XXIIIrd INTERNATIONAL CONGRESS OF GENETICS

Biodiversity Genomics - a Global Perspective

Sunday 16 July 2023

MELBOURNE CONVENTION AND EXHIBITION CENTRE **AUSTRALIA**

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Biodiversity faces many threats resulting from human activity around the world. There are an extraordinary number of species and ecosystems known to be threatened, with many more to be identified and registered. Urgent and sustained action is required. Genomics offers a powerful set of tools that provide critical information to underpin and guide the development and implementation strategies to preserve biodiversity. These genomic tools include genome sequencing, genotyping of populations and e-DNA. In 2018, an audacious plan to sequence, catalog and characterize the genomes of all of the Earth's eukaryotic biodiversity over a period of 10 years was announced. Five years on, what progress is being made on this *moonshot for biology*? What benefits are being derived from this research and what needs to be done to expedite progress? Starting with the shared opening session, this Biodiversity Genomics meeting will divide into two streams, one on genome sequencing and genotyping and the other on the use of e-DNA to study ecosystems. This meeting will be an important step towards a national dialogue on how systematic and sustained genomic analysis can be used to identify, preserve and protect Australia's unique biodiversity.

SUNDAY 16TH JULY 2023

8.45am	**Arrival – Registration, Coffee/Tea provided**
9.15-9.45	**Welcome, introduction to the meeting and overview of the Biodiversity Genomics Australia agenda**
9.45-10.00	**Brendan Wintle**, Lead Councillor, Biodiversity Council *Growing policy momentum to tackle the global biodiversity crisis* Biodiversity underpins all aspects of our life, from food systems to culture and identity, economy, and health. Animals pollinate 90% of crops; 70% of medicines are derived from animals and plants; natural ecosystems remain the only viable large-scale carbon sink, and half of the global economy is directly dependent on nature. Yet biodiversity is in precipitous decline globally, and particularly so in Australia. The World Economic Forum ranks biodiversity loss in the top three risks to the global economy. In Australia, catastrophic policy failures have led to dramatic biodiversity losses and ecosystem declines. But winds of change bring hope. Responding to the IPBES global assessment and growing pressure from business and community, the new UN Global Biodiversity Framework sets a bold new agenda and commitments to protection and recovery of biodiversity. The Taskforce for Nature related Financial Disclosure looms as a key driver of change and the European Parliament has now legislated the prohibition of products with land clearing in their supply chain. The domestic biodiversity policy agenda has been energized by an ambitious new minister and her nature-positive plan. But there is much work to be done to make the most of these opportunities and to mitigate against the prominent risk of greenwashing and attendant cynicism. The role of science and expert evidence has never been more important to support positive societal, policy and regulatory transformations. I highlight key knowledge challenges and emerging opportunities to harness a growing global appreciation of the existential crisis we face.

10.00-10.20	**Mark Blaxter**, Program Lead, Tree of Life Program, Wellcome Sanger Institute, UK *Sequencing life for the future of life* The Linnaean project – the formal naming of all species on our planet – remains one of the largest and most successful science megaprojects ever, and has delivered a universal language through which we as humans can share understanding of the natural world. However, the Linnaean catalogue of Life only gives us the titles of the books that should be in the library. In the Earth BioGenome Project a global community of genome, biodiversity and analytic scientists is responding to the sixth great extinction by delivering as fast as we can the text of the Books of Life – the complete genome sequences of all eukaryotes on earth. This decadal project will, we believe, transform understanding of diversity and evolution, and provide foundational data onto which new conservation, biomonitoring, bioindustry and basic science can be built. I will introduce the Earth BioGenome Project as a network of networks that ensures cooperation, collaboration and delivery to our goals of sequencing all 1.8 million eukaryotes, and present some of our early and growing successes.
10.20-10.40	**Carolyn Hogg**, Senior Research Manager, Australasian Wildlife Genomics Group, University of Sydney *Biodiversity Genomics in the Age of Extinction* Genetic diversity is biodiversity permitting variation between species and ecosystems. Human activity and actions are changing our planet resulting in over 1 million species under threat of extinction. As the biodiversity crisis deepens, we are turning to technological solutions to meet the ever-increasing demands of humanity on the natural world. For over 50 years, ecologists have monitored changes to both ecosystems, and species. However, it has only been in the last decade that characterising and monitoring genetic diversity has accelerated. Yet, there is an underlying assumption in the broader community that the successes of human genomics in medicine are easily replicated for biodiversity conservation. Sadly, this is not the case. Of the 15,521 animal species listed as threatened by the International Union for the Conservation of Nature (IUCN), less than 2.5% have genomic resources. To combat this, global genome initiatives are generating genomes for all eukaryotic life on earth. Yet a reference genome does not conserve a species – but it allows us to develop a suite of tools to understand both genome-wide and functional diversity within and between species. These tools allow for the integration of genetic diversity into decision-making, providing conservation practitioners and policy makers with the ability to maintain species' adaptive potential. Solutions to closing the space between when genomes are produced, and how the information is used by conservation practitioners are currently in development. In this talk I will use Australian case studies to highlight the benefits of applying genomic research in real-time to management actions, discuss our systematic approach to integrating genomics into biodiversity protection through a large collaboration of different scientific disciplines, government agencies, conservation organisations and 'big tech' companies, and present key knowledge gaps that still exist in the biodiversity genomics/conservation space.
10.40 – 11.00	**Morning Tea followed by two concurrent streams – (1) Genomics & (2) eDNA**

