ALLAN WILSON CENTRE

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Lee Dugatkin is a Professor and Distinguished University Scholar in the Department of Biology at the University of Louisville

THE EVOLUTION OF **GOODNESS**

This year's Allan Wilson Centre (AWC) public lecture series begins with a fast-moving, action-packed talk entitled *The Evolution of Goodness*. Lee Dugatkin is a Professor of Biology and a Distinguished University Scholar at the University of Louisville in the United States, and one of the world's leading experts on the subject of the evolution of animal behaviour. His talk focuses on the core issue of what drives humans and other animals to help each other out, through acts of kindness, generosity and protection, even when these altruistic behaviours can be detrimental to themselves.

Professor Lee Dugatkin's current research projects include studies of the evolution of cooperation, interactions between genetic and cultural evolution, and the evolution of aggressive and risk-taking behaviours. He is the author and co-author of textbooks on animal behaviour and evolution, and has written more than 150 academic articles on evolution and behaviour. He has also written several books and articles for non-specialist audiences, including three books on the evolution of goodness, and several articles published in the widely-read *Scientific American* and *New Scientist* magazines.

One of his recent books, *Mr Jefferson and the Giant Moose* (2009), describes the lengths Thomas Jefferson went to in the late eighteenth century to counter an argument that the American environment was degenerate – that as a result of living in a cold and wet climate, all of the species found in America were weak and feeble. This theory was set out by one of France's most prominent Enlightenment thinkers, Count Georges-Louis Leclerc Buffon, in his influential natural history encyclopedia *Histoire Naturelle*. Lee's book provides a fascinating account of Jefferson's attempts to prove Buffon wrong, which included bringing a stuffed giant moose to Paris as a demonstration of the mighty native animals of America.

In *The Altruism Equation: Seven Scientists Search for the Origins of Goodness* (2006), Lee follows the history of evolutionary explanations of altruistic behaviours, from Charles Darwin's work in the mid-19th century, through to the mathematical equation for kinship selection formulated by William Hamilton in the 1960s. He explains how Darwin struggled to explain how the behaviour of honeybees and other insects could fit within his newly formulated ideas of natural selection, under which small beneficial changes within individuals are passed on to their descendants. Worker bees spend their lives providing resources to the hive, yet they are sterile and as individuals do not contribute to later generations – behaviour which is difficult to reconcile with the theory of natural selection.

INSIDE THIS ISSUE

The existence of sterile individuals within species was a major problem for Darwin which he later described in *The Origin of Species* as 'one special difficulty, which at first appeared to me to be insuperable, and actually fatal to the whole theory'. His eventual answer to the problem was the argument that in these examples selection was in fact acting at the level of families as well as individuals – that the altruistic behaviours of individual members of a group were beneficial to themselves as it increased the likelihood of survival and reproduction of their closely related group members.

Lee examines the impact and development of evolutionary arguments for altruistic behaviours in *The Altruism Equation*, from Darwin's contemporaries to 20th century scientists, including the prominent Russian anarchist Prince Peter Kropotkin. Kropotkin rejected Darwin's explanation that altruism was due to natural selection acting at a family level, instead seeing and promoting acts of goodness amongst people as independent of biological processes. In his most recent book, *The Prince of Evolution: Peter Kropotkin's Adventures in Science and Politics* (2012), Lee provides a more detailed account of Kropotkin's fascinating life and times.

> *At its heart, altruism is about incurring a personal cost in order to help others, and that is close to what most of us mean when we speak of doing good.*
>
> *Lee Dugatkin, in The Altruism Equation: Seven Scientists Search for the Origins of Goodness 2006:ix*

In his AWC public lecture, *The Evolution of Goodness*, Lee combines his extensive knowledge of the history of evolution and behaviour with the results and insights emerging from the latest research in the field, including his own projects on altruism, to provide his expert view of this compelling topic. Lee will be speaking at six venues nationally from late April to early May – see below and our website for details.

