ALLAN WILSON CENTRE
FOR MOLECULAR ECOLOGY AND EVOLUTION

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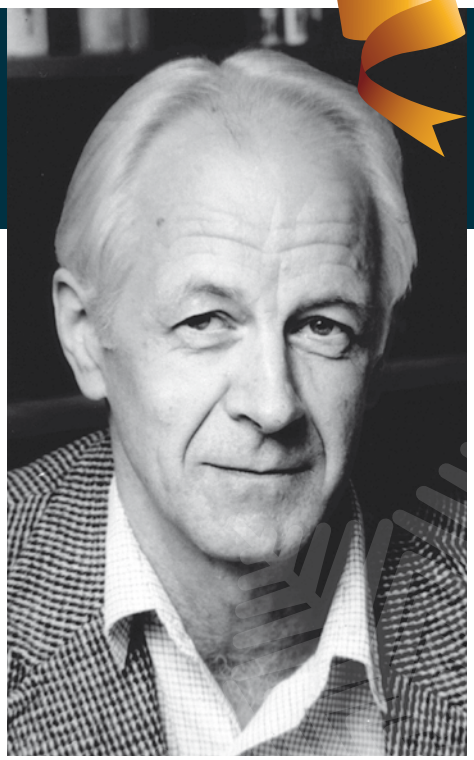
THE Allan Wilson LEGACY

ALLAN WILSON'S COLLABORATOR, REBECCA CANN, TO TOUR NEW ZEALAND

Professor Rebecca Cann from the University of Hawaii will commemorate the life and work of Allan Wilson on the twentieth anniversary of his death. She will speak at six venues throughout the country, including at Wilson's secondary school, King's College.



Allan Wilson

One of New Zealand's greatest scientists, Allan Wilson's innovative mind and creative talent shaped the field of molecular biology. His many achievements are recognised in naming the Allan Wilson Centre for Molecular Ecology and Evolution after him.

Wilson was born and educated in New Zealand, gaining a Bachelor of Science from the University of Otago and a PhD at the University of California, Berkeley, in 1955, where he remained until his death in 1991.

Wilson was a prolific scientist, producing many publications with his collaborators and students. Amongst these, two landmark papers, published 20 years apart, stand out. Each literally re-wrote history.

The publication in 1967 of *Immunological time-scale for human evolution in Science*, co-authored with Vincent Sarich, changed our understanding of human ancestry. Showing that humans and apes have a very recent common ancestor and introduced the concept of the evolutionary or molecular clock.

Then, in 1987, with Rebecca Cann and Mark Stoneking, Wilson published *Mitochondrial DNA and human evolution in Nature*. This paper used emerging molecular technology to peer into the origins of modern humans.

In her lecture series, Professor Cann will talk about Wilson's life, his work, and his scientific legacy.

Lecture dates and times

- **Dunedin:** 1 August at 6pm, St David's Lecture Theatre, University of Otago.
- **Nelson:** 3 August at 6pm, The Suter Art Gallery.
- **Palmerston North:** 4 August at 7pm, Public Library.
- **Wellington:** 5 August at 5.15pm, Rutherford Lecture Theatre 1, Victoria University of Wellington.
- **Auckland:** 8 August at 6pm, Fisher & Paykel Theatre, Owen Glenn Building, The University of Auckland.

INSIDE THIS ISSUE

Our divergence from apes, and the molecular clock

In the mid-1960s, it was generally agreed that apes are our closest living relatives. However, the time of divergence of the human and ape lineages was a subject of controversy.

DNA technologies did not exist at the time, so Allan Wilson and Vincent Sarich investigated the ape-human relationship by comparing differences among proteins in these species.

Traditional studies relied on the human fossil record, but because it is so incomplete, estimates ranged enormously, from 4 to 30 million years.

DNA technologies did not exist at the time, so Allan Wilson and Vincent Sarich investigated the ape-human relationship by comparing differences among proteins in these species. Because proteins are the products of DNA, this was an indirect estimate of genetic relationships.