	Genomics (Room 219)	eDNA (Room 218)
11.00 – 11.20	**Anne Muigai**, Chair African Biogenome Project, National Defence University, Kenya *The African Biogenome Project: An African Initiative to conserve and document Africa's biodiversity.* Africa, as a continent, is currently experiencing an unprecedented loss of its biodiversity, partly due to climate change, but mainly due to overexploitation by humans and human activities. The International Union for the Conservation of Nature (IUCN) indicates that over 6,400 animals and 3,100 plants are at risk of extinction. Their surveys have also shown that 39 percent of African vertebrate species have declined over the last 25 years. This data is an indication of the severe biodiversity crisis facing Africa. To mitigate this and document African biodiversity, the African BioGenome Project was instituted to galvanize African scientists, those on the continent and across the globe, to come together and characterize African plants, animals, and microbes. The project aims to coordinate the sequencing of 100,000 indigenous African non-human species with a special focus on species that play significant roles in African communities by providing food, shelter, and medicine, or through the enhancement of cultural experiences of communities. AfricaBP partners and collaborators and African communities across the continent were invited to nominate species for sequencing, from which shortlists of species in various categories were shortlisted. Sequencing efforts are currently underway and a total of nine (9) genomes have been sequenced to completion with more planned for the near future. To ensure the sustainability of the Project, AfricaBP established an institute, the AfricaBP Open Institute for Genomics and Bioinformatics whose main goal is to facilitate knowledge exchange, with a special focus on young and early-career African scientists located on the continent. During this conference, an update on AfricaBPs activities will be provided with the aim of sharing lessons learned and future prospects of the project.	**Mike Bunce**, Chief Science Advisor, Department of Conservation, New Zealand *Why eDNA has a key role to play in protecting nature, keeping score and engaging people.* Environmental DNA (eDNA) has the ability to transform how we monitor and manage both species and the ecosystems they live within. Put simply, eDNA has the ability to change how we listen to the natural world, and 'keep score'. The latter of these is vital as measuring biodiversity and ecological integrity is difficult to do well. Biodiversity measurement is also vital as Australasia explores biodiversity certificates/credits. Within its recent long-term insights briefing the Department of Conservation (DOC) flagged eDNA as a game-changing technology that needed to be interwoven into the biomonitoring toolkit. This presentation will reach into the future and speculate how eDNA technologies and data might be used (and re-used) listen to nature. How we take people on their 'eDNA journey' will likely be a key driver on the integration and acceptance of eDNA as a biomonitoring tool. If, as eDNA researchers, we can make data accessible, collaborate with non-experts, empower tradition owners and partner with industry, I believe we can positively influence environmental stewardship.

