IN THE NEWS

Peer review — the big secret?

Three quarters of the British public have no idea what peer review is, according to a new poll that was commissioned by the Science Media Centre and *Nature*.

The poll, conducted by the MORI Social Research Institute, involved interviewing more than a 1,000 adults aged 15 and over. The results were startling or unsurprising, depending on your point of view — only a quarter of those interviewed described peer review as "society's scrutiny of other scientists' work, generally" (BBC Radio 4, Today programme). Intriguingly, however, the survey also showed that the public supports rigorous scrutiny of scientific results before publication, and if peer review did not exist already they would want to create it. "The vast majority (71%) of the public favour either the kind of scrutiny provided by peer review or more stringent controls in which experiments are repeated independently before being published" (*The Guardian*). Fiona Fox, director of the Science Media Centre, encouraged the scientists to "get out there and share their big secret" of peer review.

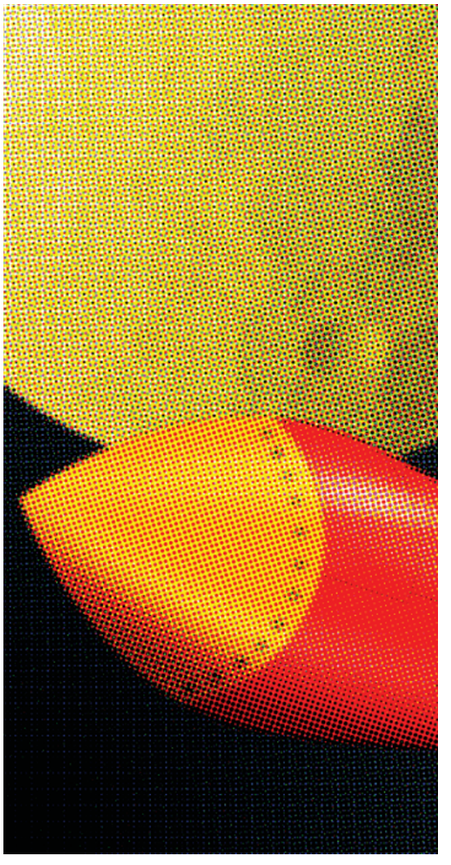
These findings are of course timely — they were published only a few days after the "IVF specialist Dr Panos Zavos announced to the press that he had cloned a baby" having "refused to submit his experiment to peer review" (*The Guardian*). So, the poll's results seem to say that it is not only the scientists who are frustrated with this kind of science reporting, but that the public is weary as well.

There is a constructive outcome to this survey — the Science Media Centre has published a new guide for scientists "in an effort to help them better communicate their work" (*The Guardian*).

Magdalena Skipper

GENOME EVOLUTION

Escape from Planet X



Genes on the mammalian X chromosome just can't wait to get off.

J. J. Emerson and colleagues' analysis of the human and mouse genomes shows that the X chromosome has a clear excess of genes that have functional duplicates on other chromosomes. Of the 94 genes that the authors identified to have been functionally retroposed between chromosomes in the human genome, 15 were derived from X-chromosome genes: far more than the 3 or 4 expected on the basis of the size of this chromosome. Similarly, the 17 out of 105 functional retropositions in the mouse genome were of X-chromosome genes, although only 4 or 5 were expected.

So why do genes want out of the X chromosome? One possibility is that genes that benefit males at a cost to females are moving because, compared with the X chromosome, an autosome spends on average less time in females and so would be more difficult to select against. Alternatively, the inactivation of X-linked genes during meiosis might favour the export of genes to the autosomes, where they are more likely to be expressed to the benefit of the male during meiosis. Either of these mechanisms could cause functional retrogenes that are exported from the X to be selectively favoured over genes that are retroposed from other chromosomes.

Despite the X chromosome being a popular place for genes to leave, paradoxically, it also seems that it is a favourite destination. The authors show that there are relatively many more functional retrogenes recruited to the X than any other chromosome in both human and mouse genomes. However, they also show that human pseudoretrogenes, which are less likely to be subject to selection, are also more common than expected on the X chromosome. So, although selection once again has a key role in causing this bias, in this case there is likely to be a purely mechanistic component to the bias.

So, it seems that selection primarily powers the genic traffic that

TECHNOLOGY

A robot scientist

Thanks to a new system developed by Ross King *et al.*, scientists could soon be spending less time formulating and testing hypotheses and more time making "…the high-level creative leaps at which they excel".

King *et al.* have developed a 'robot scientist' that takes the integration of robotics and scientific discovery to a new level. It consists of a master computer that controls the system and carries out the scientific reasoning, a liquid-handling robot and a plate reader, along with their control computers. It runs software that includes background biological information, a logical inference engine and codes that generate hypotheses, select experiments and integrate the whole system.

Functional genomics was the testing ground for the robot scientist: specifically, dissection of the yeast aromatic amino acid (AAA)-synthesis pathway. First, the authors developed a 'logical formalism', which translates biological data into formulae for the computer. For the AAA pathway, data were taken from the *Kyoto Encyclopedia of Genes and Genomes* (KEGG). Using the logical formulae, Prolog, the robot scientist's logic-programming language, then generated a model of the AAA pathway. Next, the robot scientist formulated hypotheses about the relationships between AAA-enzymatic reactions and open reading frames, devised and ran experiments to test them, interpreted the results to discount inconsistent hypotheses, and so on. The robot scientist essentially performed as well as human scientists, predicting at least 80% of all possible experiments.

Next, King *et al.* compared the accuracy (that is, the number of correct predictions made) versus the monetary cost of different experimental selection strategies. In the long term, the robot scientist's machine-learning system — active selection of experiments (ASE)-Progol — was more cost effective than choosing the cheapest experiment or a random experiment.