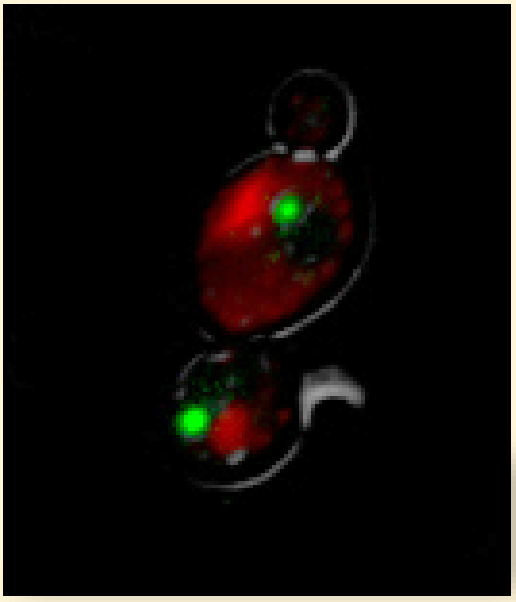
13ª Reunión de la Red Española de Levaduras



El Escorial,
14-16 de Diciembre de 2022

Coordinadores:
Jesús Pla & Joaquín Ariño

Rpb4 phosphorylation as a new mechanism to regulate gene expression in *Saccharomyces cerevisiae*

González-Jiménez, Araceli[1]; Jordán, Antonio[2]; González-Jiménez, M. Carmen[1]; Medina, Ithaisa[1]; Alfonso, Manuel J[1]; Calvo, Olga[1].

[1]Instituto de Biología Funcional y Genómica, Consejo Superior de Investigaciones Científicas, Universidad de Salamanca, Calle Zacarías González 2, 37007 Salamanca, Spain.
[2]Instituto de Biomedicina de Valencia. Developmental Neurobiology Unit, Instituto de Biomedicina de Valencia IBV-CSIC, Valencia, Spain.

Contact e-mail: **ocalvo@usal.es**

In eukaryotes, cellular RNAs are produced by three nuclear RNA polymerases (RNAPI, II, and III), which are multi-subunit complexes. They share structural and functional features, although they are specialized in the synthesis of specific RNAs. RNAPII transcribes the vast majority of cellular RNAs, including mRNAs and a large number of noncoding RNAs. The structure of RNAPII is highly conserved in all eukaryotes, consisting of 12 subunits (Rpb1-12) organized into four structural modules, among which the Rpb4 and Rpb7 subunits form the stalk [1]. Rpb4 and Rpb7 appear to be unique and unconventional RNAPII subunits because of their versatility to function in different cellular compartments and biological processes. It participates in processes ranging from transcription to translation and mRNA degradation in a cyclical process. For this reason, Rpb4/7 is considered a coordinator of gene expression [2,3].

How Rpb4/7 performs so many different -spatially and temporally separated- functions to regulate gene expression is explained in part by its ability to interact with different nuclear and cytosolic complexes. However, how these interactions are regulated are fundamental unanswered questions. We hypothesize that post-translational modifications regulate Rpb4/7 functions. More specifically, based on our work, we propose that Rpb4 is subject to phosphorylation with a regulatory role in gene expression. Up to the date, only the carboxyl-terminal domain (CTD) of Rpb1, the largest subunit of the RNAPII, has been shown to be phosphorylated with a key role in gene expression regulation [4].

Here, we present data demonstrating that indeed Rpb4 is phosphorylated *in vivo*, and that Rpb4-P levels are important for transcription elongation, regulating RNAPII gene occupancy. Our results also suggest that phosphorylation/dephosphorylation of Rpb1 and Rpb4 might be coordinated to regulate gene expression.

REFERENCES

[1] Bushnell, D.A, and Kornberg, R. (2003). Complete 12-subunit RNA polymerase II at 4.1-A resolution: implications for the initiation of transcription. Proc Natl Acad Sci USA.100:6969-73.

[2] Harel-Sharvit L, et al. (2010). RNA polymerase II subunits link transcription and mRNA decay to translation. Cell. 143:552-63.

[3] Calvo, O. (2020) RNA polymerase II phosphorylation and gene looping: new roles for the Rpb4/7 heterodimer in regulating gene expression. Curr Genet. 66: 927-937.

[4] Gonzalez-Jimenez, A., et al. (2021). Regulation of Eukaryotic RNAPs Activities by Phosphorylation. Front Mol Biosci. 8:681865. doi: 10.3389/fmolb.2021.681865.