11.20 – 11.35	**Peter Dearden**, Director, Genomics Aotearoa, New Zealand *Conservation and biodiversity genomics, a Genomics Aotearoa perspective* Aotearoa-New Zealand is biologically unique. Its high degree of endemicity, and its geography and history, have led to significant challenges for our native taonga (treasured) species. These challenges are increasing with climate change. Genomics can provide data to better understand our unique biology, and inform managers of our conservation species and environments. Genomics Aotearoa has been tasked to develop tools and technologies and build capability in Aotearoa-New Zealand. I will talk about new genomic tools we have generated to support conservation management, new approaches to genome sequencing, and the future of genomic environment monitoring.
	Matthew Barnes, Dept of Natural Resources Management, Texas Tech University, USA *Environmental DNA innovations for conservation* In a little over a decade, eDNA analysis has emerged as a powerful research and management tool, and the innovative spirit which motivated analysis of the first water samples continues to this day. This presentation will propose four themes of research innovation where I think the field has much to gain by focusing our efforts. “Foundation Innovations” relate to the ecology of eDNA, which has been occasionally overlooked during the rapid expansion of the field, even though eDNA itself represents an ecological entity worthy of study in its own right. On the other hand, one of the most consistent forms of eDNA innovation has been the excitement of confronting eDNA methods with new species targets in novel ecosystems, and the advancement of technological and methodological boundaries and the deployment of eDNA methods in novel habitats and with new targets, which I term “Application Innovations.” Comparisons between eDNA and more traditional survey methods have contributed to the quantification of sensitivity and accuracy of eDNA methods. I refer to such comparisons as “Calibration Innovations” and argue that they are critical for placing eDNA analysis within the broader toolbox of biodiversity surveillance methods. Finally, “Interpretation Innovations” push the bounds of what we can learn using eDNA analysis. Overall, prioritizing these four themes of innovation will help researchers identify opportunities for continued eDNA innovation in the future.
11.35 – 11.50	**Sarah Richmond**, General Manager – Science Programs, Bioplatforms Australia *Exploring the genomic frontier: Uniting national expertise to discover, monitor and manage Australia's biodiversity*. Bioplatforms Australia supports Australian life science research through investments in cutting-edge infrastructure and expertise in genomics, proteomics, metabolomics, synthetic biology, and bioinformatics. We organise and deploy these capabilities in national collaborative data initiatives to support innovation and transform scientific outcomes into tangible benefits for Australians. This presentation provides an overview of Bioplatforms Australia, focusing on our role in genomics and our remit to support Australia's national research priorities. The presentation showcases the collaborative model that serves as the foundation of our initiatives and highlights the outcomes of completed and ongoing projects that enhance our understanding and conservation of Australia's unique flora and fauna. We will discuss projects currently in the planning phase and provide insights into our future strategy, emphasising our ongoing dedication to advancing genomics research and its application in addressing critical challenges for Australia's biodiversity.

	Toshifumi Minamoto, Graduate School of Human Development & Environment, Kobe University, Japan *Development of eDNA research in Japan and its application to environmental studies.* Japanese researchers have been working on eDNA research in macroorganisms from a relatively early stage. In 2018, they began efforts to implement such advanced technologies in society by establishing the eDNA Society, which includes members not only from academia, but also from government and the private sector. The eDNA Society has promoted the standardization of the technology by publishing standard technical manuals in Japanese and English. In addition, a roundtable discussion was held among relevant ministries and agencies to ensure comparability of results even among surveys conducted by different agencies. The eDNA method has been piloted in Japan's largest wildlife survey, the National Census on River Environment, and will be fully implemented in the near future. In this talk, I would like to review the history of the development and social implementation of eDNA methods in Japan, and discuss issues for future development.
11.50 – 12.05	**Rahul Rane**, Senior Research Consultant Applied Genomics, CSIRO *Democratising Genomics for decision making: a national science agency perspective*. Genomics is rapidly becoming commoditised and transforming the way we manage ecosystems. CSIRO routinely leverages cutting-edge 'omics technologies to drive biodiversity management and decision-making in collaboration with public/private partners. Our biodiversity related work genomics work is focused on: Conservation genomics: using genomics/multi-omics to understand the genetic diversity and distribution of Australian organisms, and to identify genes critical for adaptation and resilience. Environmental genomics: using genomics to study/develop ways to understand, monitor and manage the impact of environmental change on organisms. Biosecurity/Agri-genomics: using distribution, diversity and trait-based whole genome sequencing to inform real-time decisions for pest/disease management. Our state-of-the-art genomics infrastructure (facilities and compute) enables enterprise grade automation of software tools for analysing genomic data. These analysis platforms have also significantly reduced the cost and time for generating reference genomic datasets from biodiversity specimens. CSIRO is also committed to working with other organizations to maximize the impact of our genomics research. We partner globally with universities, research institutions, and government agencies, allowing shared expertise, resources, and data, progressively moving towards FAIR collaborations. Recent biosecurity case studies demonstrate how CSIRO in partnership with multiple governments, companies, and industry bodies, used genomics to demonstrate pest/disease trait incursion pathways and genetic diversity impacts management strategies. Automation workflows enabled at-scale delivery, reducing the time required from study inception to project outcome. This process improved government and industry decision making in Australia and neighbouring countries. These partnerships will enable wider adoption of genomic technology and more broadly revolutionise conservation management.

