



CONNECTIONS

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ACROPORA MILLEPORA

Photo courtesy of Darren Coker, ARC Centre of Excellence for Coral Reef Studies.

CORAL GENOME COMPLETED

Australian scientists have sequenced the genome of the staghorn coral *Acropora millepora*, a major component of the Great Barrier Reef and coral reefs worldwide.

The coral genome sequence has been a national collaborative effort by the Australian Genome Research Facility (AGRF) and researchers in the ARC Centre of Excellence for Coral Reef Studies (CoECRS) based at James Cook University, the Australian National University, Monash University, the Walter and Eliza Hall Institute and the University of Queensland. The project kicked off in mid 2009 and brought together some of the best young minds in Australian genome science to tackle the daunting task of stitching together the approximately 400 million letters of DNA that make up the coral genome.

This is the first animal genome project carried out entirely in Australia and has both practical and scientific significance. Corals are the backbone of the Great Barrier Reef but face significant environmental stress. The availability of the genome sequence will enable major advances in understanding many aspects of coral biology, including the responses of corals to climate change, ocean acidification, pollution

and disease. Greater insight into how corals build reefs and why they fail to do so when under stress will offer an invaluable contribution to coral preservation and an iconic element of Australia's tourism industry.

Their study shows that corals may look like simple animals, but their DNA is surprisingly complex. In fact, corals have about the same number of genes as man, and many of them are remarkably like ours. Their genome comprises 28 chromosomes and the project revealed a high level of polymorphism. Like most animals, the coral is diploid (each individual contains two near-identical sets of genes – one from the father, and one from the mother), but the two haplotypes (the father and the mother halves of the genome) are more different in corals than in other animal species. This feature amplified the challenge of assembling the sequence given the daunting number of short reads produced by the next generation sequencing technology employed for the project. Addressing these challenges prompted a number of pioneering genome assembly methods.

The first draft assembly of the *Acropora millepora* sequence is available to the scientific community under specific conditions.

Contact Professor David Miller, CoECRS and JCU, (07) 4781 4473 or Dr Kirby Siemering, AGRF (03) 9321 3707 for further information.

EBI MIRROR GIVES FAST ACCESS TO BIOTECH DATA

On behalf of EMBL Australia, the University of Queensland has launched a 'mirror' facility of the most-used data services of the European Bioinformatics Institute (EBI) within the European Molecular Biology Laboratory (EMBL).

The mirror provides Australian-based entry to a growing selection of EBI's databases, software frameworks, and on-line tools for data retrieval, querying, analysis, comparison, integration and visualisation. It is co-located with the National Computational Infrastructure (NCI) Specialised Facility in Bioinformatics.

According to University of Queensland professor, Mark Ragan, Australia currently produces only two to three per cent of the world's bioinformatics data. Like other data internationally in bioscience, these datasets are collected in the US, UK and/or Japan, where they are subjected to quality control, formatted in standard ways, integrated with other data types and aggregated into value-added data services. The mirror will allow Australian researchers to access these data and data services at least 10 times faster than it would normally take to download from the EBI. Scientists can download the data to their own research institutions via AARNet's fibre network or use them in experiments on the NCI supercomputer.

The mirror facility, the first of its kind outside the UK, will enable new opportunities for large-scale research and collaboration in Australia. It offers significant potential to attract investment to Australian life sciences, biotechnology and information and communications technology. Scientists have welcomed the initiative and expect it to play a crucial role in the development of personalised medicine and other breakthrough genomics applications.



Dr Ng's research aims to better understand the molecular mechanisms that drive cardiovascular disease



EBI MIRROR TEAM. *Front row from left:* Lanna Wong, Jeremy Barker, Gavin Graham, Terry Clark, Elham Gharazi. *Back row from left:* Mark Ragan, Peter Scott, David Green, Gerald Hartig, Jeremy Parsons, Dominique Gorse.



The mirror facility is funded and supported by EMBL Australia, The University of Queensland, Queensland Government, and the Australian Government through Bioplatforms Australia, and Australian National Data Service.

Together, the EMBL Australia EBI Mirror and the NCI Specialised Facility in Bioinformatics comprise 3,144 cores in 384 nodes, 11.25 terabytes of RAM and more than 500 terabytes of disk storage which will be further increased.

Contact: Prof. Mark Ragan, Genomics & Computational Biology, Institute for Molecular Bioscience, University of Queensland, E: m.ragan@uq.edu.au, T: 07 3346 2616.

NEW DATASET FOR SOIL BIODIVERSITY

Bioplatforms Australia has launched a new dataset project to benchmark Australia's soil biodiversity.

