XIII REUNIÓN DE BIOLOGÍA MOLECULAR DE PLANTAS

FORMULARIO PARA EL ENVÍO DE COMUNICACIONES

DATOS DE CONTACTO
NOMBRE Y APELLIDOS: Catharina Merchante
CENTRO: Universidad de Málaga
e-mail: merchante@uma.es **TELÉFONO: 952134268**
SESIÓN: Vías de Señalización **TIPO: (X)** Oral ( ) Póster

Hormone-Mediated Gene-Specific Translation Regulation

Catharina Merchante[1,2], Javier Brumós[2], Jeonga Yun[2], Anna Stepanova[2], José Alonso[2]

[1]Departmento de Biología Molecular y Bioquímica, UMA, Málaga, Spain
[2]Department of Plant and Microbial Biology, NCSU, Raleigh, USA

The central role of translation regulation in the control of critical cellular processes has long been recognized. Yet the systematic exploration of quantitative changes in translation at a genome-wide scale in response to specific stimuli has only recently become technically feasible. Using a genetic approach, we have identified new Arabidopsis weak-ethylene insensitive mutants that also display defects in translation, which suggested the existence of a previously unknown molecular module involved in ethylene-mediated translation regulation of components of this signaling pathway. To explore this link in detail, we implemented for Arabidopsis the ribosome-footprinting technology, which enables the study of translation at a whole-genome level at single codon resolution[1]. Using ribosome-footprinting we examined the effects of short exposure to ethylene on the Arabidopsis translatome looking for ethylene-triggered changes in translation rates that could not be explained by changes in transcript levels. The results of this research, in combination with the characterization of a subset of the aforementioned weak-ethylene insensitive mutants that are defective in the UPF genes (core-components of the nonsense-mediated mRNA decay machinery), uncovered a translation-based branch of the ethylene signaling pathway[2]. In the presence of ethylene, translation of a negative regulator of ethylene signaling EBF2 is repressed, despite induced transcription of this gene. These translational effects of ethylene require the long 3´UTR of *EBF2* (3´*EBF2*), which is recognized by the C-terminal end of the key ethylene-signaling protein EIN2 (EIN2C) in the cytoplasm once EIN2C is released from the ER-membrane by proteolytic cleavage. EIN2C binds the 3´*EBF2*, recruits the UPF proteins and moves to P-bodies, where the translation of *EBF2* in inhibited despite its mRNA accumulation. Once the ethylene signal is withdrawn, the translation of the stored *EBF2* mRNAs is resumed, thus rapidly dampening the ethylene response. These findings represent a mechanistic paradigm of gene-specific regulation of translation in response to a key growth regulator.

Translation regulatory elements can be located in both 3′ and 5′ UTRs. We are now focusing on the *ead1* and *ead2* mutants, another set of ethylene-signaling mutants defective in translational regulation. Ribosome-footprinting on the *ead1* mutant revealed an accumulation of translating ribosomes in the 5´UTRs of uORF-containing genes and reduction in the levels of ribosomes in the main ORF. The mutant is also impaired in the translation of GFP when this reporter is fused to WT 5´UTR of potential EAD1 targets but not when GFP is fused to the uORF-less versions of the same 5´UTRs. Our hypothesis is that EAD1/2 work as a complex that is required for the efficient translation of mRNAs that have common structural (complex 5´UTR with uORFs) and functional (regulation of key cellular processes) features. We are working towards the identification of the conditions where the EAD1 regulation of translation is required.

[1] Ingolia, N. et al. (2009) Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. Science, 324; 218-222

[2] Merchante, C. et al. (2015) Gene-Specific Translation Regulation Mediated by the Hormone-Signaling Molecule EIN2. Cell, 163(3): 684-697