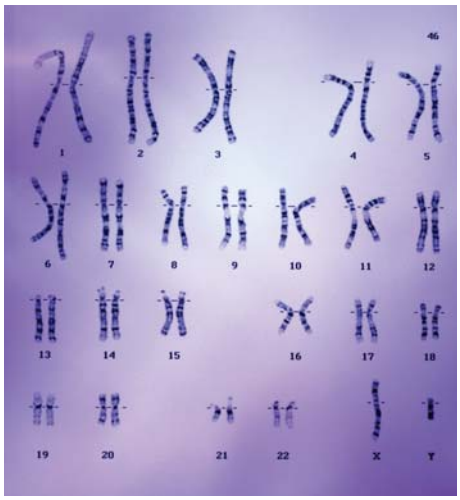
Genomes ahead



This time last year, Melbourne was gripped by genetics fever. Did the International Congress leave a mark on genetics in Australia? Susan Williamson reports.

ONE YEAR on from last year's XIX International Congress of Genetics, its organiser Dr Phil Batterham is at it again, organising this year's 51st annual meeting of the Genetics Society of Australia.

To state the obvious: it's a smaller organisational job for Batterham than last year's event – about a tenth the size, he says.

Last year the International Congress of Genetics was held in Melbourne, incorporated the 50th annual Genetics Society of Australian conference, the 50th anniversary of the discovery of the structure of DNA and saw thousands of delegates pass through the Melbourne Exhibition Centre. Batterham says he raised $1.5 million in sponsorship for the event – not such a small task.

And he is just as enthusiastic about organising this year's conference, despite its much smaller scale. "There's always a fresh challenge," he says.

DEFINING A DISCIPLINE

Organising conferences is something Batterham has been doing for years. He believes they play an important role in defining a discipline by fostering linkages and providing great benefits – tangible and otherwise – to those involved, by allowing researchers to improve their work through discussions with peers and providing a forum for introducing students to the discipline.

"Genetics in Australia, or around the world, is talked about in so many different areas," he says. "People use genetic skills and techniques in cell biology, molecular biology, environmental biology – the talks at meetings involve the use of genetics in all contexts."

The International Congress of Genetics provided just this environment, covering a broad range of areas in genetic science and, as Batterham said, "brought it all together".

One thing that came out of the congress was that the technologies that are now available to genetics researchers are allowing them to take things further – in the past sequencing genes provided the way forward, but now researchers can look at whole genomes. Tools such as microarrays, gene silencing techniques, and bioinformatics are enabling genetics research to step up to the next level and look at how genes work to produce a functioning organism.

"We know a lot about individual genes but we don't know how the complete gene set interacts to produce that organism," Batterham says. "How do genes work, what switches them on and off, how do they act in partnership to make a fish from a *Drosophila*, human or chimp?"

Batterham speaks of students in his lab using microarrays to look at which *Drosophila* genes are being expressed under certain conditions, and the ability they have to pick one gene out of the 14,000 in the *Drosophila* genome. But not that long ago, even looking at one gene was a big undertaking.

CLOSER TIES

The annual meeting of the Human Genetics Society of Australasia is also coming up in August in Fremantle.

At the moment the two societies remain separate – the division between the Genetics Society of Australia and the Human Genetics Society of Australasia goes back 23 years, but Batterham believes it is a division that may not remain so clear-cut as genetics moves into the future.

According to Batterham, this is one of things that became evident at last year's international congress.

The Human Genetics Society focuses

A boost for insect research

Batterham is currently based at the University of Melbourne as deputy director of the Centre for Environmental Stress and Adaptive Research (CESAR), an ARC-funded special research centre with nodes at Melbourne, Monash and La Trobe Universities.

The director of CESAR, Prof Ary Hoffmann, was recently awarded a Federation Fellowship and will be moving from La Trobe to Melbourne University. Hoffmann will also be the new president for the Genetics Society of Australia this year, taking over from Prof Rob Saint.

"It's great that Ary is coming to Melbourne, the co-location will be great," says an enthusiastic Batterham. "The fellowship gives us a tremendous capacity to build research and the centre.

"Ary brings to the mix a lot of expertise in biological control and integrated pest management (IPM). We think IPM means using all of the possible methods so as you deal with insect pests in a more benign way in terms of the environment."