Professor Lee Dugatkin will be touring New Zealand as a guest of the Allan Wilson Centre

Nelson	Christchurch	Dunedin	Wellington	Tauranga	Auckland
Monday 28 April, 6.00pm, Old St Johns, 320 Hardy Street	Tuesday 29 April, 6.00pm, University of Canterbury, Central Lecture Theatre 1	Thursday 01 May, 6.30pm, St David's Lecture Theatre, University of Otago	Friday 02 May, 6.00pm, Te Papa Soundings Theatre	Monday 05 May, 6.00pm,Tauranga Yacht and Power Boat Club, 90 Keith Allan Drive, Sulphur Point	Tuesday 06 May, 6.15pm, Auckland Museum Events Centre, $15 for general public $10 for Auckland Museum Institute members, Auckland Writers & Readers Festival Patrons and Friends or students with ID

BOOKINGS: To ensure a seat, and to purchase tickets (Auckland only), go to **http://www.allanwilsoncentre.ac.nz** Click 'Register Online' under 'News and Events'. Reservations are essential for the Tauranga event for catering purposes.

Africa to Aotearoa

The Allan Wilson Centre organised and hosted a visit in late February/early March by Dr Spencer Wells and his team from the National Geographic Genographic Project (www.genographic.com). AWC member, Professor Lisa Matisoo-Smith, is their Oceanic Investigator, and is currently extending the Project's worldwide DNA survey by sampling 2000 New Zealanders, thanks to additional funding from a James Cook Research Fellowship and the Allan Wilson Centre. (See the next article, which explains how these samples are analysed in the University of Otago laboratory).

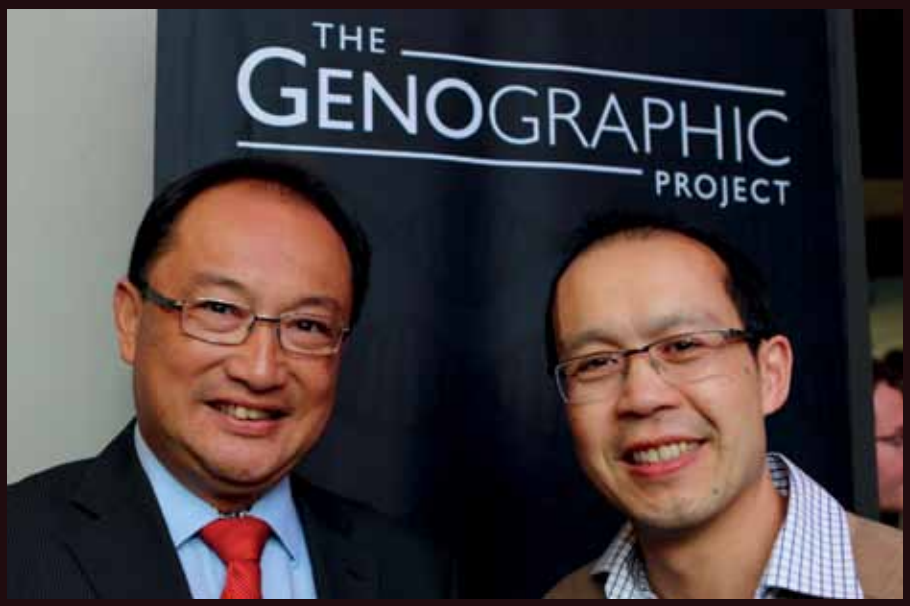
Spencer wanted to be there when Lisa reported her analysis of the DNA samples contributed by 13 Ngai Tamanuhiri people at Muriwai. A film crew making a documentary for the American Public Broadcasting Service, accompanied the expedition to record the event.

The team then travelled to Wellington to sample 100 (mainly) Wellingtonians following a lecture by Spencer, in which he used results from Allan Wilson's brother Gary, and Richard Brooking from Ngai Tamanuhiri, to illustrate the sort of information that can be inferred using the latest methods of analysis from the USA, including how much Neanderthal and Denisovan DNA each person has (yes, really!).

The Centre intends to organise a report-back event once the 'Wellington DNA' has been processed. The DNA sample included pioneering contributions from Sir Anand Satyanand, Hon Tariana Turia, Mayor of Gisborne Meng Foon, and Professor Sir Peter Gluckman.

