IN BRIEF

DEVELOPMENTAL BIOLOGY

Coordinate activation of maternal protein degradation during the egg-to-embryo transition in *C. elegans*.

Pellettieri, J. *et al*. *Dev. Cell* **5**, 451–462 (2003)

One early step in development is the transition from an asymmetric egg to a dividing patterned embryo. Controlled translation of maternal mRNAs has been implicated in this process; however, this paper shows that in *Caenorhabditis elegans*, coordinated protein degradation is also involved. Characterization of the *mbk-2* gene, which the authors identified, indicates that the encoded kinase coordinates the degradation of several maternal proteins and thereby regulates the transition from meiosis to mitosis, and also initiates the patterning of the anterior–posterior axis.

POPULATION GENETICS

Assessing the performance of the haplotype block model of linkage disequilibrium.

Wall, J. D. & Pritchard, J. K. *Am. J. Hum. Genet*. **73**, 502–515 (2003)

It has been suggested that the seemingly complex pattern of linkage disequilibrium (LD) across the human genome has a block-like structure: sites within a block would be in LD with each other, with the block boundaries corresponding to recombination hotspots. But is the haplotype model generally valid? By applying three quantitative criteria to both real and simulated data sets, the authors believe the answer to be yes, although the results obtained were complex.

GENE EXPRESSION

Use of genetic profiling in leprosy to discriminate clinical forms of the disease.

Bleharski, J. R. *et al. Science* **301**, 1527–1530 (2003)

Having compared the expression patterns of ~12,000 genes in skin-biopsy specimens from the lesions of diagnosed and classified leprosy patients, the authors show that the clinical forms of leprosy — which range from tuberculoid to lepromatous — correlate with distinct patterns of gene expression and can be defined by gene-expression profiling. This approach could provide insights into how the immune response to pathogens is regulated.

TECHNOLOGY

Maize-targeted mutagenesis: a knockout resource for maize.

May, B. P. *et al. Proc. Natl Acad. Sci. USA* **100**, 11541–11546 (2003)

May *et al.* report the development of 43,776 plants that each contain a stabilized and unique *Mu*-transposon insertion. As part of this maize-targeted mutagenesis (MTM) project, pedigree, knockout, sequence, phenotype and other data can be accessed through the MTM database web site. The collection, which is openly available to the scientific community, promises to be a valuable resource for those interested in maize genetics and developmental biology.