Batterham will be moving to the Bio21 institute, a multidisciplinary research centre specialising in medical, agricultural and environmental biotechnology, something he describes as "a wonderful opportunity to be able to collaborate and use new technologies".

The research focus of CESAR includes looking at the mode of action of insecticides by finding and identifying the targets of insecticides currently in use, and to look at insect resistance.

"We are looking for more rational ways to control pests," says Batterham. "For a long time people would just hurl insecticides at pests without knowing the effects on the insect or the resistance of the insects. Insects have a detoxification system that involves enzymes that are able to degrade xenobiotic chemicals – just like humans have the P450 enzymes that metabolise drugs."

on human genetics, while the Genetics Society looks at all organisms, including humans.

"The human genome project has made it clear that humans are not all that different from other organisms," says Batterham. "All organisms have the same basic gene set that has been around for 600 million years. There's not that much difference between worms, chimps and humans."

So in the wake of the human genome project and last year's international congress, Batterham says the two groups are likely to come closer together.

The science of the two groups overlaps not only in content, but also in the techniques used to pursue research as well as comparative studies that enable a cross-pollination of ideas and information.

And the future looks bright for Australian genetics as far as fostering such linkages go, with two international congresses coming up – the International Congress of Human Genetics and the International Congress of Entomology – both to be held in Brisbane in August 2006, which will bring the two societies together yet again.

NETWORKING THE REGION

Last year's international congress also highlighted the vast amount of genetic research going on in Australia's next door neighbours – such as New Zealand and Asia – and the mutual benefits and opportunities that could arise in networking this region.

The Genetics Society of Australia is taking a step in this direction and is poised to change its name to the Genetics Society of AustralAsia – Batterham says he is keen to emphasise the second capital 'A' for New Zealand and Asia.

"To recognise the links we already have with New Zealand and to begin to build bridges with Asia," he says.

Batterham believes that having a regional focus is important for Australia and points out that the opportunities, research and industry-based, are just as available to Australia in the Asia-Pacific region, and if not more relevant, to those in the US and Europe.

"We sometimes forget the growing strength in our region," he says. "In the world economy at the moment our region is doing well, and partnership with Asia, I think, is worthwhile."

INTERNATIONAL GENETICS

One of Batterham's passions is promoting genetics in the developing world and international congresses provide an ideal forum for him to pursue this. His new role as secretary for the International Genetics Federation will also feed this passion.

The International Genetics Federation is an umbrella body that overarches a collection of genetics societies from around the world. It is governed by an interim council that meets every five years at the International Congress of Genetics. The Federation gave Melbourne the stewardship of the International Genetics Congress last year, and has allocated the next congress to Berlin in 2008.

In his new position as secretary Batterham is working with organisations in Berlin on the next congress and will be pursuing the developing world as he believes Australia has a lot to offer in this regard.

> "The human genome project has made it clear that humans are not all that different from other organisms"
>
> *– Dr Phil Batterham*

"It [genetics research] is incredibly empowering," says Batterham. "But it comes with responsibility. The public needs to be engaged for they decide what technology gets accepted or not. And regulation is important too as the government acts on the public good. We need to be literate on these issues."

IMPORTANT LINKS

Genetics Society of Australia conference
www.gsa2004.org.au
Human Genetics Society of Australasia conference
www.geneswest-hgsa2004.org
International Congress of Human Genetics
www.icms.com.au/ICHG2006
International Congress of Entomology
www.ccm.com.au/icoe/home

GENETICS IN ALL ITS BREADTH

The control of pests, environmental cleanup, the kangaroo genome, and tracking fruit flies – these are just some of the research topics that will be under the spotlight at this year's Genetics Society of Australia conference. Melissa Trudinger and Graeme O'Neill spoke with some of the researchers who will be presenting at the conference.

Shoo fly

GRAEME O'NEILL

BACTROCERA TRYONI is a drifter from Queensland's tropical north, whose taste for temperate as well as tropical fruit has drawn it far south and inland, since European settlement, to haunt the orchards of the NSW Riverina and the Murray Valley.

