IV MEETING

RED DE EXCELENCIA TEMÁTICA

BFU2015-71978-REDT/RED2018-102467-T

12-13 Julio 2021

SEVILLA

Monday, 12 July

15:50 RNA Life II: Presentation. José E. Pérez

SESSION 1 (Chairwoman Puri Fortes)

16:00-16:35 José Carlos Reyes

Regulation of enhancers, co-expression domains and splicing efficiency by TGFβ

16:45-17:20 E. Rovira (lab Puri Fortes)

U1A is a positive regulator of the expression of heterologous and cellular genes involved in cell proliferation and migration

17:30-18:05 Sebastián Chávez

Human prefoldin modulates co-transcriptional pre-mRNA splicing

18:15-18:45 COFFEE BREAK

SESSION 2 (Chairman Sergi Puig)

18:45-19:20 Olga Calvo & Araceli González-Jiménez

Functions and regulation of the RNAPII stalk domain

19:30-20:05 Carlos Fernánez-Tornero

Transcriptional regulation and DNA lesion detection by RNA polymerase I

Tuesday, 13 July

SESSION 3 (Chairman Julio Salinas)

9:00-09:15 Rafael Catalá (lab. Julio Salinas)

Exploring the function of the LSM2-8 complex through the characterization of a suppressor of the lsm8 mutation

9:15-09:35 Eduardo Tranque (lab. Julio Salinas)

Differential regulation of stress responses in plants by PAT1 proteins

09:45-10:20 Cristina Moreno-Castro & María Duarte (lab C. Suñé)

Investigating the roles of TCERG1 and PRPF40B in transcription and RNA splicing

10:30-11:00 COFFEE BREAK

SESSION 4 (Chairwoman Xenia Peñate)

11:00-11:35 José E Pérez-Ortín

Study of the cellular component-dependent functions of Xrn1

11:45-12:00 Ana I. Garrido-Godino (lab F. Navarro)

Rpb4 as a key element between the synthesis and degradation of mRNAs

12:00-12:20 Francisco Navarro

Bud27 and RNAs: some results and many questions

12:30-13:00. I.P. Meeting

13:00-15:00 Lunch

SESSION 5 (Chairwoman S. Rodríguez-Navarro)

15:00-15:35 Carme Nuño-Cabanes & Ana Tejada-Colón (lab S. Rodríguez-Navarro)

Mip6 participates at different steps during RNA metabolism

15:45-16:00 Tania Jordá (lab S. Puig)

The lipid composition of yeast cells modulates the response to iron deficiency mediated by the transcriptional factor Aft1

16:00-16:20 Antonia María Romero (lab S. Puig)

The yeast mRNA-binding protein Cth2 regulates gene expression at the transcriptional and post-transcriptional level in iron deficiency.

16:30- 17:05 Sergio Camero & José M. Pérez Cañadillas

NMR studies of the low complexity domain of hnRNP A1: Conformational properties and nucleic acid recognition

17:15-18:00. Coffee-break

SESSION 6 (Chair A. Jordán)

18:00-18:15 José Fernández (lab J. de la Cruz)

Early role of ribosomal protein eL15 during the assembly of 60S ribosomal subunits in Saccharomyces cerevisiae

18:15-18:35 Sara Martín (lab J. de la Cruz)

The RNA helicase Dbp7 is required for the release of the snR190 snoRNA chaperone from early pre-60S ribosomal particles in Saccharomyces cerevisiae

18:45-19:20 Rosario Francisco-Velilla (lab E. Martínez-Salas)

Gemin5, a multifunctional RNA-binding protein involved in translation control

19:30 Debate sobre el estado de la Red ***RNA life*** *y su futuro*

RNA life

ABSTRACTS

SESSION 1

REGULATION OF ENHANCERS, CO-EXPRESSION DOMAINS AND SPLICING EFFICIENCY BY TGFβ.

Jose A. Guerrero-Martínez, Elena Sanchez-Escabias, Elena Gómez-Marín, Laura Basurto-Cayuela, Isabel Pozuelo-Sánchez, María Ceballos-Chávez, and Jose C. Reyes

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TGFβ cytokines have crucial roles in development, proliferation, tissue homeostasis, differentiation and immune regulation. Consequently, alterations in TGFβ signaling underlie numerous diseases, including cancer. TGFβ is one of the most potent inductors of epithelial to mesenchymal transition (EMT) in normal and oncogenic epithelial cells from different origins. EMT and its reversion (MET) are common processes during embryonic development and have attracted considerable interest due to the fact that they seem to be related to tumor cells dissemination and migration, generation of tumor circulating cells, cancer stem cells and metastasis formation. TGFβ causes a large reorganization of gene expression patterns and epigenetic information, that we are only starting to understand. In our group we are investigating how TGFβ causes these reorganization of gene expression patterns.

We have cartographied the genomic transcriptional enhancers that are regulated by TGFβ in a breast epithelial cell line. In fact, TGFβ triggers a fast and widespread increase in chromatin accessibility in about 80% of enhancers, irrespective of whether they are activated, repressed or not regulated by TGFβ. We have also shown that most TGFβ-regulated genes are located around enhancers regulated in the same way, often creating domains of several co-regulated genes that we term TGFβ regulatory domains (TRD). We are currently investigating how the 3D organization of the genome connect the enhancers with the TRDs.

We have also investigated whether regulation co-transcriptional splicing efficiency at the whole gene level is used to regulate gene expression by TGFβ. First we found that the existence of two well-differentiated strategies for co-transcriptional splicing efficiency, at the extremes of a gradient: short genes, that produces high levels of pre-mRNA display a relatively inefficient splicing while long genes with relatively low pre-mRNA levels present efficient splicing. Furthermore, we found that the TGFβ pathway regulates the general co-transcriptional splicing efficiency causing changes in mature mRNA levels. Taken together, our data indicate that co-transcriptional splicing efficiency is a gene-specific characteristic that can be regulated to control gene expression.

Finally, other members of the group are looking for chromatin factors that control gene expression changes caused by TGFβ.

This work was funded by the Spanish Ministry of Economy and Competitiveness (BFU2014-53543-P and BFU2017-85420-R), by Junta de Andalucía (P18-FR-1962) and by Fundación Vencer el Cáncer (VEC – 001/2014 FVEC-FPS)