# Web watch

## WOULD MENDEL HAVE BEEN A BLOGGER?

The web is undergoing a revolution. Web 2.0, or the 'social web', is much talked about, but are geneticists ready to make the most of it?

Web 2.0 describes internet environments — such as social networking, wikis and blogs — that allow users to collaborate and share information online. Blogs have, by now, become almost ubiquitous. A Google search for blogs related to genetics reveals some interesting sites that, as well as being informative, provide a glimpse of how geneticists use this communication tool.

Mendel's Garden is run by Hsien-Hsien Lei, and offers monthly instalments on topics that range from science policy (such as the story about a biological sample repository on the moon!) to the history of genetics.

A blog from our colleagues at *Nature Genetics* — Free Association — focuses on newly published primary papers, interviews, and so on.

The Daily Transcript, subtitled "Daily news and views from a postdoctoral fellow in cell biology", offers yet more discussion on recent publications; in August it also had a posting on laboratory fashion, which featured photos of the 'socks and sandals' look. Among other offerings are the Genomics Policy weblog from the University of Glamorgan, UK, and Pharyngula, subtitled "Evolution, development, and random biological ejaculations from a godless liberal".

Based on this survey, most genetics blogs tend to discuss general topics sparked off by recent scientific publications or general press coverage. But another potential application of blogging springs to mind. Benefits of such rapid exchanges of information are clear to anyone who has struggled with experiments that don't work for no apparent reason, or with problematic data analysis. In fact, the 'world wide lab' concept predates blogging itself: BIOSCI/Bionet is a set of newsgroups and parallel e-mail lists used by biological scientists worldwide.

*Magdalena Skipper*

GENE REGULATION

# The insulating role of an RNAi architect

> This study adds the control of chromatin architecture to the growing list of skills of the RNAi machinery.

Small RNA pathways are skilled multi-taskers, regulating gene expression in various ways. A study of insulator activity has now uncovered a new role for the RNAi machinery: in organizing chromatin structure.

The *gypsy* transposable element of *Drosophila melanogaster* is widely used to study insulator function in assays because of its ability to shield genes from enhancers when it is inserted between them. *gypsy* recruits a protein complex that is thought to promote the formation of higher-order chromatin structures that prevent enhancers and promoters from meeting.

Lei and Corces identified a putative RNA helicase, Rm62, as a new component of the *gypsy* insulator complex that only interacts with the other components in the presence of an RNA molecule. Rm62 is essential for dsRNA-mediated silencing in flies, providing a potential link between the RNAi pathway and insulator function.

To check the functional significance of their finding, the authors tested the effects of mutating either Rm62 or other RNAi-pathway components on the insulating abilities of *gypsy*. *Rm62* mutations increased insulator activity, indicating that the encoded helicase somehow inhibits *gypsy* function. By contrast, mutations in *piwi* and *aubergine* — which encode Argonaute proteins that are needed for RNAi-induced chromatin modifications — had the opposite effect. Epistasis analysis that used

SYSTEMS BIOLOGY

# Network fundamentals, via hub genes

A thorough investigation of the molecular interactions that take place in, arguably, the most interesting of animal cells — our own — is currently beyond our practical means. But while technologies catch up, simpler eukaryotes can tell us a great deal about the nature of genetic networks in animals. The first systematic study of such interactions to be carried out on a large scale in any animal has now been reported for *Caenorhabditis elegans*. The most striking general finding to emerge from this RNAi screen — which tested ~65,000 pairwise interactions — is that a handful of genes interact with an unexpectedly large number of signalling pathways, and so might be common modifiers of different developmental processes.

The new screen, reported by Ben Lehner and colleagues, was designed to detect interactions between a member of an RNAi library and genes that were individually mutated in 'query' strains. In practice, one of a library of RNAi reagents was delivered to both mutant and wild-type worms, and the treated animals were then scored for a synthetic phenotype. The assay, therefore, involved asking: is the phenotype caused by combining a library RNAi reagent and any mutant allele more severe than the product of the phenotype seen in the mutant and in the library-treated wild-type worm alone? If the answer is yes, then an interaction between the two genes is deemed to be likely.

> If genetic hub genes also exist in humans (and they most probably will) then they might function as modifier genes in seemingly unrelated genetic diseases.

The authors were particularly interested in assessing the interaction between components of signalling pathways, as there is much evidence that, when mutated, these molecules cause disease in mammals. The RNAi library consisted of about 1,750 genes that, based on sequence homology, are involved in signal transduction; likewise, each of the 37 query strains carried a mutation in a known signalling molecule. Of the 65,000 pairwise interactions that were tested ~350 interactions, involving 162 genes, were identified.

The resulting interaction map is notable for two reasons. First, it highlights an unexpected level of sharing between pathways: six genes