del linaje eritroide primitivo, desde su fase de progenitor temprano. Dispongo también de una sólida experiencia en biología molecular, adquirida durante mi tesis doctoral, que realicé en el Hospital Valle de Hebron de Barcelona. Experiencia investigadora: Oct 2010-presente. Investigador Postdoctoral, Departamento de Biología del desarrollo Cardiovascular, Instituto de Investigaciones Cardiovasculares Carlos III (CNIC), Madrid. Tema: Estudio de la ontogénia del sistema hematopoyético y del nicho hematopoyético/mesenquimal. Ene-Sep 2010. ¿Assistant Professor¿, Dept. of Medicine, Hematology/Oncology Division, Mount Sinai School of Medicine, New York, USA. Tema: Developmental hematopoyesis. 2004-2010. Becario Postdoctoral, Dept. of Medicine, Hematology/Oncology Division, Mount Sinai School of Medicine, New York, USA. Tema: Developmental hematopoyesis. 1997-2003. Estudiante de Doctorado. Mecanismos moleculares de regulación genica mediada por andrógenos en el riñón de ratón (supervisora: Dr. Anna Meseguer), ¿Centre d¿Investigacions en Bioquímica i Biologia Molecular¿ (CIBBIM). Hospital Valle de Hebron, Barcelona. Feb-May 2000. Estudiante visitante. Estudio funcional de los transportadores Oatp-1 y Oatp-d en oocitos de Xenopus laevis, University Hospital Zurich, Zurich, Suiza. Formación Académica: Doctor en Bioquímica (Universidad Autónoma de Barcelona, Bellaterra, 2003). Licenciado en Bioquímica (Universidad Autónoma de Barcelona, Bellaterra,1996) Publicaciones: Isern, J. et al. (2011) Blood ; Isern, J. et al. (2010) Blood (Portada) ; Isern, J. et al. (2010) Blood Cell Mol Dis ; Fraser S.T., Isern, J. et al. (2010) Methods Enzymol ; Isern, J. et al. (2008) PNAS ; Fraser S.T.*, Isern, J. *et al. (2007) Blood (*contribución igual); Kwon, G.S., Fraser, S.T., Eakin, G.,S., Mangano, M., Isern, J., et al. (2006) Dev. Dyn.; Aresté, C., Melià, M.J., Isern, J., et al. (2005) J Endocrinol ; Isern, J. and A. Meseguer (2004) BBRC; Isern, J., et al. (2001) Bba ; Lopez-Ferrer, A., de Bolos, C., Barranco, C., Garrido, M., Isern, J. et al.

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CONVOCATORIA 2011

Nombre: **VERGARA TINOCO, ALEXANDER** **Referencia:** RYC-2011-09547

Area: Tecnología Electrónica y de las Comunicaciones

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Titulo:

Biological inspired Olfactory Radar for Indoor Chemical Threat Identification and Localization

Resumen de la Memoria:

Many species owe their survival in nature to an advanced chemical information processing capability. In contrast to other sensory domains (e.g., vision, sound, or touch), chemo-sensing is subject to the stochasticity of the percept due to unpredictable changes in environmental parameters. However, despite such ambiguities biological olfactory systems have the extraordinary ability to recognize chemicals and locate their sources reliably. The evolution has equipped these systems with an information fusion mechanism that produces a coherent and more reliable response to a target odor using multiple and multi-modal sensory inputs. They make use of the basic principle that a parallel reading from a diversity of sensors reduces the probability of misreading, increasing thereby the confidence of their readings. Recent progress in chemo-sensory signal processing has been stimulated by inter-disciplinary perspectives at the intersection of biology and signal processing/pattern recognition. However, it remains as a standing question how to maximize the information gain that can be obtained from a group of sensors, and even more importantly, how to incorporate information about the location of the odor-source into the sensory system. In this project I aim at developing a biologically-inspired odor identification system-radar, which will predict an airborne chemical¿s identity and the location of its source by one or several real-time measurements taken at distant locations from the odor source. The radar system will consist of a multi-modal acquisition sensory layer that will interface a variety of sensor technologies, including those from the chemo-resistive family and one from analytical chemistry. I will prescribe a principled data fusion methodology to operate a variety of chemical/odor sensors in an optimum way, with respect to an information-theoretic objective. As observed in the biological olfaction, the solution will have an adaptive nature, in the sense that the sensory elements¿ operating conditions will be dynamically adjusted on-the-fly as new information is gathered on the identification problem at hand. This will eventually allow us to improve the decision of making and modifying the collection of the type of information, in a dynamical manner.

Resumen del Curriculum Vitae:

Alexander Vergara Tinoco BioCircutis Institute/Chemosignals Laboratory University of California, San Diego E-mail: vergara@ucsd.edu I am currently a Postdoctoral Scientist Associate at UC, San Diego. I have been working on a Multi-University Research Initiative (ONR-MURI) project entitled "Chemical Discrimination and Localization of Odor Sources using biologically based Olfactory Processing". This joint effort of UCSD, Caltech, and University of Pittsburg, aims at designing and deploying autonomous systems with sensing capabilities on board to identify, discriminate, quantify, and spatially localize odor sources through biomimetic algorithms resembling the olfactory processing of living organisms. This valuable experience has afforded me the opportunity to design and construct an artificial olfaction research laboratory, a test-bed in which I investigate on the development of algorithms that resemble the biological basis of the sense of smell; to design intelligent systems for the analysis of complex odors; to develop dynamic methods for the optimization of micro gas-sensory systems; and to build autonomous vehicles with sensing capabilities on board to spatially localize odor sources. My areas of interest also include working on the design of pattern recognition and feature extraction methods, ameliorating the performance of chemical sensor arrays, and machine olfaction. My present research areas of interest summarize on the following topics: Detection and Estimation: ¿ Detection, identification, quantification, and spatial localization of events from multi-modal sensory data, particularly in the chemical context. Extensively used, developed, and customized machine learning tools for sensor conditioning, sensor optimization, sensory fusion, feature extraction, feature selection, and inference. Modelling ¿ Model building and validation in the following areas: ¿ Memory: Information storage and retrieval in nonlinear/complex dynamical systems ¿ Biological: Olfactory processing and conditioning in honey-bee. ¿ Bio-mimetic: Signal processing of biological and artificial olfactory receptors. Optimization ¿ Basic knowledge on and hand-on experience with linear and non-linear programming, making contributions in the following lines: ¿ Sensor optimization: Developed and implemented a complete dynamical and theoretical scheme for the optimization and conditioning of artificial chemical receptors. ¿ Numerical solvers: Co-developed tools for real-time approximation of variational problems. ¿ Maximum margin classifier/regressor design: Co-developed a unified formalism for a support vector machine (SVM) classification and regression. Experimental Design¿Designed and completely developed the artificial-olfactory-system research laboratory at BioCircuits Intitute/ChemoSignals lab¿UC, San Diego: ¿ ChemoSignals laboratory: Designed and implemented the olfactory research laboratory facility. ¿ Wind-tunnel facilities: Designed and implemented the wind-Tunnel facility to run on gas distribution mapping and gas plume track applications with a robotic platform. My publication record consists of almost 50 publications (H-factor of 7 with more than 130 citations) including publications on peer-reviewed journals (9 as first author), top international conference papers, 3 book chapters, 1 edited book, and 1 US patent.