

Wallaby genome begins to reveal its secrets

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The first sequence data from the wallaby genome project has revealed 68 per cent similarity between the human and wallaby genes encoding NADH dehydrogenase, an essential protein in the cell's energy power-houses, the mitochondria.

"It's very useful to see a house-keeping gene with such a level of conservation," said Sue Forrest, director of the Australian Genome Research Facility (AGRF), which generated the sequence. "It confirms the wallaby's position in the evolutionary tree."

Forrest said finding similarities between human and other mammalian genomes and the wallaby was an important part of the genome project, as it would allow researchers to identify valuable regulatory sequences and essential genes. "We can learn just as much from the similarities as the differences," she said.

The release of the sequence data marks the first milestone of the

multimillion dollar project, which has been funded by the US NIH's National Human Genome Research Institute, the Victorian government, AGRF and Applied Biosystems. Forrest is still seeking AUD\$2.5 million in funding for the project,



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which has recently been boosted by a \$50,000 contribution from the philanthropic Jack Brockhoff Foundation.

And the importance of the project is not lost on expatriate Australian Richard Gibbs, whose Human Genome Sequencing Centre at Baylor College of Medicine in Houston, Texas, is responsible for

generating the other half of the data.

"This project is an important contribution for understanding the tree of life – and for advancing collaborative research between the United States of America and

Australia. The magnitude of the contribution of the National Human Genome Research Institute indicates strong confidence in the ability of the Australian groups to generate these important data," he said.

According to Marilyn Renfree, who leads the marsupial research team at Melbourne University, Australian marsupial researchers

are eagerly awaiting the genome data.

"Our team has already learnt much about mammalian reproduction, development and genetics from the Tammar wallaby. In many cases marsupial genes are closer to humans than are the equivalent mouse genes," she said.

"Australian researchers will be well placed to harness the genome information to speed up our understanding of human and marsupial evolution, help us conserve Australia's unique marsupials, and develop unique biomedical research applications."

And the program may also be bringing funding benefits. Renfree and her colleagues have secured ongoing funding from the Australian Research Council and the National Health and Medical Research Council to support their marsupial biology research program, and this week were short-listed for an ARC Centre of Excellence in Mammalian Genomics and Sex in conjunction with ANU and UNSW. ❄

Australian genomics alliance calls for funds

A heavyweight group of Australian researchers has called on the federal government to provide AUD\$250 million in funding for genomics research over the next five years.

The Australian Genome Alliance, led by the Australian Genome Research Facility's director Sue Forrest and Phil Batterham, the deputy director of the ARC-funded Centre for Environmental Stress and Adaptation Research, has filed a budget submission with federal treasurer Peter Costello requesting that \$50 million be allocated annually for the next five years as a special budget allocation toward genomic research, citing the "social and economic benefits of the genetics revolution triggered by the human genome project" and a need to ensure that Australia's unique genetic biodiversity is not usurped by other nations.

The letter points out that genomics is central to several of the federal government's national research priorities, including an environmentally sustainable

Australia, promoting and maintaining good health, frontier technologies for building and transforming Australian industries, and safeguarding Australia.

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"There is quite a demand for genome sequencing in this country," said Batterham. "The thing that has actually escaped the decision makers is that there is no logical funding source for genome projects."

While the ARC and NHMRC are able to fund small, focused sequencing projects, neither agency has the budget or the flexibility to provide funding for the larger projects, he said, and the agricul-

tural research and development corporations are similarly unable to provide the level of funding required.

Ironically, Batterham said, genome sequencing was picking up pace around the world as researchers discovered the benefits of having genomic information to hand.

"It's getting cheaper and the yield of information is getting greater," he said. "Sequencing is becoming a tool that will allow us to take an inventory of the environment."

Forrest said she hoped that the budget submission would at the very least provide an opportunity for researchers and politicians to engage in discussion about what is needed.

She and Batterham believe that genomic information should be regarded as an essential piece of 'soft' infrastructure, akin to having a synchrotron for physics.

"It doesn't look impressive, but it is a crucial underpinning to future research," Batterham said.

The alliance is also keen that the push for funding be seen as a shared vision and shared issue, not just one group pushing for funds for their own project. The submission refers to a number of current and proposed genome projects ranging from the wallaby project to projects on agriculturally important pest species *Helicoverpa armigera*, the southern blue gum and *Brassica* species.

The alliance envisages that the funding would be managed by the ARC, with a process put in place to evaluate the merits of projects.

"We need to make the process somewhat less ad hoc – form an orderly queue so that the best projects get done in good time," Batterham said.

"The government has to be convinced that there is a pipeline – that as data becomes available, Australia is in the primary position to use that data. In the case of *Helicoverpa*, I'm convinced that we are in the position to translate benefits from the sequence to affected crops." ❄

– Melissa Trudinger