For decades, fruit-growers have been pointing accusing fingers at tourists from northern climes for causing sporadic outbreaks of Queensland fruit fly – Q-fly – that put the multi-billion dollar fruit industry in and around the Murray Valley at risk.

Molecular biologist and population geneticist Dr Stuart Gilchrist and his colleagues at the Fruit Fly Research Centre at the University of Sydney, extensively sampled *B. tryoni* populations throughout the species' range during 2002, and used microsatellite DNA markers to analyse their genetic variation and population structures.

The survey region included the coastal zone between Sydney and Brisbane, including Gosford, an important citrus centre, and the western slopes of the Great Dividing Range from Dubbo down through Young, West Wyalong, and Wagga, as far south as Albury, at the eastern edge of the Murray Valley.

Gilchrist says hot, dry summers and frosty winters make the Murray Valley and Riverina, and the western slopes of the Great Divide in NSW, climatically marginal for the Q-fly. But in warmer years, more flies can survive over winter and breed to larger numbers the following summer.

In 2001 and 2002, unusually mild, wet conditions saw several severe Q-fly outbreaks in the Riverina region, in and around towns including Leeton, Narrandera, and Deniliquin, and as far west as Hay.

These centres lie within the Fruit Fly Exclusion Zone (FFEZ), a quarantine region established in 1994 in an effort to limit the Q-fly's spread. The FFEZ encompasses the Riverina and the entire the Murray Valley, from east of Albury to Murray Bridge in South Australia, Australia's most important regions for horticultural production.

Fruit-fly road signs on major highways request travelers to eat any remaining fruit, or dump it in roadside bins before they enter the FFEZ.


Bactrocera tryoni

Gilchrist says the migratory inclinations of *B. tryoni* contrast with the sedentary habits of its cousin, *B. neohumoralis*, with which it is sympatric through much of its pre-European range. *B. tryoni* extends further from the coast, but the flies tend not to fly further than a kilometre under their own steam during their brief lifetime, clearly implicating careless human travelers in the Riverina outbreaks.

But did the flies come from nearby or from greater distance?

Using microsatellite markers to genetically fingerprint the different populations, Gilchrist's research group has now absolved long-distance travelers of blame – he will describe his conclusions in a presentation to this month's annual conference of the Genetics Society of Australia.

The immigrants came from the hardy Q-fly populations west of the Great Divide, on the periphery of the FFEZ. "The flies responsible for outbreaks within the FFEZ tended to be a close match with the closest populations outside the FFEZ," Gilchrist says. "None of them had come in from the west or north."


Bactrocera neohumoralis

Gilchrist says measures by the NSW Department of Agriculture to eradicate outbreaks from Riverina fruit-growing centres like Leeton and Narrandera provided a clue as to the flies' mode of travel.

NSW Agriculture officers released tens of millions of sterile male flies bred at a production facility in Camden, NSW, jointly funded by the NSW, Victorian and South Australian governments.

The facility produces 10 to 13 million sterile male flies per week. Before being dispatched to outbreak areas, they are dyed pink allowing the releases to be monitored. During the 2004 summer season, sterile male flies released in the Leeton-Narrandera area, were found in pheromone-baited traps in Wagga, 100 km east. Significantly, they turned up in traps proximal to local McDonalds and Kentucky Fried Chicken restaurants.

The discoveries indicate the flies had hitch-hiked in cars passing through the release areas in Leeton and Narrandera, perhaps attracted by the scent of fruit on board, and escaped when the occupants wound down the car windows for a takeaway meal at Wagga. Flies could also have survived impacts with car windshields and mudguards, Gilchrist said.

A severe Q-fly outbreak in Deniliquin in the 2003/4 summer taught locals a lesson – when some people expressed concerns about the use of bait sprays in residential areas, the tactic was discontinued. The surviving flies caused such a severe infestation in early 2004 that residents demanded the spraying program be resumed.

The survey conducted by the Sydney University researchers highlights the importance of rapid

Stuart Gilchrist

eradication of infestations in and around the FFEZ.

The microsatellite markers have resolved another mystery about the genetic relationships of the sympatric species *B. tryoni* and *B. neohumoralis* in their original range. Normally, strong selection pressure for the two populations not to hybridise results in the rapid evolution of pre-mating isolating mechanisms. Any hybrids are unlikely to survive because they are at a competitive disadvantage to the parent species in the environments in which they evolved.