We'll keep you posted on future events, and Lisa's ongoing research into the New Zealand identity. To register to receive this information directly, email awc-lectures@massey.ac.nz.

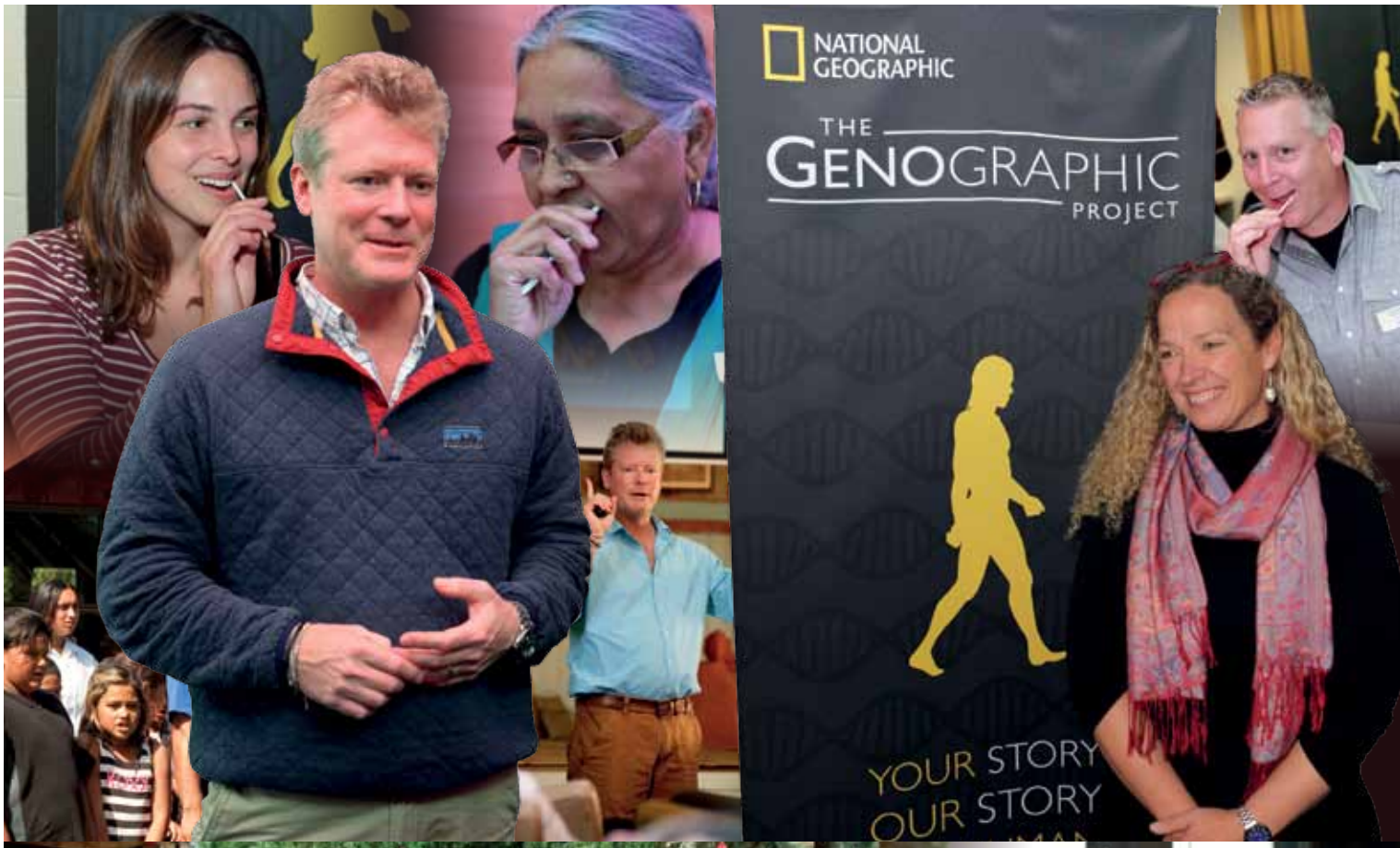
Dr Spencer Wells



Mayor of Gisborne, Meng Foon, and Murray Wu (Kiwibank)