	Shannon Corrigan, Vertebrate Genomics Research Officer, Minderoo Foundation *Oceanomics: Bolstering marine research and conservation with genomic technologies* The ocean covers around 71% of Earth’s surface and supports 90% of its biosphere. Despite being the largest and most exploited realm on our planet, more than 80% of the ocean is unmapped, unexplored, and unobserved. The OceanOmics program at the Minderoo Foundation set out to revolutionise how we observe, measure, and understand life in our ocean. We are working with globally renowned scientists and industry partners to innovate eDNA-based marine genomics technologies to transform how we collect biodiversity data across dynamic space and time. This involves optimisation and scaling of eDNA collection, processing, and characterisation, including the development of novel approaches for species and individual detection and quantification. To enable ocean-scale eDNA-based biodiversity surveys, OceanOmics is committed to generating and openly publishing reference genomic resources for thousands of species of marine vertebrates, as well as developing computational tools for marine sequencing data based on standardised, reproducible processes and artificial intelligence. We have demonstrated the scalability of eDNA technologies by deployment from our shipboard sequencing laboratory in multiple research expeditions across Australia. We develop these marine genomics tools, and generate large-scale marine vertebrate biodiversity baselines as powerful assets to facilitate rapid, accurate and large-scale generation of biodiversity data and ultimately accelerate ocean conservation efforts that can halt biodiversity loss.
12.05 – 12.20	**Ary Hoffmann**, Chair of Ecological Genetics, University of Melbourne, Australia *Applications from genomic studies of local and invasive mosquitoes*. Mosquitoes that transmit diseases but are absent from much of Australia are being detected at airports and ports. At the same time, native mosquitoes are being increasingly implicated in the spread of diseases even though they also constitute important biodiversity values. To reduce incursions of invasive into Australia (and within Australia once they arrive), we need to understand where they are coming from so that control strategies can be implemented at the source. To establish the risk of disease spread by native mosquitoes and how to suppress them, we need to understand their patterns of connectedness and movement so that local control programs can be implemented. In this talk I explain why genomic tools provide answers to these important issues. We used collections of Aedes mosquitoes from various countries and isolated areas in Australia and sequenced genomes to identify thousands of genetic markers for invasive and native species. These markers provided a “fingerprint” representing an unambiguous signature of the origin of the mosquitoes detected as incursions at ports, airports and in isolated areas within the mainland. They were also used to establish pathways of local incursions within Australia. The same tools provided information on movement patterns of native mosquitoes which in turn sets boundaries for local mosquito control.

	Gert-Jan Jeunen, Senior Research Fellow, University of Otago, New Zealand *From genomes to identifications: enhancing antarctic eDNA surveys with curated reference databases.* Environmental DNA surveys have transformed our ability to monitor the natural world, enabling species identification by matching DNA sequences obtained from environmental samples to reference barcodes. However, incomplete genomic reference databases hinder the effectiveness of eDNA surveys within a biodiversity conservation context. Here, we discuss how highly-curated genomic reference databases underpin eDNA surveys to aid conservation efforts in Antarctica. Antarctic fish reference databases for multiple molecular markers were generated using CRABS, while optimusPrimer facilitated appropriate assay choice by comparing databases from different molecular markers through barcode gap analysis, taxonomic resolution, amplification efficiency, and potential for co-amplification of non-target taxa. These highly-curated reference databases enabled eDNA surveys, obtained from marine sponge specimens caught as bycatch, to identify all fish species caught onboard Antarctic toothfish fishing vessels, as well as estimate fish community composition on a regional scale (R2 = 0.9575), and predict catch abundance on a specific fishing line for demersal fishes (R2 = 0.8302). These results provide evidence for the potential of eDNA surveys to aid fisheries management. The curated reference database was also employed to investigate dietary preferences between Adélie penguin (Pygoscelis adeliae) populations. Metabarcoding from guano DNA extracts revealed significant phylodiversity differences between populations, potentially affected by the geographical location of the colony with distance to the open ocean. Additionally, metabarcoding revealed, for the first time, crocodile icefishes (Channichthyidae) to be an important food source for the Cape Bird colony. These findings show the importance of metabarcoding to aid in the conservation of this iconic species.
12.20 – 1.00	**LUNCH**

