IN BRIEF

DEVELOPMENT

Working together for the greater good

Cooperation between cells in multicellular organisms is essential to ensure the fitness of the whole organism; however, 'cheater' mutants (which do not cooperate but benefit from the cooperation between others) can emerge, lowering fitness unless the organism can re-equilibrate towards cooperation. Here, the authors hypothesized that regulatory mechanisms operate during mammalian development to remove aberrant clones that reduce fitness. To test this, they developed a genome-wide 'cheater screen' in mouse pluripotent stem cells to identify cooperation genes, loss of which would allow cheater mutants to obtain a competitive advantage. Among the genes identified were those encoding p53, topoisomerase 1 and olfactory receptors, knockdown of which allowed mutant cells to expand disproportionately compared with wild-type cells *in vitro* and *in vivo*. Thus, these genes seem to have key roles in fostering cell cooperation in mammals.

ORIGINAL RESEARCH PAPER Dejosez, M. *et al.* Safeguards for cell cooperation in mouse embryogenesis shown by genome-wide cheater screen. *Science* http://dx.doi.org/10.1126/science.1241628 (2013)

RNA METABOLISM

Visualizing RNA splicing

This study reports an experimental system that allows the visualization of transcription and mRNA splicing in living human cells, with single-molecule resolution. Using this approach, the authors obtained key insights into splicing dynamics. First, they inserted GFP-tagged versions of the coat protein of bacteriophage MS2 or the antiterminator protein N of bacteriophage λ into each of the two introns of the β-globin gene and followed splicing dynamics using microscopy. They observed that β-globin intron excision occurs in 20–30 seconds, with the first intron having a shorter lifetime than the second (terminal) intron, which suggests that it is excised while the terminal intron is still present. Moreover, using a mouse immunoglobulin M (IgM) gene engineered to contain one intron between exons M1 and M2, the authors showed that splice site strength also influences splicing kinetics, as introns with a strong polypyrimidine tract (Py tract; an essential splicing signal) had a shorter lifetime than those with a weak Py tract.

ORIGINAL RESEARCH PAPER Martin, R. M. *et al.* Live-cell visualization of pre-mRNA splicing with single-molecule sensitivity. *Cell Rep.* http://dx.doi.org/10.1016/j.celrep.2013.08.013 (2013)

ORGANELLE DYNAMICS

Degrading the signal

Proteins imported into mitochondria and chloroplasts are processed to remove the targeting (signal) sequence. In plants, this is known to be mediated by mitochondrial processing peptidase and stromal processing peptidase, respectively, and the peptides themselves are degraded by presequence protease (PreP). In addition to PreP, M3A family proteases have been suggested to degrade the signal peptide in many species, and this study identifies organellar oligopeptidase (OOP) as an M3A protease that carries out this function in plants. OOP was targeted to both the mitochondrial matrix and the chloroplast stroma. Moreover, it showed a substrate length restriction (8–23 amino acids; which matches many signal sequences as well as other peptide substrates) and a weak preference for hydrophobic residues but did not have a strict cleavage pattern.

ORIGINAL RESEARCH PAPER Kmiec, B. *et al.* Organellar oligopeptidase (OOP) provides a complementary pathway for targeting peptide degradation in mitochondria and chloroplasts. *Proc. Natl Acad. Sci. USA* http://dx.doi.org/10.1073/pnas.1307637110 (2013)