Joshua Anstey and Lisa Matisoo-Smith

Film crew interview Nellie Brooking about her DNA result


NATIONAL GEOGRAPHIC
THE GENOGRAPHIC PROJECT
YOUR STORY
OUR STORY

Africa to Aotearoa: analysing the DNA of 2000 New Zealanders

Olga Kardailsky

The laboratory work for Principal Investigator Lisa Matisoo-Smith's Africa to Aotearoa research project is progressing quickly in her University of Otago laboratory. More than 500 samples are being analysed at present, and a further ~1500 New Zealanders will get a chance to be a part of this exciting study in 2014. Below we take a brief look at what happens to the samples in the lab.

Lisa and Olga take DNA swabs in Wellington

1. Collecting the sample

The samples are obtained by rubbing a swab on the inside of the subject's cheek. Cheek cells (and other microbial cells present in the mouth) stick to the swab, which is given a unique number code, and placed in a tube containing a buffer solution. The buffer stabilises the sample so that it can be kept at room temperature until it gets to the lab.

2. DNA extraction

The samples are taken to Lisa's laboratory in the Department of Anatomy at the University of Otago, where Olga Kardailsky performs the next few steps of the process. DNA is separated from the other cellular material in the swab sample using a DNA extraction kit, which contains an enzyme, Proteinase K, to break down protein structures. DNA is captured from the sample using magnetic beads, and finally the purified DNA is re-suspended in a new buffer solution. If the subject is male, a small subsample is taken from the purified DNA and sent to La Trobe University in Melbourne for Y-chromosome typing.

3. mtDNA amplification

The DNA sample contains DNA from the entire genome of the subject, and is also likely to contain DNA from many microbes living in the mouth. This step targets the non-chromosomal mitochondrial DNA (mtDNA) which is used in the Africa to Aotearoa study to trace maternal lineages, and copies it repeatedly. This amplification of the mtDNA builds up the concentration of the desired molecules so that they are present in much greater numbers than other DNA present in the original sample.

Two large overlapping DNA fragments of about 9000 and 11,000 bases are copied using the polymerase chain reaction (PCR). Together these fragments cover the entire ~16,550 bases of the mtDNA genome. This is a time-consuming step - the PCR process takes about 13 hours. It requires special PCR enzymes which have been developed to cope with the large number of cycles and long extension times required, and to minimise any replication errors.

4. Whole mtDNA genome sequencing

The large mtDNA molecules created through the PCR process have to be broken up into smaller fragments for the sequencing step. A sonicator machine uses sound waves to break the long DNA molecules into ~500bp pieces.

Special DNA tags, which function like barcodes, are then applied to the small fragments. These tags are used to identify individual samples, and enable 130 samples to be sequenced simultaneously using the Roche 454 next generation sequencing machine.

The sequencing results consist of multiple copies of short DNA reads, most of which are copied from the mtDNA. Bioinformatic techniques are used to separate the sequence run results back into individual samples using the tags, and combine and align the short sequences into mtDNA genomes.

5. Final steps

Lisa and other team members analyse the genomic mtDNA sequence, seeing where it fits on the global mtDNA tree. An mtDNA haplogroup is assigned, along with a Y-chromosome haplotype for male samples, and the results returned to individual participants. Finally, when all of the samples (~2000) have been processed, Lisa will analyse all of the results together to gain insights into the many different paths taken by our ancestors to form the New Zealanders we are today.

Teaching suggestions

- Curriculum links: Nature of Science – Understanding about Science, Living World: Evolution Level 6
- The Biotechnology Learning Hub's DNA Lab theme has sections on DNA extraction, amplification and sequencing **http://www.biotechlearn.org.nz/themes/dna_lab**
- Follow this link for an example of a magnetic bead DNA extraction kit, with an illustrated overview of how it works: **http://www.lifetechnologies.com/nz/en/home/brands/product-brand/chargeswitch.html**
- The Africa to Aotearoa website: **http://africatoaotearoa.otago.ac.nz/**
- Lisa is a Principal Investigator for the National Geographic's Genographic Project. Find out more about this global study here: **https://genographic.nationalgeographic.com**

Controlling the transmission of disease from animals to humans

Professor Nigel French was invited to travel to North America in early March this year to give presentations at the Centre for Disease Control (CDC) in Atlanta, and the University of Saskatchewan in Canada.