The project will generate large scale genomic datasets that will create a reference map and new data resource of Australian soil biomes across a range of different sites.

Soil provides the very basis for all our lives, largely through the provision of nutrients to plants that can feed and shelter us. At a microscopic level, soil hosts diverse microbial communities that drive ecological processes such as nutrient and carbon recycling as well as

being intimately involved in a range of symbiotic relationships with plants and animals. As such, microbial communities play a critical but largely unquantified role in determining broad-scale patterns of plant species abundance and resilience. Soil is rarely viewed as a natural resource but it is a crucial element for primary production, land and water management, environmental pollution and site remediation and conservation.

Like Bioplatforms Australia's wheat dataset project, this initiative will serve broad national interests and rely on the collaborative efforts of prominent researchers and industry experts. Bioplatforms Australia will co-ordinate the project which will collate metagenomics measurements across different sites in order to create a reference map of Australian soil. These datasets will be linked with existing overland surveys, meteorological data, geological knowledge and other portals of information to enhance the ecological knowledge of the Australian continent and contribute to land management strategies.

Titled the Biome of Australia Soil Environments (BASE), the project will be supported by CSIRO, the Commonwealth Department of Sustainability, the Environment, Water, Population and Communities (SEWPAC), State Departments of Primary Industry, the Grains Research Development Corporation (GRDC) together with a number of universities and other research organisations. The resulting datasets will be made publicly available and involve advanced bioinformatics to ensure usability and

accessibility by all researchers.

The BASE project will align with the Earth Microbiome Project, an international effort to characterise more than 200,000 microbial samples around the world. The project aims to better understand the microbial diversity that exists on earth and provide a publicly available global data repository and data-analysis portal.

For further information, please contact Anna Fitzgerald at Bioplatforms Australia afitzgerald@bioplatforms.com.

BPA ACCESS VOUCHER SUPPORTS CARDIOVASCULAR DISEASE



Dr Dominic Ng, ASBMB's Bioplatforms Australia Award recipient.

Dr Dominic Ng from the Bio21 Molecular Science and Biotechnology Institute at the University of Melbourne has been awarded a Bioplatforms Australia access voucher to advance his research into cardiovascular disease.

The voucher is to be awarded annually by the Australian Society for Biochemistry and Molecular Biology (ASBMB) to recognise young, post-doctoral researchers who are performing outstanding research in the field of genomics, transcriptomics, proteomics, metabolomics or relevant bioinformatics. The access voucher provides \$10,000 worth of services provided by any node of Bioplatforms Australia.

Dr Ng is the inaugural awardee of ASBMB's Bioplatforms Australia award. His research aims to better understand the molecular mechanisms that drive cardiovascular disease so that early stages of heart failure can be better detected and aid the development of new diagnostics and treatment strategies. Dr Ng intends to use the award to conduct gene expression profiling by microarray at the Australian Genome Research Facility (AGRF).

7TH ANNUAL METABOLOMICS SOCIETY MEETING - CAIRNS, AUSTRALIA

The Metabolomics Society's 7th annual conference, Metabolomics 2011, held in Cairns last June demonstrated the increasingly translational nature of metabolomics research.

Only a few years ago, the major component of the research being reported at these conferences related to the development and optimisation of wet and dry technologies for the delivery, management and mining of metabolomics data. At Metabolomics 2011, it was evident that a great and growing variety of metabolomics applications are being actively pursued and leading to some impressive examples of translational metabolomics. Conference highlights covered Keio University's CE-MS "metabolomics factory" which is being used to identify novel biomarkers for multiple liver diseases, major depression and colon

cancer. Prof. Holmes, of the Imperial College, London demonstrated how NMR and MS are being combined to help identify the human "exposome" and to create an "intelligent scalpel" for the emerging field of surgical metabolomics. Dr Meikle of the Baker Institute in Melbourne showed how quantitative lipidomics is leading to novel biomarker profiles for cardiovascular disease and type II diabetes.

Despite the biological advances of metabolomics approaches, it would be incorrect to say that the technology is now mature. Better tools for metabolite identification and quantification together with robust procedures for multi-omics integration are on-going requirements. Bioinformatics capabilities, such as the growing demand for database design, data management and data co-ordination also require attention with conference sessions illustrating the growing need for more effective analytical tools.

In the field of animal and human metabolomics, the primary focus was on biomarker identification, either with regard to markers of disease or markers of exposure. Cancer remains a major topic with obesity and type II diabetes the second most commonly discussed subjects.

