IN BRIEF

TRANSCRIPTION

PAF1 regulates promoter-proximal pausing

Promoter-proximal pausing of RNA polymerase II (Pol II) precedes transcription elongation, but how Pol II is restrained is unknown. Chen *et al.* discovered that depletion of Pol II-associated factor 1 (PAF1) in human and fly cells resulted in redistribution of Pol II from promoter-proximal regions to gene bodies in thousands of genes; this was more pronounced in highly paused genes (indicating a strong dependence on PAF1 for pausing) and was accompanied by an increase in the proportion of elongating Pol II, which is phosphorylated on Ser2, at these genes. Ser2 phosphorylation and release from pausing upon PAF1 depletion were mediated by the recruitment to promoter-proximal regions of the super elongation complex (SEC), which includes the Pol II-activating kinase P-TEFb. This indicates that PAF1 restricts the access of SEC to promoters.

ORIGINAL RESEARCH PAPER Chen, F. X. *et al.* PAF1, a molecular regulator of promoter-proximal pausing by RNA polymerase II. *Cell* http://dx.doi.org/10.1016/j.cell.2015.07.042 (2015)

METABOLISM

Human bone marrow can make fat

White adipose tissue (WAT) is the main type of adipose tissue in human adults. Whether white adipocyte progenitors derive only from permanently WAT-residing cells or whether cells migrating from other tissues may contribute to adipogenesis is unclear. Rydén *et al.* investigated subcutaneous WAT from 65 patients who had undergone allogeneic transplantation with either whole bone marrow (BM) or mobilized peripheral blood stem cells (PBSCs). By taking advantage of genomic differences between donor and recipient cells, and using mathematical modelling, they estimated that BM- or PBSC-derived progenitors contribute ~10% to the adipocyte population over the entire lifespan. The contribution was up to 2.5 times higher in obese patients, indicating that the increased need for adipocytes in obesity can be met, in part, by BM- or PBSC-derived progenitors. Exome and whole-genome sequencing of single adipocytes suggested that these progenitors incorporate into WAT by cell differentiation and cell fusion. However, single-cell fate studies to provide direct proof for such processes cannot be performed.

ORIGINAL RESEARCH PAPER Rydén, M. *et al.* Transplanted bone marrow-derived cells contribute to human adipogenesis. *Cell Metab.* http://dx.doi.org/10.1016/j.cmet.2015.06.011 (2015)

GENE EXPRESSION

PolyQ repeats regulate transcription

Polyglutamine (polyQ) repeats shrink and expand. PolyQ expansion over a certain threshold is associated with several neurodegenerative diseases, but the consequences of moderate repeat variations and their physiological role are unclear. PolyQ repeats are found in eukaryotic transcription regulator genes; by generating multiple repeat variants (with normal and excessive lengths) of the yeast transcription factor Ssn6, followed by transcriptome sequencing, Gemayel *et al.* found that repeat length affects the expression levels of Ssn6 target genes. Analysis of the Ssn6 interactome indicated that repeat length regulates Ssn6 solubility and functional protein interactions. Moreover, Ssn6 with repeats over a certain length had the tendency to misfold and aggregate, which is typical of polyQ-containing proteins; the Hsp70 chaperone Ssa2 was found to reduce aggregation.

ORIGINAL RESEARCH PAPER Gemayel, T. *et al.* Variable glutamine-rich repeats modulate transcription factor activity. *Mol. Cell* http://dx.doi.org/10.1016/j.molcel.2015.07.003 (2015)