IN BRIEF

ANIMAL MODELS

Correction of Fragile X Syndrome in mice.

Dölen, G. *et al. Neuron* **56**, 955–962 (2007)

Fragile X Syndrome (FXS) results from transcriptional silencing of the *FMR1* gene, but how this defect results in disease is unclear. These authors tested the hypothesis that key FXS symptoms are caused by a loss of regulation of the metabotropic glutamate receptor mGluR5. Consistent with this theory, several phenotypes that parallel human neurological and psychiatric FXS symptoms were rescued in *FMR1*-null mice that were also engineered to give a 50% reduction in mGluR5 expression. This finding suggests new avenues for developing therapies for FXS.

EVOLUTION

cis-regulatory changes in *Kit ligand* expression and parallel evolution of pigmentation in sticklebacks and humans.

Miller, C. T. *et al. Cell* **131**, 1179–1189 (2007)

This paper shows that regulatory changes in the *Kit ligand* (*Kitlg*) gene contribute to variation in pigmentation in sticklebacks and humans, suggesting that similar genetic changes might underlie morphological evolution across vertebrates. By using genome-wide linkage mapping in sticklebacks, the authors identified mutations in *Kitlg* that are also associated with reduced pigmentation in freshwater populations. Strong signatures of selection around human *KITLG* and the results of admixture mapping suggest that similar genetic changes influence human skin colour.

DISEASE GENETICS

Clustered environments and randomized genes: a fundamental distinction between conventional and genetic epidemiology.

Davey Smith, G. *et al. PLoS Med.* **4**, e352 (2007)

This study demonstrates, for the first time, the validity of using Mendelian randomization in epidemiological studies. In this approach, a genetic variant that is associated with a non-genetic risk factor is used to determine whether the latter has a causal role in disease risk. Using data from an established prospective cohort study, the authors confirm that genetic associations are far less susceptible to confounding (in which a factor appears to be associated with disease risk owing to its correlation with other causal factors) than are non-genetic factors.

GENOMICS

The *Physcomitrella* genome reveals evolutionary insights into the conquest of land by plants.

Rensing, S. A. *et al. Science* **319**, 64–69 (2008)

The first Bryophyte genome sequence has been reported. Because Bryophytes are remnants of early diverging lineages of land plants, they are important in evolutionary studies — most notably for studying the conquest of land by plants. The sequence revealed that this event was associated with an increase in gene-family complexity, acquisition of genes for terrestrial stress tolerance, and the development of auxin and abscisic acid signalling, which coordinates multicellular growth and responses to dehydration.