Nigel is the Professor of Food Safety and Veterinary Public Health at Massey University and an Allan Wilson Centre Principal Investigator. He is the Director of the Infectious Disease Research Centre situated at Massey's Palmerston North campus and his research group is internationally recognised for their studies of pathogenic organisms which infect humans and other animals. At the CDC Nigel presented a lecture on enteric zoonoses (a zoonosis is an infectious disease transmitted from an animal species to humans, or vice versa). In Canada, Nigel gave the prestigious DLT Smith Lecture at the University of Saskatchewan on the topic: 'Controlling zoonoses: how advances in microbial genetics and evolutionary biology are transforming epidemiology and public health'.

SCIENCE WHICH MAKES A **DIFFERENCE** BY JAMES RUSSELL

As a tenured academic at a New Zealand University my job description contains equal measures of research and teaching. Research is a fantastic joy and every time I lift my head in the field or lab I remember how lucky I am to be able to contribute to expanding the boundaries of human knowledge. Teaching is also as important.

For one, it brings in the largest share of income to most academic institutions, which secures employment. But that is only part of it. Almost all the students I encounter in my ecology classes are studying ecology because they want to make the world a better place (the same reason I enrolled in the very same courses I now teach). My job as a teacher is to share my knowledge, along with that of so many other people, with these students and empower them to use that knowledge to change the world as they so desire. Teaching is also a fantastic joy, and like each scientific paper published, each trained student will go out into the wide world to hopefully make a difference.

Research and teaching go hand in hand in so far as what we publish is not knowledge unless there is someone to teach it to, who can take it out in to the real-world. Most people do not spend their days downloading scientific papers and reading them, instead taking their information in from the news, from face to face communication, and increasingly from the un-moderated 'internet' in its entirety. With so much information out there the job of a teacher is now more of a broker of knowledge, rather than a disseminator. The information people find is then used, and filtered, in complex ways. One of the strongest results in information and social science is that simply giving people more information doesn't lead to changes in attitudes or behaviour. And so I often find myself wondering with every scientific paper I publish: who will read this? who will use this? what will this result change? It's reassuring to see my work cited by other scientists, but it's equally as rewarding to see government agencies implement it as policy, or journalists consider its merits (or often as not flaws). Only then do you know that you have created knowledge.

And so I often find myself saying that scientists will create the knowledge which changes the world, but they won't be the ones that implement it. That task is instead done by politicians, journalists, NGOs, community groups, and everyday members of the public. Scientists can also be great advocates, but these other people are the ones that all begin as students in our classrooms, or audience members in our outreach. It is them who we must prepare as well as possible to interpret the knowledge we provide to them and then go forth in the real world to implement meaningful change.

Senior lecturer James Russell checks the health of a juvenile greyfaced petrel

THREE YEARS WORK IN THREE MINUTES BY TOM FINN

The Challenge

For science to have maximum impact, it needs to be appreciated by the public. A crucial aspect of this is that it must be understandable. This can be a challenging task, to turn complicated subject matter into a form that is readily comprehensible to a wider audience. The discipline of science is immense; with a seemingly endless stream of new technologies becoming available, it is often easy for the scientist to get carried away. Regardless, a scientist must always endeavour to present their work so that it may capture the imagination of the public.