The pair purified serum albumin from apes, old world monkeys, and humans, showing that human, chimpanzee, and gorilla albumins are extremely similar. This had been demonstrated before, but the conclusion they drew from this was ground breaking, not only for human evolution, but for the field of molecular biology as a whole.
"We have recently shown that albumin evolution in primates is a remarkably regular process," said Wilson and Sarich. "Thus, albumin molecules can serve as an evolutionary clock or dating device. The calibration of that clock… would allow us to calculate the time of divergence between apes and man." Now known as the molecular clock, this idea is used throughout evolutionary biology to calculate the timing of divergence of species in their evolutionary history.

Despite limited ability to calibrate the rate of evolutionary change in albumin, Wilson and Sarich estimated that the human-ape divergence occurred 5 million years ago – much more recently than most studies based on anatomy. Their paper created a major scientific controversy but this date is still widely accepted today.

Mitochondrial DNA and human evolution

When and where did modern humans (*Homo sapiens*) evolve? Again, the incomplete human fossil record provided some clues to this question, but left much room for controversy.

"Africa is a likely source of the human gene pool," the trio concluded.

In 1987 Rebecca Cann, Mark Stoneking and Allan Wilson used forefront molecular genetic technologies to examine and compare mitochondrial DNA from 147 people of African, Asian, European, Aboriginal and New Guinean descent.

"Africa is a likely source of the human gene pool," the trio concluded. Invoking the molecular clock hypothesis, they assumed that mitochondrial DNA evolves at a constant rate in humans and that the common ancestor of all surviving mitochondrial DNA existed 140,000-290,000 years ago. This ancestor is now known as Mitochondrial Eve. This paper generated a scientific controversy even greater than their 1967 paper, but again their ideas have come to be widely accepted by the scientific community.

RESEARCHER PROFILE: PROFESSOR REBECCA CANN

Rebecca Cann began her scientific career as a graduate student in Allan Wilson's lab at the University of California, Berkeley in the late 1970s. She was drawn there by his idea that evolution could be studied by measuring the rate of mutation of DNA. At that stage, however, the theory was unable to be tested directly as technology did not exist to sequence comparable DNA fragments from multiple individuals.

The early 1980s was a time of great change in molecular technology, though, and soon after the completion of her thesis, Cann and colleagues were able to publish their ground-breaking paper on human evolution in *Nature*.

Professor Cann's current research focuses on the mechanisms by which genetic variants arise and are maintained in populations. In particular, she is interested in genetic conflicts within individuals and between the sexes. Her research also looks at conservation biology in her home state of Hawaii.

"SAVING THE WORLD" AT THE WRITERS AND READERS FESTIVAL

Are we facing the sixth mass extinction? At the Auckland Writers and Readers Festival held in May this year, the Allan Wilson Centre sponsored a discussion of just that question. Entitled *Saving the World* and in front of an audience of more than 500, four panel members: Paul Gilding, Professor Naomi Oreskes, Grant Redvers, and Professor Fred Allendorf debated the role humans play in evolution, and if this might provide a pathway towards ethical action directed at saving the world.

Fred Allendorf

Fred Allendorf participated in this event as an expert in the application of population and evolutionary genetics to conservation biology. Allendorf is a Regents Professor of Biology at the University of Montana, a Professorial Research Fellow at Victoria University of Wellington, and a member of the International Scientific Advisory Panel for the Allan Wilson Centre. He is passionate about the importance of understanding the likely effects of humans actions on the evolution of many organisms.

In *Saving the World*, Allendorf argued that together overpopulation and overconsumption are stressing the planet and posing the risk of a sixth mass extinction. Others on the panel argued that overconsumption, particularly in the developed world, is the entire problem, but Allendorf disagreed. "Our current population growth is unsustainable. It's not just overconsumption, not just stuff that we buy. Production of the food that we need to support this many people is just not sustainable." To support this contention, Allendorf cited David Suzuki's recent book which points out that humans currently use 40% of the total photosynthetic activity on the planet.

However, solving the problem of overpopulation will not be easy. "The issue of personal reproduction is one of the most difficult choices that environmentalists face.

> ***"Our current population growth is unsustainable. It's not just overconsumption, not just stuff that we buy. Production of the food that we need to support this many people is just not sustainable."***

Successful reproduction drives evolutionary change, and reproductive success has been rewarded for billions of years. And so for people to voluntarily decide not to reproduce because they think it's going to be harmful, that really is a tough choice."

