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IN BRIEF

RNA METABOLISM

ADAR1 suppresses the recognition of self dsRNA

The conversion of adenosine to inosine is catalysed on double-stranded RNA (dsRNA) by ADAR deaminases. ADAR1-null mice die *in utero* owing to failed erythropoiesis and liver disintegration, but whether this is caused by defects in RNA editing was unknown. Liddicoat *et al.* confirmed that this is the case by recapitulating a similar phenotype in mice with editing-deficient ADAR1 (*Adar1*$^{E861A/E861A}$). The absence of RNA editing led to upregulation of interferon-stimulated genes, similar to those activated *in vitro* by dsRNAs containing adenosine, but not inosine, demonstrating that editing by ADAR1 suppresses the interferon response in homeostatic conditions. Many editing sites were found in the 3′ UTRs of three erythropoiesis genes; these were predicted to form long dsRNA stretches in unedited but not in edited transcripts. Knocking out MDA5 — which is a sensor of viral dsRNA and activator of the interferon response — in *Adar1*$^{E861A/E861A}$ mice rescued their phenotype. Thus, sensing of unedited endogenous dsRNAs by MDA5 activates erythropoiesis-detrimental interferon responses.

ORIGINAL RESEARCH PAPER Liddicoat, B. J. *et al.* RNA editing by ADAR1 prevents MDA5 sensing of endogenous dsRNA as nonself. *Science* http://dx.doi.org/10.1126/science.aac7049 (2015)

CELL DIVISION

Relaxation at the poles

During cell division, chromosome movement and cytokinesis must be precisely coordinated to ensure accurate segregation of chromosomes to daughter cells. Baum and colleagues report the existence of a signalling pathway that triggers polar relaxation — that is, the local softening, at cell poles, of the otherwise rigid actomyosin cortex — which enables cell elongation during anaphase and orderly cell division. Live-cell imaging revealed that actin was cleared from cell poles before furrow formation at the cell equator in *Drosophila melanogaster* and in human cells. Loss of F-actin and cortical relaxation occurred in response to chromatin coming closer to the poles at mid-anaphase. The authors found that this was dependent on protein phosphatase 1 and its regulatory subunit SDS22, which localize at kinetochores and induce the dephosphorylation and inactivation of ezrin–radixin–moesin proteins, which link actin to the plasma membrane, at the cell poles.

ORIGINAL RESEARCH PAPER Rodrigues, N. T. L. *et al.* Kinetochore-localized PP1–Sds22 couples chromosome segregation to polar relaxation. *Nature* http://dx.doi.org/10.1038/nature14496 (2015)

TECHNIQUE

Mapping DNA G-quadruplex structures

DNA G-quadruplexes (G4) are guanine-rich structures that are stable in physiological conditions and can affect gene expression and genomic stability. Chambers *et al.* developed G4-seq for high-resolution, genome-wide G4 mapping. This mapping technique is based on DNA polymerase stalling at stabilized G4 structures, which can be precisely localized by high-throughput sequencing, as stalling results in a drop in sequencing quality. Applying G4-seq in primary lymphocytes revealed >500,000 G4 structures in the human genome. Notably, ~70% of these were not predicted computationally, because they contain bulges or long loops. Such non-canonical G4 structures were exceptionally prevalent in gene regulatory regions, especially in 5′ UTRs and splicing sites, and also in oncogenes and (other) regions that are amplified in cancers.

ORIGINAL RESEARCH PAPER Chambers, V. S. *et al.* High-throughput sequencing of DNA G-quadruplex structures in the human genome. *Nat. Biotechnol.* **33**, 877–881 (2015)