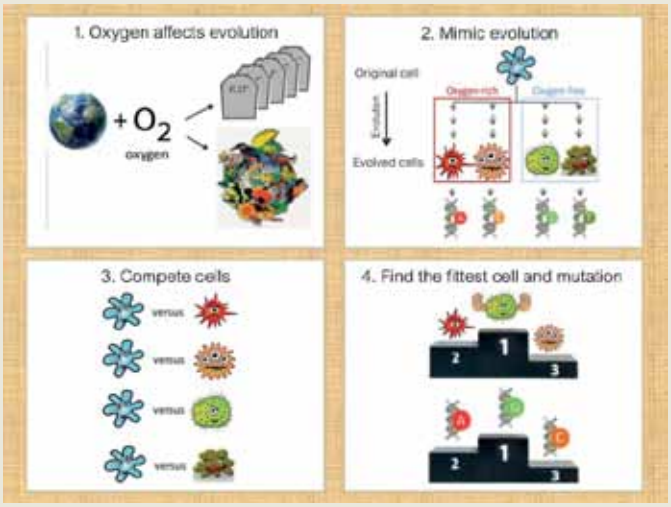
The Competition

Communicating my work is a problem I have faced in my own studies. An opportunity to test my scientific communication skills came with the 3 Minute Thesis Competition. This academic, multi-disciplinary presentation-based contest was started at the University of Queensland in 2008. Due to its popularity, it quickly became an annual Australasia-wide competition. The competition is aptly summed up in the slogan "3 years' work in 3 minutes". A daunting task for sure. Each contestant is required to present their work to an "intelligent but non-specialised audience". Rules of the competition dictate that the presenter cannot use props, may only use one slide (without animations) and crucially, must present within three minutes. Universities put forward only one contestant each year. The contestant is selected by winning preliminary rounds in their own university. Thinking it would be good practice, I entered the Massey preliminary rounds of the contest.

The Process

Clearly I have a great deal of interest in my own research. However, after three years of work, it is very easy to get lost in the details. For the competition I knew I had to take a step back and think of what it was that initially attracted me to the project.

Initially I felt I was at a disadvantage, as I was competing against other students, each with very interesting and arguably easier to understand subject matter. My project in itself is quite fundamental, but relies on complicated genome-based genetic analyses that are not so easy to grasp. The title of my project itself is quite detailed; "Understanding bacterial adaptation to aerobic and anaerobic environments, through experimental evolution and whole genome analysis".



Tom's single powerpoint slide

To grasp the big picture aim of my project an understanding of these techniques is essential. For this task, I employed a rather simple gimmick. I used the instantly recognisable world of Hollywood, and drew similarities between my experiments and movies particularly, the pop-culture favourites *Jurassic Park* and *The Hunger Games*. Another concept that very much aided the audience's understanding was that of eliminating what I call "snooze words". These are words that are just not that interesting to the public - jargon words like "aerobic and anaerobic treatments", "next-generation sequencing pipelines" and "sub-culturing of replicate samples" that are common in my research field but not to a wider audience.

The visual component of the competition i.e. the slide, is also crucial. If four years of undergrad education has taught me anything, it is that complicated slides do not help. Slides should aid rather than interfere with understanding. I wanted the slide to be easy to follow, so just by looking at it, someone could easily grasp the concept of my experiment and how it works.

The Outcome

I competed and won two rounds at Massey University's competition, competing against 50 other Massey PhD students from all three of the University's campuses. I was also elected the audience favourite. As a result of this, I was selected to be Massey University's entry for the Trans-Tasman Finals (which is broadcast internationally) at the University of Western Sydney in October 2013.

Here, I competed against 44 other winners of their respective universities throughout Australia, New Zealand and Hong Kong. The same presentation saw me reach the grand final, and for the first time ever, Massey University was represented among the Final 8 contestants.

The last point I would like to make is that science isn't a one person job. This presentation was the product of much advice and support. Many valuable insights were given from my colleagues, supervisors and support staff at the University, for which I would very much like to acknowledge and thank them.

About Tom Finn

Tom at the Wellington premiere of the Hobbit

Tom is in the final year of his PhD, which focuses on how life evolves with and without oxygen. The Marsden funded project is being carried out in conjunction with the New Zealand Institute of Advanced Studies (Professor Paul Rainey), AgResearch Ltd (Drs Christina Moon and Sinead Leahy), and the University of Ottawa (Professor Rees Kassen).