Allendorf has used the recent resurgence of bed bugs in the United States and around the world as a vivid example of the importance of considering the evolutionary implications of human actions. The U.S. Centers for Disease Control and Prevention recently have concluded that the primary reason for recent problems with bed bugs is that they have evolved resistance to a variety of pesticides that have been used to control them.

Allendorf also has put forward the view that health policy must include evolutionary considerations – that we must recognise that disease organisms evolve, sometimes in response to our efforts to deal with them. For example, in the 1970s the United Nations resolved to eradicate infectious disease by the year 2000. However, when the year 2000 arrived, the situation was actually worse. "Part of the problem was they did not recognise that disease organisms are evolving, and that we have to treat them in a way that will minimise them evolving to become more harmful for humans." An example of this is that as a result of overuse and misuse of antibiotics, many of today's disease-causing bacteria are resistant to the very drugs designed to deal with them.

Overall, says Allendorf, humans need to be aware of how our actions influence the evolution of other species on Earth and the important ramifications of this for society.

Close-up of a bed bug

FOCUSSING THE LENS ON PROFESSOR LISA MATISOO-SMITH

In April this year, Allan Wilson Centre researcher Professor Lisa Matisoo-Smith presented a seminar as part of the Liggins Institute's LENScience Senior Biology Seminar Series. Designed as an extension programme for Year 13 biology students, the series links our promising future biologists with cutting-edge science being carried out on their doorstep. Lisa's seminar focussed on how our understanding of the human settlement of the Pacific has developed as a result of evidence collected using molecular technology. As part of the seminar series, students are invited to ask questions. Below is an edited selection of these.

Professor Lisa Matisoo-Smith

Andrew Clarke

Student: *Kumara arrived in New Zealand before South Americans began moving around Polynesia. Is this evidence for contact of Polynesians with South American indigenous culture? Are there any studies which have been done on commensal plant migration?*

Lisa: The presence of the kumara is indeed evidence of contact and Andrew Clarke, who is working in our labs here in Dunedin, is looking at genetic variation in kumara and other commensal plants (plants that people take with them when they migrate).

Plant genetics are much more complicated than human or animal genetics though – and the remains rarely are recovered from the archaeological record, so we have to consider the possibility of recent mixture, which can complicate the picture. We have also identified the prehistoric introduction of chickens from Polynesia to the Americas, using ancient DNA studies.

Student: *Can you explain the relationship between exposure to new diseases and migration?*

Lisa: If a population is constantly exposed to a disease, then it will eventually develop resistance. European populations developed resistance to many diseases over a long period of time, whereas other populations were not exposed and therefore didn't develop resistance. So when Europeans arrived in the Pacific, they were carrying disease-causing organisms that had little impact on their own health, but when introduced to a population that had no resistance had a significant impact on the new population. This was a major problem wherever Old World populations came into contact with New World populations such as in the Pacific and the Americas.

Student: *I was under the impression that a set of seven substantially different Mitochondrial Eves had been traced rather than just one. Can you shed some light on this?*

Lisa: This shows the power of the popular press. The Seven Daughters of Eve is a book written about the various mitochondrial lineages that we see primarily in European populations. The seven lineages all share a common maternal ancestor – Mitochondrial Eve – who existed in Africa around 100 000 to 150 000 years ago.

Student: *How is ancient DNA extracted and preserved?*

Lisa: As soon as an organism dies, its DNA starts to break down. This process is affected by environmental factors. We find the best-preserved DNA in teeth because the enamel is very strong and protects it. We can also get DNA from other biological material such as bones, but it is generally damaged and mixed with DNA from the environment, for example, from bacteria.

We grind the bone, burst the cells and extract the DNA. We then have to amplify (make lots of copies of) the particular bit we are interested in using the Polymerase Chain Reaction (PCR) so we can study it.

When we extract the DNA, we extract all that is in the sample – not just from the organism that we're interested in, but all of the other organisms that have invaded that bone. This is a big problem for researchers as it contaminates the sample and makes it difficult to interpret the results.

