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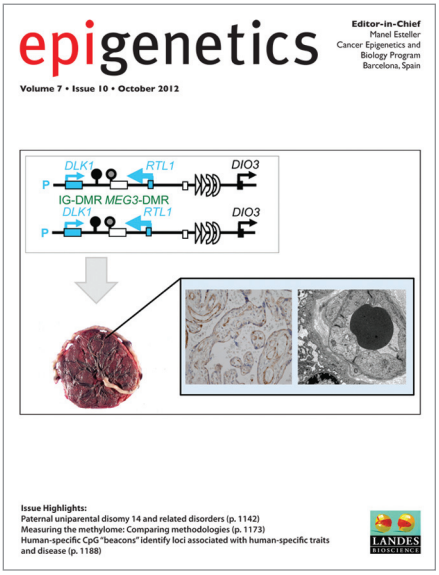
# Landes Highlights

## Histone phosphorylation involved in diverse nuclear events

Different mechanisms exist to modify chromatin compaction, thereby allowing to control DNA accessibility. One example are histone posttranslational modifications (PTMs), such as acetylation, methylation, phosphorylation and ubiquitination. These marks function as signals during various chromatin-based processes and act as platforms for recruitment, assembly or retention of chromatin-associated factors. A recent Review by Dr Jacques Côté and co-workers focuses specifically on the regulation and functions of histone phosphorylation. The authors summarize the current knowledge of histone phosphorylation and describe the many kinases and phosphatases that regulate it. The key roles played by this histone mark in DNA repair, transcription and chromatin compaction during cell division and apoptosis are discussed. Additionally, the authors describe the intricate crosstalk that occurs between phosphorylation and other histone modifications and contributes to the sophisticated control of the chromatin remodeling processes.

**Reference**

1. Rossetto D, Avvakumov N, Côté. Histone phosphorylation: A chromatin modification involved in diverse nuclear events. Epigenetics 2012; 7:1098-1108; http://www.landesbioscience.com/journals/epigenetics/article/21975/




## Nucleoporins Nup160 and Seh1 are required for disease resistance in Arabidopsis

Plants use sophisticated defense systems against pathogen infection. Cellular resistance signaling involves the transduction of stress stimuli into the nucleus to reprogram the expression pattern of defense genes and subsequent export of transcripts for protein biosynthesis in the cytoplasm mediating an appropriate immune response. Nuclear pore complexes (NPCs), composed of various nucleoporins (Nups), mediate the regulated exchange of proteins and RNAs between the cytoplasm and the nucleus. A previous study investigated in a reverse-genetics approach whether members of the Arabidopsis Nup 107-160 nuclear pore sub-complex are required for plant immunity. Results showed that plants carrying mutations in components of this complex, Nup160 and Seh1, are compromised in basal resistance to virulent Pseudomonas bacteria. Both genes also contributed to immunity conferred by Toll interleukin 1 receptor/nucleotide-binding/leucine-rich repeat (TNL)-type R proteins and to constitutive resistance activated in a deregulated TNL mutant, snc1. Protein levels of EDS1, a central regulator of TNL-triggered resistance, were reduced in seh1 and severely depleted in nup160 single mutants. Following up on these previous findings, Drs Roth and Wiermer investigated the impact of mutations in Nup160, Seh1 and a third complex member, MOS3/Nup96, on EDS1 protein accumulation in the snc1 autoimmune mutant background. In addition, they examined the subcellular localization of Seh1 in root tissues. The study results suggest that Nup160 and Seh1 differently affect TNL-type R protein triggered resistance and autoimmunity in snc1 mutants, possibly because of the different subcellular localization of the proteins or due to partial compensation of Seh1-linked defects by Nup160 or other Nups.

**Reference**

1. Roth C, Wiermer M. Nucleoporins Nup160 and Seh1 are required for disease resistance in Arabidopsis. Plant Signaling & Behavior 2012; 7:1212-1214; http://www.landesbioscience.com/journals/psb/article/21426/

## Size matters in RNA export

In eukaryotic cells, many RNA species have to be exported from the nucleus to the cytoplasm. Different RNA species form distinct ribonucleoprotein (RNP) complexes for export, indicating specific RNA recognition by export proteins. Specific RNA recognition is usually achieved by specific RNA sequences or structures, but recently a new molecular mechanism by which the formation of export RNP complexes is specified by RNA length has been reported. RNA polymerase II (Pol II) is known to synthesize not only mRNAs but also shorter RNAs, including spliceosomal U snRNAs. Both types of RNAs initially acquire an m7G-cap structure at their 5′ ends, to which the common factor cap-binding complex (CBC) binds. However, beyond this initial event, the subsequent assembly of their export complexes differs. Since neither class of RNAs contains clearly conserved RNA sequences or structures that could mediate this distinguishing features, Dr Mutsuhito Ohno set out to identify other special features of these RNAs that are recognized by the cellular RNA export machinery. Although the key U snRNA export factor, PHAX, could bind to mRNA in vitro, PHAX was excluded from mRNA in vivo. The heterotetramer of the heterogeneous nuclear RNP (hnRNP) C1/C2 specifically bound Pol II transcripts longer than 200–300 nt, and funneled them into the mRNA export pathway by inhibiting their binding by PHAX, whereas shorter transcripts not bound by the heterotetramer were committed to the U snRNA export pathway. This finding revealed a novel function of the C1/C2 heterotetramer and highlighted the biological importance of RNA recognition by length. In a recent Point-of-View, Dr Ohno discusses questions raised by these results, together with some historical background of this finding.


### Reference

1. Ohno M. Size matters in RNA export. RNA Biology 2012; 9:1413-1417; http://www.landesbioscience.com/journals/rnabiology/article/22569/

## Deubiquitinating protein USP24 interacts with NER pathway component DDB2

Nucleotide excision repair (NER) is the major pathway for repair of UV-induced cyclobutane pyrimidine dimers (CPDs) in human cells. Damage-specific DNA-binding protein 2 (DDB2) was first isolated as a subunit of the UV-DDB heterodimeric complex that is involved in DNA damage recognition in the NER pathway. DDB2 is required for efficient repair of CPDs in chromatin and is a component of the CUL4-RING E3 ubiquitin ligase complex (CRL4DDB2) that targets XPC protein, histones and DDB2 itself for ubiquitination. Recently, a yeast two-hybrid screen of a human cDNA library was performed to identify potential DDB2 partners. Dr Feng Gong and colleagues identified a deubiquitinating enzyme, USP24, as a likely DDB2-interacting protein. Interaction between DDB2 and USP24 was confirmed by co-precipitation. Importantly, knockdown of USP24 in two human cell lines decreased the steady-state levels of DDB2, indicating that USP24-mediated DDB2 deubiquitination prevents DDB2 degradation. In addition, the authors demonstrated that USP24 can cleave an ubiquitinated form of DDB2 in vitro. Taken together, these results suggest that the ubiquitin-specific protease USP24 is a novel regulator of DDB2 stability.


### Reference

1. Zhang L, Lubin A, Chen H, Sun Z, Gong F. The deubiquitinating protein USP24 interacts with DDB2 and regulates DDB2 stability. Cell Cycle 2012; 11:4378-4384; http://www.landesbioscience.com/journals/cc/article/22688/