

# Landes Highlights

## The role of the Mediator complex in plant immunity

Chuanfu An and Zhonglin Mou

Upon pathogen infection, plants undergo dramatic transcriptome reprogramming to shift from normal growth and development to immune response. During this rapid process, the multiprotein Mediator complex has been recognized as an important player to fine-tune gene-specific and pathway-specific transcriptional reprogramming by acting as an adaptor/coregulator between sequence-specific transcription factor and RNA polymerase II (RNAPII). In their recent review, Drs An and Mou present the current understanding of the role of five functionally characterized Mediator subunits—MED8, MED15, MED16, MED21 and MED25—in plant immunity. All of them positively regulate resistance against leaf-infecting biotrophic bacteria or necrotrophic fungi. While MED21 appears to regulate

defense against fungal pathogens via relaying signals from upstream regulators and chromatin modification to RNAPII, the other four Mediator subunits locate at different positions of the defense network to convey phytohormone signals. To fully understand the role of Mediator in plant immunity, the characterization of additional mediator subunits in both Arabidopsis and other plant species will be necessary. The identification of interacting proteins of Mediator subunits will further help to reveal their specific regulatory mechanisms in plant immunity.

[www.landesbioscience.com/journals/psb/article/23182](http://www.landesbioscience.com/journals/psb/article/23182)

### Reference

An C, et al. Plant Signal Behav 2013; 8:8.



## HuR controls mitochondrial morphology through the regulation of BclxL translation

Danielle Durie, Maria Hatzoglou, Pranesh Chakraborty and Martin Holcik

Mitochondrial dynamics has recently emerged as an important regulatory process in cellular bioenergetics, apoptosis and disease. One well-studied regulatory mechanism that is intimately linked to mitochondrial morphology is the cellular apoptotic machinery, and key factors participating in this process are members of the Bcl-2 family of proteins which regulate membrane permeabilization and the release of pro-apoptotic factors, thus triggering cell death. BclxL is a key prosurvival factor that in addition to controlling mitochondrial membrane permeability, regulates mitochondrial network dynamics. The expression of BclxL is regulated at the level of transcription, splicing and selective translation. In a recent study, Dr Martin Holcik and co-workers showed that the RNA-binding protein HuR, which is known

to orchestrate an anti-apoptotic cellular program, functions as a translational repressor of BclxL. They showed that HuR binds directly to the 5'UTR of BclxL, and represses BclxL translation through the inhibition of its internal ribosome entry site (IRES). Reduction of HuR levels led to the derepression of BclxL translation and subsequent rearrangement of the mitochondrial network. The results of this study place BclxL into the HuR-regulated operon and provide further insight into the regulation of cellular stress response by HuR.

[www.landesbioscience.com/journals/translation/article/23980](http://www.landesbioscience.com/journals/translation/article/23980)

### Reference

Durie D, et al. Translation 2013; 1:e23980.



# The dynamic pathway of nuclear RNA in eukaryotes

Jonathan Sheinberger and Yaron Shav-Tal

The passage of mRNA molecules from the site of synthesis, through the nucleoplasm and the nuclear pore, en route to the cytoplasm, might seem straightforward. Nonetheless, several decades of detailed examination of this pathway, from high-resolution electron microscopy in fixed specimens, through the development of immunodetection techniques and fluorescence toolkits, to the current era of live-cell imaging, show this to be an eventful journey. In addition to mRNAs, several species of noncoding RNAs travel and function

in the nucleus, some being retained within throughout their lifetime. A recent review by Drs Sheinberger and Shav-Tal highlights the nucleoplasmic paths taken by mRNAs and noncoding RNAs in eukaryotic cells with special focus on live-cell data and in concurrence with the biophysical nature of the nucleus. [www.landesbioscience.com/journals/nucleus/article/24434/](http://www.landesbioscience.com/journals/nucleus/article/24434/)

## Reference

Sheinberger J, et al. *Nucleus* 2013; 4:195-205.