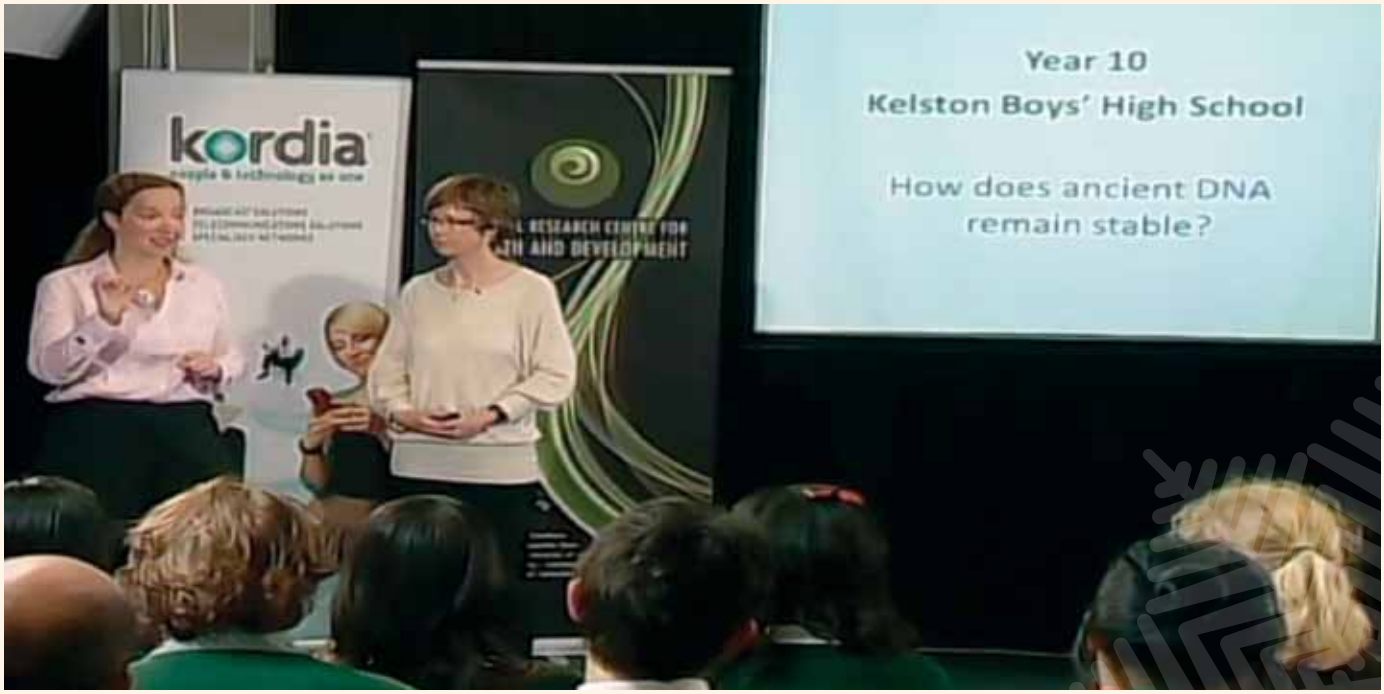
The degradation process is another problem – the DNA is often broken into small pieces and changes to it may also have occurred. That was a real problem with the Neanderthal DNA, as it was in such small fragments that most of it couldn't be amplified using traditional approaches. This is where new DNA sequencing technology is very useful – it can amplify tiny fragments of DNA.

Student: *What are the differences between early Polynesian settlers and modern-day humans? Are we simply more evolved or an entirely different species? If both types of people still existed, would inter-breeding be possible?*

Lisa: There are no differences at all between early Polynesians and people living in those regions of the Pacific today. With few exceptions, all people living for the last 30,000 years belong to the same species – Homo sapiens – and could interbreed. If an early Polynesian were sitting next to you in class today, you wouldn't spot them as being any different from the population of New Zealand in general. They are only removed from you by about 120 generations – or 3,000 years.

Student: *When working out evolutionary relationships to create a phylogenetic tree, how do you calculate when a mutation happened?*

Lisa: There have been many studies that have shown that mutations occur at a predictable rate, and these can be used to estimate when a mutation first appeared. We also use dated fossil remains to test the assumptions that underpin these calculations.



Professor Lisa Matisoo-Smith presenting at the Liggins Institute's LENScience Senior Biology Seminar Series

Genetic Signposts Mark the Way

Genographic researchers use parts of the genome that are passed down almost unchanged from parent to child to trace human lineages back through time. For most of our genome, we inherit half from our father and half from our mother but the chromosomes are shuffled and recombined at each generation, meaning a child is a genetic mixture of each parent. However, two types of DNA are passed down unshuffled – mitochondrial DNA and the Y chromosome. Mitochondria are cellular structures containing their own DNA. Because mitochondria are present in eggs, but not the heads of sperm, they are passed down only from mother to child. The Y chromosome is the sex-determining chromosome in humans and is found only in males, so is passed down only from father to son.

