NEW DATASET PROJECT LEADS TO FIRST DRAFT KOALA GENOME

Bioplatforms Australia's new dataset project to sequence the koala genome with researchers from the Australian Museum and Queensland University of Technology (QUT) has resulted in the first draft genome of Australia's iconic koala together with a new research consortium.

The high level of international interest in the koala has made winning the race to fully map its genome a fitting Australian accomplishment. However, this achievement is more important for the far reaching scientific benefits and research outcomes the genome offers.

For the first time, scientists working on koala biology will have access to their complete genetic blueprint. Until now, only a handful of koala genes have been available in public databases. The developing genetic map is expected to include 20,000 genes when completed.

So far, the data has already uncovered many unique koala genes such as those related to their remarkable ability to survive on a specialised diet as well as the surprising finding that some koala genes are associated with human diseases such as bowel and breast cancer.

The datasets will be used for many broad research interests such as the evolution of koalas but will also be immediately applied to addressing the alarming susceptibility of koalas to Chlamydia and Koala retrovirus. These diseases are having a devastating impact koala populations in NSW and Queensland and the sequencing data generated by the Koala Genome Consortium is providing critical information on koala immunity.

Professor Timms from QUT, and one of the Koala Genome Consortium leaders, is most excited about the discovery of the koala interferon gamma (IFN-g) gene - a chemical messenger that plays a key role in the marsupials' defence against cancer, viruses and intracellular bacteria. His team is now using this new insight to better diagnose and treat diseased koalas and is currently trialling Chlamydia vaccines.

The wealth of data and the new knowledge being generated by this project is also relevant to biologists working to protect other species with similar genetic sequences as the koala.

The genome sequencing completed to date has been funded by Bioplatforms Australia, the Australian Museum Foundation, QUT and the ARC Linkage Scheme. The project will also utilise specialist bioinformatics resources. This initial funding has now seeded a broadening commitment to koala research.

Currently, the Koala Genome Consortium involves more than 12 scientists, veterinarians and bioinformaticians, including experts from the Ramaciotti Centre, a Bioplatforms Australia node, for library preparation, sequencing and technical expertise. The Consortium is actively seeking greater researcher support to supplement the sequencing data and has invited Australian and international experts to expand the consortium and generate more extensive research programs.

BASE – IMPACTS TO MICROBE DIVERSITY AND FUNCTION IN SOIL

Healthy and productive soils are crucial elements of natural ecosystem function and central to the sustainability of production landscapes.

BASE aims to measure what soil microbes Australia has and how microbial diversity and function change in relation to soil environment and landuse

Australia's unique geological and evolutionary history has resulted in the development of a complex set of soil environments and along with these go diverse, novel and potentially unique microbial communities. Despite this, relatively little is known about the distribution and abundance of soil microbes in Australia, and their relationship to ecological function.

Bioplatforms Australia's soil dataset project titled 'Biomes of Australian Soil Environments' (BASE) is an attempt to provide the first comprehensive national framework dataset of soil microbial diversity across the Australian continent. The project is using metagenomic analysis to examine fungal and bacterial communities at 300 sites in natural environments ranging from temperate grasslands, to arid shrublands, coastal dune systems and tropical forest. It is also analysing soil environments from around 200 agricultural and horticultural sites representing the country's major production industries (eg. wheat, cotton, dairy).

The broad aims of BASE are to measure what soil microbes Australia has and how microbial diversity and function change in relation to soil environment and landuse. Specifically, combining the microbial data obtained from sequencing with information on soil and vegetation data collected locally from the sampling plots, along with modeled climate information, will allow development of a predictive model of soil microbial community structure and functional traits. Comparison of results from natural and agricultural sites will then allow a direct assessment of the effects of land use, farming system and agricultural practice on microbial community structure, function and productivity.

The data from BASE also form Australia's contribution to The Earth Microbiome Project (EMP), an international initiative exploring the microbial diversity of the planet. By generating data compatible with the EMP, BASE will facilitate studies of the global evolution of soil microbes as well as giving a picture of the relative evolutionary novelty of Australia's soil biomes.

