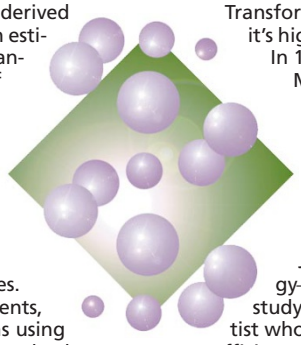
TOUCHING**base**

ORESTES—getting to the centre of genes



Existing EST collections contain mainly sequences derived from the 3′ (65%) or 5′ (26%) ends of cDNAs. Only an estimated 11% of Unigene clusters span the entire transcribed portion of the gene, and this relative lack of sequences derived from the central portions of transcripts limits genome annotation. Andrew Simpson (of the Ludwig Institute for Cancer Research in São Paolo, Brazil) and colleagues have now attempted to compensate for this deficit. They hypothesized that the use of random primers under low-stringency RT–PCR conditions would amplify a high percentage of fragments encompassing the central portions of genes. Before proceeding with 'wet' laboratory experiments, they tested their prediction in a series of simulations using the sequence of all known full-length cDNAs in GenBank. The *in silico* analysis confirmed the predicted symmetry of amplified fragments around the centre of the transcripts. Thus encouraged, the researchers proceeded with a pilot project by generating a series of 10,000 sequences (which they refer to as open reading frame ESTs, or ORESTES) from human breast tumour RNA (*Proc. Natl Acad. Sci. USA* **97**, 3491–3496; 2000). Analysis of these sequences suggests that the ORESTES collection (planned to contain 500,000 entries eventually) is a resource complementary to existing ones and will significantly extend the coverage of coding regions within ESTs. In the hope that the ORESTES will aid current attempts to annotate the human genome, Simpson and colleagues from throughout the state of São Paulo are currently depositing approximately 25,000 new sequences per month into public databases.

Genetic engineering in zero-G

Transformation efficiency in plants is poorly understood: it's high in some, such as tobacco, but quite low in others. In 1998, John Glenn, United States senator and former Mercury astronaut, carried out experiments on board the space shuttle to test whether soybean cells (which are notoriously difficult to transform) can take up foreign DNA under low-gravity conditions. The answer? They can, and it seems to be more efficient, by an order of magnitude, than on Earth. To see if this preliminary finding holds up—and whether John Glenn has a hidden talent for molecular biology—an upcoming shuttle flight will host a follow-up study. Richard Vierling (of Purdue University), the scientist who designed both experiments, hopes to discover the 'efficiency' factor of low gravity and thereby design equipment to increase gene-transfer efficiency back on Earth.

"Art upsets, science reassures."
—George Braque

"Really, I'm fine. It was just a fleeting sense of purpose—I'm sure it will pass."

Spot the scientist

"Defining Features: Scientific and Medical Portraits 1660–2000," an exhibition in London, is concerned with the traditions and conventions of scientific portraiture over the past four centuries—a time span during which the roles of those whom we now think of as scientists and medical practitioners have changed dramatically. The exhibit is divided into four sections: Setting the Scene, Boundaries, a Case Study of Edward Jenner and Portraiture in Practice. It is also meant to provoke thoughts on the role of women in science, with portraits of Caroline Herschel, a fellow of the Royal Astronomical Society, Dorothy Hodgkin (who solved the structures of penicillin, vitamin B12 and insulin, is the only British woman to have won a Nobel Prize for Science, and whose hands are portrayed by Henry Moore on the right) and mouse embryologist Rosa Beddington. "Defining Features" is on display at the National Portrait Gallery in London through 17 September 2000.

Muscling in on the mouse

Recent announcements by the Human Genome Project and Celera Genomics Corporation regarding the human genome inspire the reaction: "what next?" Enter the mouse. In addition to its obvious utility to mouse geneticists, the mouse genome sequence can assist in the annotation of human sequence (see page 31 of this issue). This realization has motivated a combined shotgun and clone-by-clone approach to sequencing the genome. The National Institutes of Health have established the Mouse Genome Sequencing Network (http://mouse.info.nih.gov/) to ensure that regions of "particularly high biomedical interest"—of the genome of the C57BL6/J mouse—are sequenced first. To this end, a competitive program has been established. Applications comprised of a short, web-based description of the region, its importance and its readiness to be sequenced are considered once every two months; sequences consequent to the 14 successful applications submitted 1 February 2000 are soon to be delivered. Any investigator may submit a request to sequence a BAC clone or BAC contig identified in the RPCI-23 library: the next deadline for applications is 1 June 2000.