Both mitochondrial DNA and the Y chromosome are changed by only the occasional mutation. These mutations can be used as genetic markers or signposts to trace lines of descent – the female line for mitochondrial DNA and the male line for the Y chromosome. As populations migrate around the globe, their DNA gradually changes so that each population will have some mutations that are specific to their area, and others that reflect where that population came from. The more DNA changes two populations have in common, the more closely related those populations are likely to be. By tracing the DNA changes back in time, researchers can re-trace the migratory history of a population.

By Hilary Miller

TRACKING HUMAN MIGRATIONS

Where did we come from? How did we get to where we live today? Genetic and fossil evidence suggests that humans began migrating out of Africa about 100,000 years ago. The Genographic Project is now tracking where they went, using the largest collection of human DNA ever assembled.

DNA has already contributed much to what we know about the origin of humans. Allan Wilson used DNA to show that we are all descended from a common ancestor who lived in Africa around 150,000 to 200,000 years ago – a startling discovery that changed existing views about human evolution.

Humans started migrating out of Africa around 100,000 years ago, spreading to Europe, Asia, Australia and New Guinea, the Americas and finally Polynesia. The Genographic Project is using DNA sequences to answer many of the unresolved questions about these migrations, such as the origin of particular populations and the precise routes and timing of migration events. Funded by the National Geographic Society in partnership with IBM and the Waitt Family Foundation, the project involves twelve teams of researchers from all over the world, including one in New Zealand.

The research teams are collecting DNA samples from indigenous populations in their region and looking for differences in their DNA that provide clues to their ancestry. Added to this is a public participation kit, where for $US100 anyone can have their DNA collected, sequenced and added to the Genographic database. Together, these will produce a database of DNA sequences from hundreds of thousands of individuals.

Involvement with local communities is a central part of the Genographic Project. As well as providing a DNA sample, the participants in the project often share knowledge of their family history, such as the family groups they belong to and the languages spoken by their immediate ancestors. All of this information can be used to help interpret the genetic results. Individual results are also returned, in person, to the participants, and the meaning of the results is explained.

By Hilary Miller

THE GENOGRAPHIC PROJECT AT THE ALLAN WILSON CENTRE

Lisa Matisoo-Smith explaining results

Allan Wilson Centre Principal Investigator Lisa Matisoo-Smith leads the Genographic Project's Oceania team, who are studying human settlement in the Pacific. The settlement of the Pacific was a key event in human history, and happened on an incredibly large scale in a very short period of time. Some of the unanswered questions that Lisa's team are addressing include: Who were the biological ancestors of the Polynesians? Do males and females show different migratory patterns? How much variation exists in isolated populations, such as those of French Polynesia? The team is sampling from a number of populations across the Pacific and is also collaborating with Dr John Mitchell at La Trobe University who is sampling New Zealand Māori and Australian Aboriginal populations.

Post-doctoral fellow Andrew Clarke is responsible for processing the DNA samples once they come back from the field. This involves extracting DNA from cheek swabs, sequencing the DNA, and – in collaboration with other researchers – interpreting the data. Some interesting findings are starting to emerge.

On the small island of Emirau off the coast of Papua New Guinea, mitochondrial and Y chromosome DNA show very different patterns

For instance, on the small island of Emirau off the coast of Papua New Guinea, mitochondrial and Y chromosome DNA show very different patterns. The majority of people have mitochondrial DNA with typical East Asian genetic signatures, whereas the majority of males have Y chromosomes that are shared with males living on mainland New Guinea. This shows that in some of the small off-shore island populations of New Guinea, males and females have moved around in very different ways. The team are currently exploring a number of scenarios of migration events and societal systems that might explain these patterns.

Although the primary focus of Lisa's team is Pacific migrations, by combining their data with those from other Genographic labs they are also able to look at broader-scale migration patterns. Many of the markers that Andrew is sequencing are also used by the other labs, and can broadly distinguish between European, Papuan and East Asian heritage. To make collaboration between Genographic labs easier, all genetic data is transferred to a master database called the DNA Analysis Repository that is located at National Geographic headquarters in Washington, D.C.