1.00 – 1.15	**Parwinder Kaur**, Director, DNA Zoo Australia, University of Western Australia, Australia *West Australian Genome Atlas: Building a data legacy for future!* Australia was once part of the ancient continent Gondwana, which began to break up more than 154 million years ago. The region that supports the Southwest’s unique wildlife formed when India broke away from the supercontinent around 120 million years ago. While there are some young sand dunes, much of the southwest has been geologically undisturbed for tens of millions of years. Southwest Australia, also known as the Kwongan, is home to 10% of world’s biodiversity and some of Australia’s most iconic species. Western Australia’s unique biodiversity will shortly be much better understood thanks to this seed funding support by Lotterywest, advanced research and high-performance computing infrastructures. WA Genome Atlas initiative is sequencing genomes for over a 100 WA endemic species including fauna and flora which will allow us to monitor and support endangered species, discover evolutionary patterns, understand zoonosis better preparing for future pandemic situations, enhance agriculture and food security, bioprospecting for new drugs and vaccines, and intervene against highly significant but neglected disease-agents. WA Genome Atlas initiative is delivering a coordinated, higher-level management with a strategic scientific workflow and platform capacity towards WA’s vision for a world leading approach to species conservation and development. WA with its 8 out 15 Australian biodiversity hotspots, can now begin to focus on the existing data gaps and managing what we will soon be able to understand at the fundamental DNA level and measure. It heralds a new opportunity for fundamental science as well as policymaking aimed at improving human lives and the environment.
	Dianne Gleeson, Director, National eDNA Reference Centre, University of Canberra, Australia *Ensuring eDNA applications are fit-for-purpose through a national collaborative network in Australia.* The use of eDNA in general as a tool for species detection, biomonitoring and surveillance has been extremely rapid in recent times and often demonstrates greater sensitivity than traditional methods and with greater efficiency. The promise of eDNA is vast with many publications extolling the virtues of these approaches and advocating strongly for eDNA as a revolutionary approach for practitioners. The Australian Federal Government has established the National eDNA Reference Centre (NRC) in order to sustain national eDNA testing capability, capacity and competency under the National eDNA Testing program primarily in response to increased biosecurity threats. The NRC has responsibility to establish and administer a network of Australian State and Territory-based eDNA Collaboration Centres across the private/public laboratory sectors. A key component has been the accreditation of the NRC in accordance to a newly developed Schedule by the National Association of Testing Authorities for Laboratories conducting sampling and/or testing of DNA/RNA from environmental samples. The NRC is also the facility that provides operational support including implementation, training, sampling, testing and undertakes confirmatory testing through an Environmental DNA Proficiency Testing Scheme. All of these functions require underpinning genomic information that can ensure the best practise in assay design and data interpretation. Examples from the NRC’s work in biosecurity will be discussed that highlights this capacity need.

1.15 – 1.30	**Kris Helgen**, Chief Scientist & Director of the Australian Museum Research Institute, Australia *Biodiversity Genomics and the Indispensability of Natural History Museums*
	Manpreet Dhami, Senior Researcher Manaaki Whenua-Landcare Research, New Zealand *Te huinga ira taketake o Aotearoa – making the case for a te-tiriti guided reference barcode database for Aotearoa's biodiversity.* With increasing threats to biodiversity, the need for rapid and scalable biomonitoring approaches has grown dramatically. Often these approaches are based on environmental DNA and require a reference database for accurate and reliable species identification. Reference databases thus underpin a diversity of uses and decision-making, such as biomonitoring, biosecurity surveillance, and species conservation. In Aotearoa, approximately 22,000 species of invertebrates reportedly 'present' in the GBIF database do not currently have a corresponding barcode sequence, increasing the likelihood of misidentification. We address this by developing a case for a national repository for barcode sequences that will fill this gap. In the context of Aotearoa, such a collection of sequence data requires a framework that gives effect to te-tiriti (Treaty of Waitangi) - Aotearoa's founding treaty that enshrines the rights and sovereignty of the indigenous Māori peoples. I will describe our approach in applying te-tiriti guiding principles, inviting expert testimony and community aspirations in helping develop a best practice framework for the generation of a reference database for barcode sequences representing Aotearoa's biodiversity.
1.30 – 1.45	**David Cantrill**, Executive Director Science, Royal Botanic Gardens Victoria, Australia *Genomics do Australian plants: Towards national plant biodiversity genomic infrastructure* With an estimated 75% of the Australian biota yet to be described, genomic infrastructure and tools are playing an increasingly important role in describing and naming species. Techniques such as bait capture are providing improved data sets that contain fewer missing data and should lead to more robust analysis. Bait sets like the Angiosperm353 bait kit are proving useful for testing and refining predictive classification systems and long term may offer robust molecular tools for identification with implications for biosecurity detections. To date we have built a tree of life for the flowering plant flora of Australia with 92% coverage of the 2,100 known genera. However, the kit this is based on has variable recovery across the tree of life, resulting in a need for reference genomes to help improve recovery through redesigned baits. Our approach, to assemble reference genomes based on living collections means the individuals sequenced are available for further analysis if new research questions arise, providing scope for further building on the genomic resources created. The reference genomes assembled to date are from identified gaps in sequence representation in the flora. These genome are starting to reveal new insights, such as expanded gene families that may help us understand historical diversity patterns and niche partitioning. The GAP program has also had a focus on using genomics data to inform resolution of taxonomic boundaries within species complexes so that species of conservation concern can be better defined, allowing more focused conservation and management actions.

