IN BRIEF

HUMAN DISEASE

Genome-wide association study identifies variants at *CLU* and *CR1* associated with Alzheimer's disease

Lambert, J.-C. *et al. Nature Genet.* 6 Sep 2009 (doi:10.1038/ng.439)

Genome-wide association study identifies variants at *CLU* and *PICALM* associated with Alzheimer's disease

Harold, D. *et al. Nature Genet.* 6 Sep 2009 (doi:10.1038/ng.440)

Two large genome-wide association studies of late-onset Alzheimer's disease (AD) have together identified variants in three loci that are robustly associated with genetic susceptibility to the common form of this neurodegenerative disease. The newly associated genes — *CLU* (clusterin), *PICALM* (phosphatidylinositol-binding clathrin assembly protein) and *CR1* (complement component (3b/4b) receptor 1) — have plausible biological links to the progression of this disease. *CLU* encodes a major brain apolipoprotein that interacts with amyloid-β proteins and that, together with CR1, has a role in clearing the amyloid-β peptide. *PICALM* is involved in synaptic vesicle cycling and might influence cognitive decline by affecting neural synapse integrity. Previously, AD had only been robustly linked to variants in *APOE* (apolipoprotein E), but these findings bring the number of confirmed risk loci for common AD to four.

EVOLUTION

Fundamental evolutionary limits in ecological traits drive *Drosophila* species distributions

Kellermann, V. *et al. Science* **325**, 1244–1246 (2009)

These authors show that *Drosophila* species that are distributed over a narrow habitat range are less genetically diverse than those species that live in more dispersed habitats. This work indicates that in more specialist species the traits that provide tolerance to environmental stressors may lack the genetic variation that is needed to adapt to environmental change, therefore challenging the view that genetic variability does not limit evolution. The study highlights the poor evolutionary potential of tropical species (a feature that might even apply to non-insect species) and should prompt further genetic studies of ecologically important traits.

GENE REGULATORY NETWORKS

Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture

Jothi, R. *et al. Mol. Syst. Biol.* **5**, 294 (2009)

These authors applied a new algorithm to a yeast gene regulatory network to reveal a hierarchical structure in which transcription factors are grouped into three layers: top, core and bottom. The dynamic properties of transcription factors are different between these layers, with those in the top layer being more abundant, longer-lived and noisier than those in the core and bottom layers. The authors suggest that these features might allow cells within a clonal population to vary their responses to external signals while maintaining transcriptional robustness.