In addition to building a framework soil microbial dataset, the BASE project is also exploring the effects of some specific ecological processes that are important elements of Australian ecosystems. For example at Uluru, where fire is an important driver of ecosystem dynamics, samples are being collected from recently burnt and unburnt sites to examine the impact on microbial community structure.

Another specific objective is to understand the role of microbial communities in facilitating successful ecological restoration. To do this samples have been collected from the Gondwana Link revegetation corridor in south western Australia. Here bacterial and fungal communities are being measured and compared between original intact vegetation communities, agricultural fields converted from the original vegetation, and several ages of revegetated communities up to ten years old. Examining and quantifying the trajectories of change in microbial communities through the revegetation process provides an explicit understanding of how microbes may influence restoration success. Such knowledge can be used to develop microbial inoculation or management strategies to ecologically "jump-start" revegetation projects in the future.

BASE is a collaborative research initiative between Bioplatforms Australia, the CSIRO, SEWPaC Director of National Parks, SIEF, the Victorian Department of Primary Industry, the GRDC, TERN, the Australian Antarctic Division, DEC Western Australia and a number of Australian universities.

EPIGENOMICS CLUES TO GENE ACTIVATION

Epigenomics-based research by David Tremethick at the Australian National University (ANU) has employed bioinformatics and genomics expertise supported by Bioplatforms Australia to uncover an important marker for gene expression.

Elucidating the human genome sequence has enabled a better understanding of all biological processes involved in health and disease. However, there is another layer of information, epigenetic, which goes beyond DNA-stored information essential for packaging and interpreting our genome.

There are over 250 different cell types in the human body and while the DNA sequence of these entire cell types is essentially the same, their epigenetic information or profiles are very different. Our entire DNA is compacted into a structure known as chromatin. This epigenetic information controls gene expression ensuring that only genes for a specific cell type are turned on while inappropriate genes are switched off by 'opening' or 'closing' the structure of chromatin. Regulation of this epigenetic information significantly contributes to embryonic development, differentiation and cell fate, and underlies responses to environmental signals and ensures our capacity to reproduce.

Mis-regulation of our epigenetic code has been directly implicated in many common human diseases as well as contributing to human infertility. In a recent study at the ANU, researchers have characterised the epigenetic changes that occur during sperm development and identified a novel epigenetic mark, referred to as H2A.Lap1 that regulates the expression of genes only in the mouse testis. How epigenetic processes yield an 'open' chromatin structure to allow gene expression is unknown but these researchers also
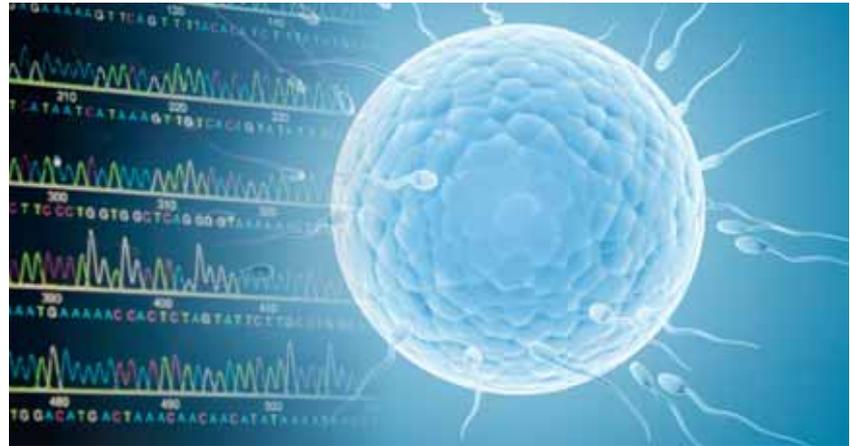
showed that H2A.Lap1 co-ordinately regulates sperm gene expression by directly opening the chromatin structure at the start site of active genes. This study has therefore uncovered a new epigenetic-based mechanism of gene activation, which will have important implications in understanding how cellular differentiation is achieved. In the future, it may also allow the development of new epigenetic-based approaches to treat male infertility.