	Jenny Giles, Director, National Biodiversity Library, CSIRO, Australia *An authoritative DNA reference library for Australia's species.* Reliable and comprehensive DNA reference data are a fundamental requirement for accurate molecular species identification and the success of eDNA metabarcoding analyses. Australia's National Biodiversity DNA Library (NBDL) is a CSIRO-led multi-partner initiative to provide comprehensive DNA reference sequences for all named Australian species of animals, plants, and macroalgae, derived from expertly identified specimens held in permanent research collections. Starting with marine taxa, the NBDL is working in targeted campaigns to generate authoritative sequence data for taxonomic identification and make these data publicly available through a dedicated data and analysis portal. CSIRO has developed a cost-effective highly miniaturised genome-skimming technology ideally suited to collection specimens to complete this library. Within Australia, we are working in partnership with philanthropic and research organisations, Australian collections, state and federal governments, and with the guidance of taxon experts and the end-user community. We are also working to identify how the NBDL can be most interoperable with similar regional and global efforts, and most effectively extend its utility for users outside Australia.
1.45 – 2.00	**Jon Daly**, University of New South Wales and Scientific Associate at Taronga Zoo *Cryopreservation and biobanking of living cells and tissues to secure biodiversity* The world is facing a biodiversity crisis caused by human impacts on the natural environment including pollution, deforestation, and climate change. While addressing these global issues will be crucial to long term species and ecosystem recovery, in the short term it is essential that we are securing as much of the current biodiversity as possible and supporting population resilience while diverse populations still exist. One of the most effective methods to secure biodiversity is the storage of cryopreserved genetic material at ultra-low temperatures in biorepositories, which can maintain living cells, tissues, and germplasm in a frozen state indefinitely. In concert with genomic analyses and reproductive technologies such as IVF or artificial insemination, strategic biobanking of living cells and tissues from healthy populations provides support for a range of recovery initiatives with ex situ and in situ management actions. Through local and international partnerships, Taronga is using this integrated approach to support a number of strategic programs, including regional management of zoo-based rhino populations, breed-for-release programs for threatened frogs, and large-scale coral reef recovery through the nationally-operated Reef Restoration and Adaptation Program. Effectiveness of these and other species and ecosystem recovery programs continues to depend on multidisciplinary partnerships among conservation practitioners and researchers within and outside of government, and with the community, including First Nations Peoples.

Antonette Walford, Senior Project Officer, Chief Plant Health Officer Unit, Agriculture Victoria; Department of Energy, Environment and Climate Action, Melbourne, Australia
Environmental DNA based detection complements biosecurity monitoring and surveillance to enhance early detection.

Environmental DNA (eDNA) is a fast-growing, innovative field that has moved to scientific integration into monitoring projects globally in the last 10 years. It is used worldwide in numerous projects across multiple applications to provide valuable information in both environmental monitoring and human and animal health. eDNA is used alongside traditional methods as a surveillance tool for marine pest surveillance in Australia and in New Zealand; human wastewater surveillance for infectious diseases and exotic snail biocontrol monitoring in broadacre crops in Australia. Most recently, eDNA detection is being tested for use in border biosecurity as a surveillance tool for exotic pest detection in shipping containers. This project has some exciting results and shows promise for future use in biosecurity more broadly. This project includes the recognition of the National eDNA Reference Centre in Canberra as Australia's leading institution of eDNA tests and standards. eDNA can provide a complimentary tool to existing surveillance methods to provide early detection of exotic pests and diseases. To enable implementation, definitions, standardisation, accepted technology, national assays and sampling validation and usage guidelines for eDNA are needed. This process has begun through initiatives such as the Southern eDNA Society (Australia and New Zealand). Clarification on appropriate application of eDNA in biosecurity settings is needed, including triggers, responses, and the implications of a positive result. Within government, the development of a framework and policies to support eDNA application is essential to enable use as an early warning system that can enhance and strengthen existing biosecurity monitoring.

LIGHTNING TALKS

2.00 – 2.30

Lightning Talks (Genomics, Room 219)

Robert Henry, Queensland Alliance for Agriculture and Food Innovation, UQ
Genomics of Australian crop wild relatives, a key resource for global food security

Australia is home to a significant proportion of global plant diversity including the wild relatives of many crop species. These genetic resources include important relatives of rice, sorghum, millet, banana, citrus, soybean, mung bean and macadamia. Genome sequencing of Australian crop wild relatives will guide improved conservation both in situ (in poorly know wild populations) and ex situ (in Australian and global seed banks). Reference genomes and re-sequencing of diversity are needed. These resources will unpin the adaptation of crop production to climate change in Australia and globally. Opportunities for de novo domestication using gene editing techniques will also be revealed.

Joanna Sumner, Museums Victoria Research Institute
Freezing cells to preserve biodiversity

Museums have long been repositories of the biodiversity, but Museums Victoria aims to preserve genetic diversity in viable living cells in our BioBank. In the last we developed a cell lab, growing fibroblasts for 5 mammal, 2 lizard and 1 bird species, storing those living cells in our cryotanks, and sending DNA from cells for whole genome sequencing. We plan to expand facilities to work with a greater diversity of fauna. These living cells will be available for future research; creating pluripotent stems cells and gametes that can return genetic diversity to wild populations.