Gilchrist says the only obvious feature that distinguishes *B. tryoni* from its otherwise identical cousin is its black shoulder pads; the pads are yellow in *B. tryoni*. But over the last 30 years, entomologsts have collected many specimens with blotchy shoulder pads, that appear to be hybrids.

Microsatellite fingerprinting has shown these colour morphs are merely natural variants of the parent species. Testing of three recent collections of the two species provided an unambiguous answer: neo-Darwinian theory rules. Researchers were unable to find a single hybrid.

A very effective pre-mating isolating mechanism keeps the two species from hybridising. Even under laboratory conditions, *D. tryoni* always mates in the evening, around 5 to 5.30 pm, whereas *D. neohumoralis* mates around noon – so the twain never tryst.

Another FFRC researcher, Dr Kathie Raphael, is searching for variations in body-clock genes that could explain the disparity in mating times.

Gilchrist says the question of why *D. neohumoralis* has never followed *D. tryoni* into southern regions, or achieved serious pest status in its native range, remains unresolved – and intriguing.

Comparative genomics

MELISSA TRUDINGER

AUSTRALIAN Genome Research Facility director Dr Sue Forrest will present a plenary session on the tammar wallaby genome sequencing project.

Forrest has been the lynchpin of the project's success to date, spending a fair proportion of her time since last October lobbying for funding for the project. That funding came through earlier this year, when the Victorian state government allocated $4.5 million to the project, allowing the program to take advantage of an unprecedented offer by the US National Human Genome Research Institute (NHGRI) to share the costs of sequencing the genome at a level of two-times (2X) coverage. Instrument specialist Applied Biosystems is also helping out, providing in-kind support and technical expertise.

Forrest credits Prof Jenny Graves, director of the Centre for the Kangaroo Genome at ANU, and her colleagues Prof Marilyn Renfree at the University of Melbourne and Prof Des Cooper at Macquarie University, as well as WEHI bioinformatician Prof Terry Speed, with spearheading the program. But the AGRF will play a key role in providing the raw sequence data to marsupial researchers at the centre and elsewhere for analysis and use in marsupial research.

According to NHGRI director Dr Francis Collins, the marsupial occupies an evolutionary 'sweet spot' for comparative genomics – at 80-130 million years old it is distant enough from the human genome for useful comparisons to be made, but as a member of the mammalian class, it is closer than, say, chicken or fish. Forrest says that the NHGRI is interested in using the sequence for comparative genomics, to glean a better understanding of the human genome and its genes, and of genome structure and function in general.

The tammar wallaby, *Macropus eugenii*, is not the only marsupial slated for sequencing by the NHGRI – in fact, at 2X coverage, it is only a minor part of the strategy. The NHGRI is focusing most of its marsupial efforts on an American species of opossum, <I>Monodelphis domestica</I>, which will get the full genome sequencing treatment. But the fact that the American marsupial species and the tammar wallaby are themselves about 50 million years apart in an evolutionary sense means that it makes sense to have the wallaby genome, too.

"Early studies I have seen, that compared equivalent regions in both species, have shown that it is worthwhile to have both sequences," Forrest says.

While the possibilities for enhancing evolutionary genomics are important to the NHGRI, Forrest says Australian researchers are far more focused on the tangible downstream benefits offered by the project. Among the areas of interest are the unique reproductive and lactation characteristics of marsupials, including the ability to make several different types of milk simultaneously and the remarkable process of diapause or suspended pregnancy, physiological puzzles such as the unique proteins that protect the immature lungs of the newborn marsupial and other aspects of marsupial biology.

Forrest says the AGRF is currently ramping up to start the sequencing, with more automation, new state-of-the-art sequencing equipment to be installed, and stringent quality assurance procedures to be put in place. She estimates that the sequencing will have commenced by November this year at the latest, and current timelines are projecting complete 1X coverage within two years. The US sequencing partner – Dr Richard Gibbs' group at Baylor College in Texas – is likely to start their 1X coverage in the latter half of next year.

As with other public genome projects, the data will be made available to researchers as it is generated, although the final assembly and annotation will not happen until sequencing is complete. But Forrest expects that researchers will start to make use of the data in their own work and to compare with the *Monodelphis* sequence from an early stage.