To watch Tom's winning presentation online go to **www.youtube.com/watch?v=dukJGi7Qe90**

GENOME MERGERS A MAJOR FORCE IN EVOLUTION

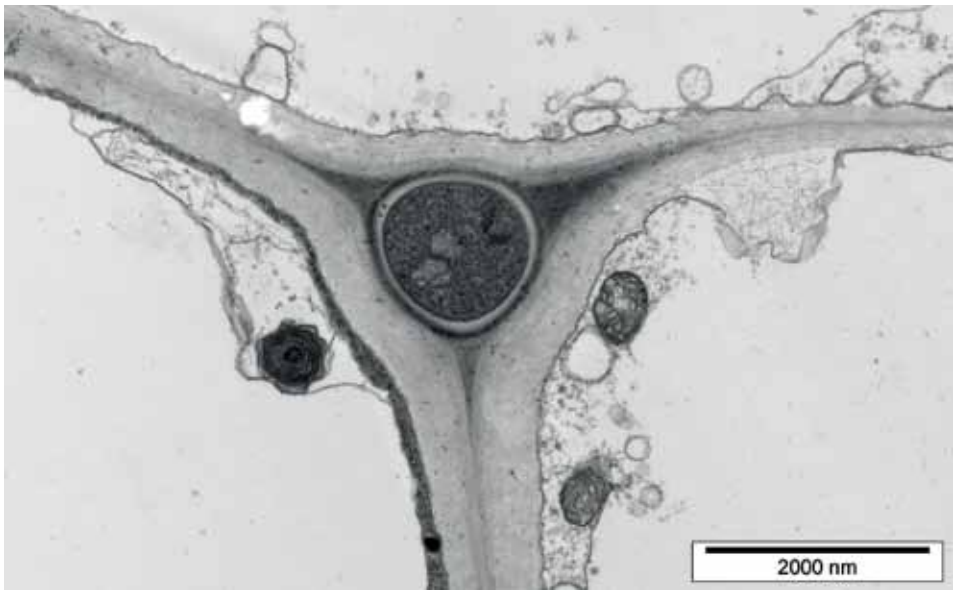
The results of a major study by Allan Wilson Centre Associate Investigator Murray Cox and colleagues was published in March in the prestigious open access journal *PLoS Genetics*. Murray leads the Computational Biology Research Group at the Institute of Fundamental Sciences at Massey University, where his work encompasses a wide range of projects which take a computational approach to exploring issues in evolutionary biology.

The *PLoS Genetics* article investigates the genetic consequences of a merger of previously separate species into a single new organism carrying both sets of the parental genomes.

The sudden increase in the number of chromosome sets carried by an organism is called polyploidisation, and it can result from genome duplication (autopolyploidy) or, as in this case, the hybridization of two different species or genera (allopolyploidy). While less common in vertebrates, polyploids are often found among plants and fungal species, and polyploidisation events are a major force in evolution. Allopolyploids can be very successful in establishing themselves ecologically, as in some cases their new combination of genes gains them an advantage over one, or even both, of the parental species.

In the project, Murray and colleagues used the latest technologies to provide an in-depth look at the effects of allopolyploidisation on gene expression (the process by which information from a gene is used in the synthesis of a functional protein). Their experimental subject was a naturally occurring fungal allopolyploid from a group known as the epichloë endophytes. These fungi are ecologically and economically important, forming a symbiotic relationship with pasture grasses. Many produce substances that can protect the grasses from insect damage.

The study examined gene expression on a genome-wide scale, looking at the levels of expression of the two parental genomes within the allopolyploid fungus and comparing these to the patterns of expression of the same genes in the closest-known parental relatives. The results showed that genes are expressed in the allopolyploid just like one or other of the parent species, and that the overall pattern of gene expression in the new hybrid species was very similar to that found in studies of cotton allopolyploids. These common responses to allopolyploidisation seen in such evolutionarily distant examples – plant and fungus – led Murray and his co-authors to suggest that genome mergers may be subject to a set of universal rules which determine how genes are expressed in new hybrid species.



A transmission electron microscope image emphasizing the close symbiotic relationship between the fungal endophyte and its grass host. A single fungal cell (dark circle in center) is growing at the junction of three grass cells (light spaces)

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