level, with decreased expression of genes that are required for fat metabolism. By contrast, mice that lack lipin upregulate these genes and convert food to body mass very inefficiently — another cause of lipodystrophy in these mice, in addition to their impaired adipose-tissue development.

Finally, to confirm that increased lipin expression exerts its effects through different pathways in fat and muscle tissue, the authors restored lipin expression in *Lpin1*-null mice in skeletal muscle only. Normal regulation of energy expenditure was restored in these mice, although there was no change to their levels of adipose tissue.

Most studies of the genetic causes of obesity have focused on pathways involved in appetite regulation and energy expenditure that are regulated by the central nervous system (see the review by Bell and colleagues in this issue). By showing how genes expressed in peripheral tissues can also contribute to weight gain, and that the same gene can have distinct effects on weight regulation in different tissues, Phan and Reue have provided new areas for future research in obesity genetics.

Louisa Flintoft

References and links

ORIGINAL RESEARCH PAPER Phan, J. & Reue, K. Lipin, a lipodystrophy and obesity gene. *Cell Metab.* **1**, 73–83 (2005)

FURTHER READING Bell, C. G., Walley, A. J. & Froguel, P. The genetics of human obesity. *Nature Rev. Genet.* **6**, 221–234 (2005)

also found to be reduced at the silenced loci.

So, transcriptional silencing does not prevent the binding of the upstream-most transcriptional activator proteins, but it does strongly reduce the binding of RNA polymerase II and its associated factors to the promoters of the silenced loci. In fact, because TFIIB recruits RNA polymerase II to promoters, it is the absence of this factor at silenced promoters that accounts for the absence of the polymerase. Although Chen and Widom have pinpointed the stage at which transcriptional silencing occurs, its exact molecular mechanisms are still open to debate.

Magdalena Skipper

References and links

ORIGINAL RESEARCH PAPER Chen, L. and Widom, J. Mechanisms of transcriptional silencing in yeast. *Cell* **120**, 37–48 (2005)

IN BRIEF

PLANT TECHNOLOGY

Targeted mutagenesis using zinc-finger nucleases in *Arabidopsis*.

Lloyd, A. *et al. Proc. Natl Acad. Sci. USA* **102**, 2232–2237 (2005)

Existing methods of targeted mutagenesis in plants that are based on homologous recombination are generally inefficient. These authors used an engineered zinc-finger nuclease to generate double-strand breaks at specific target sites in the *Arabidopsis* genome. Repair of these breaks led to a high frequency of mutations in the target sequence, potentially providing a new high-efficiency method for introducing targeted mutations in plant genomes.

DEVELOPMENT

Four-cell stage mouse blastomeres have different developmental properties.

Piotrowska-Nitsche, K. *et al. Development* **132**, 479–490 (2005)

Piotrowska-Nitsche *et al.* have tested the theory that all blastomeres of the four-cell-stage mouse embryo have equivalent developmental properties. By tracing the origins of the blastomeres with respect to earlier cell divisions, they were able to make chimeric embryos that consist of just one of the four types of blastomere. The authors showed that although all four cells have the same developmental potential, they have distinct developmental properties with respect to their abilities to differentiate in different contexts.

GENOME EVOLUTION

Evidence for widespread degradation of gene control regions in hominid genomes.

Keightley, P. D. *et al. PLoS Biol.* **3**, e42 (2005)

These authors examined the conservation of non-coding regulatory regions in hominids by comparing these regions in the human and chimpanzee genomes. Surprisingly, they found that there has been little selective constraint in the sequences compared with the equivalent regions of murid (mouse and rat) genomes. They conclude that natural selection on these non-coding regions has exerted only weak effects in humans and chimpanzees, and that this might be due to the effects of small population sizes.

EPIGENETICS

Epigenetic memory of active gene transcription is inherited through somatic cell nuclear transfer.

Ng, R. K. & Gurdon, J. B. *Proc. Natl Acad. Sci. USA* **102**, 1957–1962 (2005)

Following somatic cell nuclear transfer, genes from donor nuclei lose their epigenetic mark and are reprogrammed to adopt an embryonic expression pattern. Ng and Gurdon now show that this process is not complete. When using endoderm and neuroectoderm donor nuclei for transfer, they noticed that genes that would normally be expressed in the donor nuclei are also expressed, inappropriately, in some transplant embryos. It seems that epigenetic memory is established in differentiating cells and only applies to transcriptionally active genes.

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