IN BRIEF

EVOLUTION

DNA sequences shaped by selection for stability.

Ackermann, M. & Chao, L. *PLoS Genet.* **2**, e22 (2006)

The nucleotide composition of a DNA stretch influences the probability that it will accumulate mutations during replication and expression. Selective forces might therefore exist that make coding sequences avoid the most unstable nucleotide sequences, namely mononucleotide stretches. On the other hand, mutations are also a source of sequence variation, and therefore have adaptive potential. Sampling the genomes of several organisms showed that there is indeed selection against mononucleotide stretches. This means that selection for sequence stability against mutations is a stronger force than selection for sequence variation.

EVO–DEVO

Dorso/ventral genes are asymmetrically expressed and involved in germ-layer demarcation during cnidarian gastrulation.

Matus, D. Q. *et al. Curr. Biol.* **16**, 499–505 (2006)

In bilaterally symmetrical animals, the TGFB signalling pathway has a well-documented role in establishing the dorsal–ventral axis. A series of experiments in *Nematostella vectensis*, which is radially symmetrical, shows that the orthologues of some TGFB pathway members and interactors are expressed asymmetrically at the onset of gastrulation, and segregate into different germ layers. This work suggests that the original function of the TGFB pathway might have been in germ-layer formation or epithelial patterning rather than in axis patterning.

HUMAN DISEASE

Lamin A/C and emerin are critical for skeletal muscle satellite cell differentiation.

Frock, R. L. *et al. Genes Dev.* **20**, 486–500 (2006)

Mutations in lamin A cause several forms of human muscular dystrophy; now, a mouse model of Emery–Dreifuss muscular dystrophy reveals that this component of the nuclear envelope causes muscle wastage by interfering with myoblast differentiation. Cells in which the expression of *Lmna* (which codes for lamins A and C) was reduced by *Lmna* deficiency or siRNA-mediated knockdown showed altered expression of muscle differentiation genes and arrested muscle differentiation, effects that were reversed by expressing *Lmna* or *MyoD*.

EPIGENETICS

RNAi components are required for nuclear clustering of Polycomb group response elements.

Grimaud, C. *et al. Cell* **124**, 957–971 (2006)

Polycomb group (PcG) genes maintain homeotic genes in a silent chromatin state. Grimaud *et al.* show that components of the RNAi machinery are required for the maintenance of long-range silencing at *Fab-7*, a Polycomb response element from *Abdominal B*, a fly homeotic gene. Mutant analysis revealed an unexpected role for the RNAi machinery in spatial gene regulation — Dicer 2, PIWI and Argonaute 1 co-localize with PcG proteins and might be required to stabilize gene clustering at specific nuclear bodies, which might be important for cosuppression.