

Gene bank to offer family album of mammals

Natasha Loder

The world of ecology and evolutionary biology is about to benefit from high-throughput DNA sequencing. A joint project between the Zoological Society of San Diego and Amersham Pharmacia Biotech (AP Biotech) is set to sequence DNA from every family of mammals.

The two organizations say the result will be the world's most comprehensive database of mammalian mitochondrial DNA. They hope the database will become a major tool for research on the evolution and conservation of mammalian biodiversity. It should also be useful to researchers working on the genetic bases of species' behaviour, biology and evolution.

The collaborators say they will publish regular progress reports, and that the results of the sequencing will be made public "quickly".

Over the past 25 years, the society — which runs San Diego Zoo — has maintained a collection of cell lines known as the Frozen Zoo. This means that it already has DNA samples from over 100 of the 150 or so mammalian families.

The task of preparing the samples for sequencing is in the hands of AP Biotech company Molecular Dynamics, based in Sunnyvale, California. Robert Feldman, the production, sequencing and collaborations manager, says that his company is keen to develop the experience of broad exposure to a wide and diverse set of DNA sequencing projects. He declined to comment on the cost of the scheme.

Mitochondria are the structures in a cell



responsible for most of its respiration and energy production. They are popular with researchers interested in evolution at the molecular level, because they have a single, small (around 16,500 base pairs) chromosome which is passed down from mother to offspring. This makes them easier to analyse than full genomes.

Mitochondrial DNA contains a number of genes that evolve at different rates. This means mitochondria can be used for evolutionary analyses over different time scales.

Oliver Ryder is an adjunct professor of biology at the Center for Reproduction of Endangered Species at the Zoological Society of San Diego, a collaborator on the project and a leading figure in conservation genetics. He says that variation in mitochondrial DNA — even at the family level — will be useful for interpreting the results of conservation

genetics studies, and for analysing evolutionary differences between species.

"There are many examples where mitochondrial DNA has provided profound insights into this area of whether populations [of animals] are the same or significantly diverged," he says. For example, variation in parts of the mitochondrial DNA of cheetahs and gorillas has helped researchers understand the evolutionary diversity of regional populations and subspecies.

"Differences between families will help us understand the difference between genera and species. A lot of work is done on the tips of the evolutionary tree in the absence of the trunk and the limbs," he adds.

Ryder suggests that the database may also bring a deeper understanding of how mitochondria evolve. At a broader level, the database will offer a "scaffold of data" for interpreting mitochondrial DNA diversity.

Ryder and colleagues recently argued in favour of starting DNA banks to store the world's genomic biodiversity. They believe that collections started now would be useful in the future for reasons we cannot anticipate (see *Science* 288, 275–277; 2000). He points to the new project's use of the society's Frozen Zoo, as an example of this.

Ryder thinks the database is timely, "given the capacity in genomic sciences and the opportunity in taking the focus away from medical and therapeutic uses for a single species — humans". Feldman agrees: "This project takes the genetics of endangered species into the genomic era. That for me is very exciting," he says. ■

► <http://www.sandiegozoo.org/cres/>

Japan calls for open access to human genome data

Robert Triendl, Tokyo

The genome science committee of Japan's Council for Science and Technology is set to call for the open release of human genome data. The council coordinates Japanese research policy and is chaired by the country's prime minister.

The council's forthcoming declaration says that, to assure scientific progress, "all data and results" from human genome research should be made public. This is expected to include complementary DNA and single-nucleotide polymorphisms.

Last month, the director-general of the Science and Technology Agency, Hirofumi Nakasone, called for the creation of international rules on the release of human genome data. But although the declaration will probably cover all publicly funded

research, observers in Tokyo point out that Japanese funding agencies do not usually lay down policies for data release.

Earlier this year, the Research Association for Biotechnology, which administers biotechnology research for the Ministry of International Trade and Industry (MITI), announced the release of sequence data for 2,200 human genes — but only after the Japanese Patent Agency said that it would not approve patents for sequences that are not complete and whose functions are unknown.

The data have been produced by a MITI-sponsored consortium of private companies, which aims to sequence human full-length complementary DNA.

Patents for the genes are pending. The release of the genes' sequences will prevent overseas companies from filing patents on

them, and the period granted for revising the applications will give the companies involved some time to identify gene functions.

A spokesperson for the Research Association for Biotechnology said that although the cDNA consortium is funded entirely by public money, there are no clear rules for the release of data. Results have to be reported to the New Energy Development Organization, a MITI funding body, within 60 days of a project's completion.

Opposition from MITI has made it difficult for Japan to formulate a position on the release of human genome data. Akiyoshi Wada, director of the RIKEN Genomic Science Center, says that he recommends the regular and timely release of data to his staff, but the lack of general rules has made it difficult to draft policies for his institute. ■