Luciano Beheregaray, College of Science and Engineering, Flinders University
Genetic rescue of one of Australia's forgotten fish: the Yarra pygmy perch

Globally, freshwater fishes (FWF) are declining at twice the rate of other vertebrates. In contrast to successes of genetic-based captive breeding and reintroductions of small-bodied FWF, the Murray-Darling Basin ESU of Yarra pygmy perch (YPP) responded poorly to reintroductions and is now extinct in the wild. YPP shows higher inbreeding and lower genomic variation than other FWF. Successful hybridisation with a genetically diverse coastal ESU of YPP has been achieved in captivity. Genomic funding for this genetic rescue initiative would benefit the often neglected group of FWF by demonstrating the value of monitoring inbreeding and evolutionary potential in conservation reintroductions.

Soleille Miller, School of Biological, Earth and Environmental Sciences, UNSW
"Branching Out: Using Population Genomics to Enhance our Understanding of Biodiversity in Australia's Stick Insects"

Phasmids are a criminally understudied yet ecologically important clade with incredible morphological and reproductive diversity. I've found striking population genomic patterns in the natural range of a single phasmid species. I propose to sequence individuals from additional Australian species in both disturbed and undisturbed habitats for population genomic analyses. This will inform management by identifying new or cryptic species, quantifying genetic diversity, and understanding population dynamics under various anthropomorphic stressors. It will also underpin future projects on fundamental questions about the evolution and maintenance of sex in nature and capture some of the invaluable biodiversity of terrestrial invertebrates in Australia.

Luis Mijangos, Centre for Conservation Ecology and Genomics, University of Canberra
Bringing Genomics to the People with the dartR Platform

DNA is the original big data. It encodes all kinds of information that is useful for medicine, agriculture, and environmental management. Our challenge is to collect this information and make sense of it. The first part of this challenge is now within reach, with new technologies providing access to vast DNA sequence resources. But capitalising on this rich and much-needed source of information usually requires deep theoretical understanding, considerable computer resources, and strong programming skills. This represents a significant barrier for many people. We have designed the dartR platform to solve this challenge.

Gunjan Pandey, CSIRO Environment
Applied Genomics Initiative (AGI) – Helping scientists USE genomics and not always DO genomics

Today's research community faces a pressing need to utilize genomics, surpassing its capacity to assemble reference genomes and datasets. In CSIRO's Applied Genomics Initiative, we have successfully integrated advanced computational approaches and streamlined fully automatic high-throughput workflows, supported by hardware and software optimizations. This has enabled us the generate hundreds of diversity data assets and genomes in last 18 months. With additional funding, we would enhance multi-omics scalability, introduce advanced automation, develop sustainable computational algorithms, and integrate machine learning techniques. These advancements would empower non-expert users, drive further research, contribute to genomics advancements, and democratize access to genomics.

Mike Gardner, Lab of Evolutionary Genetics & Sociality, Flinders University
Lizards moving south – do they have the genetic variation to cope?

Pygmy bluetongues are an endangered lizard species on Australia’s 110 priority list. Currently they exist in small highly fragmented habitat and are threatened by climate change. We have preliminary work showing genes up and down regulated during the hot summer vs cooler wet spring from one demographic population. The next step would be to examine geographic variation in both gene expression and genomic variation to understand how the variation at important genes regulating adaptation to climate is distributed in the fragmented populations. These data will inform management of the species but understanding those current populations most of risk due to limited variation at these important genes, as well as providing valuable data for future planned translocations.

Alexandra Pavlova, School of Biological Sciences, Monash University
Establishing a hub for wildlife genetic management

There is growing appreciation that managing genetic variation of wildlife can help it thrive. Recent estimates suggest that over 1.4 million of threatened species may benefit from genetic management. The Wildlife Genetic Management Hub will work directly with wildlife managers to improve the health and resilience of wildlife populations. By considering genetics, we will develop effective management solutions that save time and money. We are seeking funding to support research staff of the Hub, which will make rapid genetic management advice affordable to conservation managers. The Hub is expected to improve population health of many threatened species and systems.

Lightning Talks (eDNA, Room 218)

Alexander Piper, Agriculture Victoria Research
Detecting the unexpected: Leveraging DNA Metabarcoding and Biodiversity Genomics for Biosecurity Surveillance.

Invasive insect pests present a growing threat to agriculture and the environment; however the scale and impact of new introductions can be underestimated by traditional biosecurity surveillance which often targets a limited number of priority pests. DNA metabarcoding has potential to address this gap, enabling the simultaneous detection of target pests, endemic species, and unanticipated invaders. However, achieving comprehensive insect surveillance using metabarcoding first requires coordinated efforts to document and sequence endemic biodiversity, providing a baseline for comparison. Implementing agroecosystem metabarcoding alongside biodiversity genomics initiatives has transformative potential for biosecurity surveillance and mitigating the risks posed by invasive insects.