This work by David Tremethick involves a collaboration with the ANU node of Bioplatforms Australia, comprising the Biomolecular Resource Facility and the Genome Discovery Unit (GDU). As part of the project, the GDU has developed a bioinformatics pipeline called ChipPy. This pipeline works by combining Chromatin Immunoprecipitation data with gene expression data to show the relationship between presence of a histone variant and gene expression activity. The GDU is planning a major update on this software which will allow other biologists with no computer background to use the pipeline via the popular web based portal Galaxy.

BUDGET FUNDING FOR BIOPLATFORMS AUSTRALIA

As part of the last Budget, the Australian government allocated funding of $185.9 million over two years from

1 July 2013 to continue the operation of maintenance of infrastructure projects instigated under the National Collaborative Research Infrastructure Strategy (NCRIS).

Future funding decisions by the government will be dependent on an evaluation of previous NCRIS investments.

Earlier in 2013 Bioplatforms Australia received $4.450 million under the Collaborative Research Infrastructure Scheme to bridge the period between the completion of the Super Science initiative and the start of the NCRIS program recently announced in the Commonwealth budget.

NEMO PROJECT REVEALS EFFECTS OF OCEAN ACIDIFICATION

The orange clownfish *Amphiprion percula*, also known as Nemo, has proven to be an ideal model species for understanding the ecology and evolution of reef fishes.

Research undertaken by Phil Munday and colleagues at James Cook University

(JCU) in Townsville has demonstrated that ocean acidification, caused by the uptake of additional carbon dioxide from the atmosphere, can impact the normal olfactory response of clownfish putting them in the path of predators and unsafe habitats.

The research revealed that clownfish larvae reared in seawater with elevated CO_2 levels were not able to detect the odour of common predators whereas those grown in normal levels of CO_2 were able to avoid the predator's scent more than 90 per cent of the time. Smell tests also reveal other risky behaviours that would increase the chance of the fish being eaten. This unexpected impact of ocean acidification has been demonstrated in other reef fishes, and is likely to be detected in other marine species.

With growing carbon dioxide emissions and corresponding concern for the associated environmental impacts, clownfishes are considered to be a remarkable model species for understanding the effects that climate change will have on the genetic architecture of marine species and how this may transfer to behavioural alterations that affect individual fitness.

This important research on the impact of ocean acidification on marine ecosystems is continuing and receiving support from Bioplatforms Australia for an Illumina RNAseq sequencing experiment aimed at understanding the effects of elevated CO_2 on larval gene expression in *Amphiprion*. This investigation, led by David Miller at JCU and Sylvain Forêt at the ANU and

involving Susie Sprungala and Sue-Ann Watson (JCU) as well as Mike Berumen at KAUST (Saudi Arabia), aims to precisely define the transcriptional changes that underlie the effects of elevated CO_2 on clownfish larvae.

Nemo may seem a rather exotic choice for transcriptomics experiments, but it represents a model organism for studying fish ecology and evolution, hence discoveries in the clownfish will have implications for many other marine species.

WHEAT PATHOGEN PROJECT RECEIVES POSITIVE REVIEW

Bioplatforms Australia's wheat dataset program has been generating 'omics data to support important research into fighting significant wheat diseases.

The datasets contain genomic, transcriptomic, proteomic and metabolomic datasets for a diverse range of pathogens and their interaction with their wheat host.

During the year the pathogenomics elements of the wheat dataset program were independently reviewed by Anne Osbourn, Professor and eminent researcher on the molecular basis of plant defence at the John Innes Centre in the UK. Professor Osbourn complimented the 'simple but elegant' approach of using the host (wheat) as the common link for researching diverse pathogens and infection styles. She considered that the multi-platform approach delivered an attractive, well-integrated and cohesive body of research that both consolidated and built on previous work on wheat disease that also helped to bring the wheat disease community together. Furthermore, she suggested that the project offered a proof of concept for other important crops including legumes, barley and canola.

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