The use of metabolomics approaches to study aspects of plant and

environmental interactions was a particular topic of the conference. Several examples were given where GC-MS, LC-MS and NMR-based methods are being applied to projects such as grape quality under different cropping and irrigation regimes; zinc hyperaccumulation; and carbon and/or nitrogen starvation.

Metabolomics 2011 was ably organised by Ute Roessner (University of Melbourne/Metabolomics Australia), Simone Rochfort (Dept of Primary Industries, Melbourne) and Rob Trengrove (Murdoch University/Metabolomics Australia) who pulled the conference together from scratch in just a few short months.

The location of the 2011 meeting was originally planned to be in Tsuruoka, Japan, however, the devastating tsunami and earthquake hit just 10 days after the conference registration went online forcing relocation to a new venue in Cairns.

For further information, download the Conference Abstract book from the Metabolomics Society website www.metabolomicssociety.org. Metabolomics 2012 will be held in the US next June.



7TH ANNUAL METABOLOMICS SOCIETY MEETING
Cairns Convention Centre



Bioplatforms Australia is accelerating its bioinformatics support through greater resources and strategic focus.

NEW AUSTRALIAN BIOINFORMATICS NETWORK

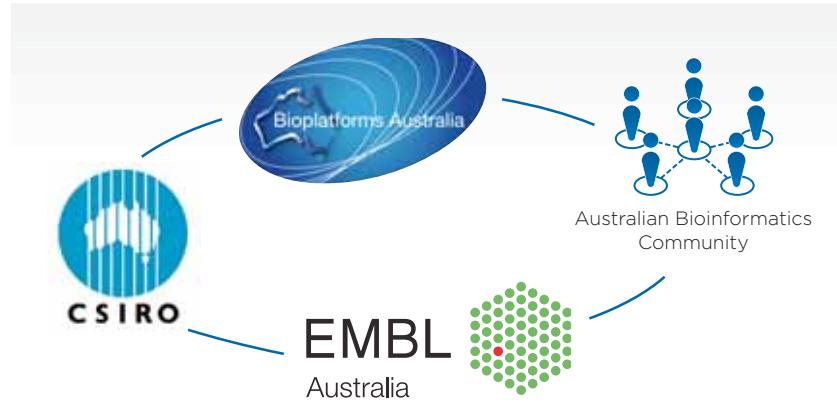
Bioplatforms Australia is pleased to announce that it is building an Australian Bioinformatics Network (ABN) in conjunction with EMBL Australia, the CSIRO and the Australian bioinformatics community.

Despite recent initiatives that have enhanced our bioinformatics capabilities, the Australian bioinformatics community remains small and fragmented relative to its counterparts in Europe and the USA. As bioinformatics is a critical discipline for life science research, Bioplatforms Australia is accelerating its bioinformatics support through greater resources and strategic focus.

Bioplatforms Australia's framework datasets strategy and our project to construct a bioinformatics analytical environment will increase accessibility of bioinformatics tools and go some way toward alleviating the computational bottlenecks and challenges of data integration faced by biologists.

The ABN is an initiative that offers broad benefit to the bioinformatics community. It aims to foster world class bioinformatics capabilities and promote cohesion by linking and supporting locally embedded practitioners with strategic bioinformatic sites at universities and research organisations across Australia. Other initiatives will focus on professional development including the creation of a Skills and Tools Registry and database of skilled practitioners. Further programs will be considered and implemented once the Director of the ABN is appointed early next year.

Bioplatforms Australia's contribution to the ABN will involve its three core centres for bioinformatics (as follows) together with expertise embedded at a number of its platform nodes:



NEW AUSTRALIAN BIOINFORMATICS NETWORK

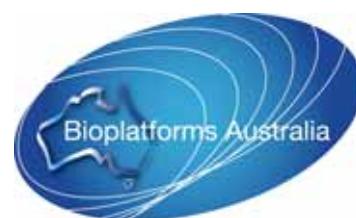
Australian Bioinformatics Network (ABN) in conjunction with EMBL Australia, the CSIRO and the Australian bioinformatics community

- *Centre for Comparative Genomics (CCG), Murdoch University* - specialists in biomedical and agricultural genomics and bioinformatics and home of the Bioinformatics Research Laboratory.
- *Systems Biology Initiative, University of New South Wales* - builds capabilities and expertise in bioinformatics for genomics and proteomics.
- *EMBL Australia EBI Mirror Facility, University of Queensland* - provides local access to EBI databases, analytical workflows and software tools.

For further information contact Catherine Shang at Bioplatforms Australia cshang@bioplatforms.com.

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Available 30 November from the Bioplatforms Australia website www.bioplatforms.com.



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