The Genographic Project has been running since 2005 and the main phase will end this year. This will represent the completion of the major period of sample collection and DNA sequencing. A lot of the results have already been published (18 scientific papers to date) but there are still many findings to come.

As data are published, they are uploaded to publicly-accessible databases enabling researchers around the world who are not directly involved in the project to verify the results, and also to use the data in their own migration studies. In this way it is likely that data generated as part of the Genographic Project will be a valuable resource for years to come.

By Hilary Miller

Andrew Clarke (far left) with other Genographic researchers from around the world at the Genographic Project meeting in Sydney, 2010

THE ABC OF PACIFIC SETTLEMENT

New Zealand was the last major landmass to be settled by humans, but where did our Polynesian ancestors come from? Otago University PhD student Stefan Prost is using new mathematical tools to investigate exactly who the Polynesian settlers were and what route they took through the Pacific.

Stefan Prost (center) and two locals from Samoa

Humans first reached Polynesia around 3,000 years ago, when they colonised Samoa and Tonga. Around 1500 years ago people began moving into the rest of Polynesia, eventually spreading north to Hawaii, east to Easter Island and south to New Zealand, arriving here only in the last 700-800 years. Although researchers have a clear picture of the general pattern of human migration through the Pacific, there are still many uncertainties. For instance, who were the ancestors of the Polynesians? How many migration events were there into the Pacific? What was the precise route taken by the Polynesian settlers, and did males and females move around in different ways?

Stefan aims to answer some of these questions using a relatively new statistical tool called Approximate Bayesian Computation (ABC). This allows researchers to test different hypotheses of human migratory history using genetic information.

Stefan uses data from both ancient and modern-day human populations around the Pacific, as well as data from one of the animals Polynesian settlers carried with them, the Pacific rat. He is working closely with researchers on the Genographic project who are gathering DNA samples from across the Pacific and measuring variation in two types of genetic marker – mitochondrial DNA and the Y chromosome. These are important tools for investigating human demographic history as both are inherited from only one parent (mitochondrial DNA from the mother, and Y chromosome from the father) and do not recombine with DNA from the other parent. This means they can be used to trace male and female lines of descent.

The Genographic project is producing a huge amount of data that contains a wealth of information about population movement through space and time. Stefan aims to use ABC to extract this information. The method is far more sensitive than previous analysis methods used to map human migrations and ideally suited to such large datasets.

While his colleagues travel to the far reaches of the Pacific to collect the data, Stefan is making yearly trips to Berkeley, home of the late Allan Wilson, to work with computational biologist Professor Rasmus Neilsen. Together, they are testing how different statistical factors influence the results of ABC. Ultimately, they aim to establish a set of guidelines for using the method to study migration patterns.

By Hilary Miller

Taking Human Evolution to the Classroom

The Allan Wilson Centre has developed a PowerPoint presentation aimed at introducing evolutionary concepts to Year 10 students, using the story of human evolution as an example. The presentation shows how humans evolved from ape-like ancestors in Africa to modern humans occupying every part of the globe, and highlights the contributions that Allan Wilson made to our understanding of human evolution.

Students will learn how scientists study our evolutionary history, using evidence such as fossil remains and genetics to form theories about evolution, and how these theories may change as new evidence is found. The presentation also covers adaptation and evolution in modern humans, discussing how natural selection acts on genetic variation with examples such as eye colour and disease resistance, and answering questions such as 'why do we look the way we do?' and 'are we still evolving?'.

The presentation was developed by Allan Wilson Centre researcher Dr Hilary Miller in collaboration with biology teacher Azra Moeed. Azra taught biology for fifteen years at Petone College and Upper Hutt College, and now trains the next generation of science teachers in her role as Curriculum Leader of Science Education in the Faculty of Education at Victoria University.

Azra will show teachers how to use the presentation at the upcoming Biolive conference, to be held in Auckland on 17-20 July. She says the presentation aims to help students to connect with their biological past and interest them in wanting to know more. Currently, teachers have little opportunity to introduce evolutionary concepts to Year 10 students. The presentation will help to clear up misconceptions students may have about evolution and will emphasise how scientists work, gather evidence and develop theories based on this evidence.

By Hilary Miller

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