Pencilfish and dolphin genetics

GRAEME O'NEILL

BEFORE MOVING FROM the US to head Macquarie University's Molecular Ecology Laboratory in Sydney, Dr Luciano Beheregaray went on a 2500 km fishing trip in the rainforests of the Amazon Basin.

The Brazilian-born population geneticist was not fishing for a feed, or for sport. He was collecting thousands of samples of pencilfish and other small forest fish in the myriad, nameless rainforest Amazonian streams.

He is using microsatellite markers and DNA sequences to reconstruct the history of fish populations in one of the world's most diverse flooded forest ecosystems, the Rio Negro floodplain in central Amazonia.

Beheregaray chose small forest fish as a model group to address a question that cuts across all biodiversity research in the Amazon Basin: why so many species?

Evolutionary biologists have used DNA approaches to investigate evolutionary relationships in Amazonian birds, mammals and butterflies, but Beheregaray is the first to attempt a comprehensive DNA study of Amazonian fish at a basin-wide scale.

Beheregaray's honours student Shannon Corrigan will present the results of a preliminary analysis of "a massive number of pencilfish samples" at the Genetics Society of Australia (GSA) annual conference.

Many of the Rio Negro's fish species, including pencilfish, are very popular with tropical fish hobbyists around the world. The local ornamental fishery accounts for about 60 per cent of the income of Rio Negro riverine communities and has inhibited their move to non-sustainable, more environmentally damaging economic activities.

> Preliminary DNA analyses have revealed the existence of numerous cryptic species in different forest streams – some separated by only a few kilometres

The trade of these very abundant small fish thus indirectly protects the rainforest against being cleared, Beheregaray said.

The Rio Negro is the major tributary of the Amazon and typically floods once a year, raising water levels in the riverine rainforests by as much as 15 metres.

Despite the extensive flooding of the rainforests, which provides opportunities for fish to disperse through the basin, the small forest fish do not seem to move across the major rivers, which may act as barriers to dispersal – in places they can be over 30km wide.

But while the forest fish may avoid these aquatic superhighways, Beheregaray says they seem to disperse laterally along their margins, wherever there is rainforest. The Amazonian fish fauna is very rich – and growing richer. Preliminary DNA analyses have revealed the existence of numerous cryptic species in different forest streams – some separated by only a few kilometres.

Beheregaray exploits this diversity in testing evolutionary hypotheses – if patterns of DNA markers in several co-distributed species tell a similar story, it's likely they have experienced similar Earth-history events.

The comparisons between DNA sequences and data from fast-evolving microsatellite markers offer clues to when populations diverged; correlations can then be sought between speciation events and major shifts in the Amazon Basin's prehistoric climate – during glacial periods, for example.

Dolphin gene flow

Beheregaray's group will also present the latest data from a microsatelite analysis of NSW populations of the coastal dolphin *Tursiops aduncus*.

Dr Luciana Möller, who coordinates the cetacean research within the group, made an initial study of the social and genetic structure of *T. Aduncus* populations as a part of her PhD project three years ago, and has continued her work, in collaboration with honours student Joanna Wiszniewski.

Her research has revealed an unusual pattern of genetic exchange among populations between Newcastle and Forster. Dolphins in the embayments are homebodies who prefer to keep their genes to themselves. Although not genetically isolated, embayment populations have only occasional contact with open-water populations.

Embayment-dwelling males make sporadic forays into open water and "hang around" with open-water groups, but gene flow in the opposite direction may be restricted by the aggression with which the embayment dolphins defend their prime habitat.

"The embayment dolphins show a high fidelity to the place they were born, especially the females," Beheregaray said.

"It's just the pattern one would expect of a mammal, yet all the earlier behavioural work predicted otherwise."

However, the microsatellite analysis shows that there is high gene flow between open-water dolphin populations along the length of the coast between Newcastle and Forster.

The laboratory's DNA studies are also resolving long-standing taxonomic questions about dolphin populations, both along the coast of south-eastern Australia and the Indo-Pacific region. The results will be published later this year – Beheregaray says dolphin-watchers can expect a surprise.

– Graeme O'Neill