Bill Sherwin, School of Biological, Earth & Environmental Sciences, UNSW
Molecules can improve biodiversity estimates

Biodiversity measures include: counts of numbers of species (or genera or genotypes) present; and Simpson/heterozygosity. However these perform poorly, because counts have huge error-ranges (confidence limits), and Simpson-het only measures highly abundant species or genes. Unfortunately, many surveys use these methods, eg eDNA species-counts. Alternative biodiversity measures minimizing both problems (eg Shannon) require abundance data, which are challenging to obtain. Available genetically-based abundance estimates can therefore help all types of biodiversity surveys, including eDNA surveys. We should actively investigate combining these abundance estimates into all biodiversity surveys.

Margaret Byrne, WA Department of Biodiversity, Conservation and Attractions
Genomics for conservation and management

Genomics is fundamental for conservation and management of Australia’s diverse plants and animals and its complex ecosystems. Work in Western Australia has demonstrated how population genomics is integral to management strategies and conservation decisions for threatened species, forest management, ecological impact assessment, climate adaptation and invasive species. Application of eDNA to ecosystem assessment and monitoring is providing advanced approaches to detecting early ecosystem change in relation to anthropogenic and climate impacts. Greater capacity to implement population genomics and eDNA applications through increased sequencing support and technological advances will provide enormous benefits through informed and effective conservation and management strategies.

Steve Cooper, South Australian Museum & University of Adelaide
The importance of genomic tools for monitoring groundwater ecosystems

Subterranean environments, such as alluvial and karst aquifers, provide crucial water resources for human consumption, agriculture, and industry, but also host highly diverse ecosystems, comprising unique species of subterranean animals, that have only recently been studied. These ecosystems are threatened by over-exploitation of the groundwater and future climatic changes, and there is an urgent need to develop genomic tools for monitoring these environmental impacts. Our team has shown the efficacy of environmental DNA metabarcoding for detecting the presence or absence of groundwater animals, but wish to develop metagenomic tools to enable the estimation of species abundance and changes to ecosystems over time.

Bruce Deagle, CSIRO Australian National Fish Collection, Hobart
A National Approach to Marine Biomonitoring with Environmental DNA (eDNA)

Environmental DNA offers an efficient way to measure biodiversity across the tree of life and is rapidly being adopted to monitor state and change in marine environments. One of eDNA’s advantages is that it allows creation of large and interoperable datasets. We present progress and a vision to monitor Australia’s coastal and blue water marine environments. The initial focus is on IMOS National Reference Stations and sampling from research vessels such as the RV Investigator. Development of efficient sampling protocols, standardised methodologies, and an inclusive nationally coordinated approach to biomonitoring will significantly improve the evidence-base for decision making in Australia’s marine environment.

Tahlia Perry, School of Biological Sciences, University of Adelaide
EchidnaCSI: where people + poo = a powerful wildlife monitoring approach

Innovative and large-scale approaches are required to make significant impacts towards the biodiversity crisis and citizen science is an under-valued method in genomics to achieve this. With EchidnaCSI, a nation-wide project, we demonstrate how more than 15,000 members of the general public have contributed to the largest faecal material collection for a highly cryptic species, the short-beaked echidna. We have used these scats to investigate diet, gut microbiome, health, and population structure. This is a method that can be replicated across many species of interest, whilst providing an avenue for the public to learn about, care for, and help our incredible wildlife.

Dawn Lewis Woolwonga, Australian Centre for Ancient DNA, University of Adelaide
The limitations and potential of sedimentary ancient DNA analysis in Indigenous Australia

Environmental ancient DNA and associated cutting-edge environmental research offer a view into the pre-European invasion Australian environment. The analysis of ancient sedimentary DNA fragments can provide evidence about changes in flora, fauna and microbiomes caused by environmental fluctuations and/or anthropogenic influence. Unfortunately, the Australian continent is largely under-represented in genomic databases and so informative species may not be identifiable. Therefore, investing in Australian reference genomes across the tree of life will be one step to enable the reclamation of Traditional Knowledge and land practices through Indigenous-led investigation of Indigenous Land history.

	Vilma Pérez Godoy, Australian Centre for Ancient DNA, University of Adelaide *Fire's Microbial Legacy: Unveiling Soil Microbiome Responses Across Time Scales* Soil microorganisms are vital for post-fire ecosystem recovery, but their responses to fire across different time scales relevant to ecosystem recovery (days to millennia) remain unclear. This research aims to reconstruct the genomic responses of soil microbiomes to fire, including community composition, function, and adaptation, over these time scales through the integration of modern and ancient environmental DNA analysis. Expected outcomes include significant advancements in knowledge regarding the ecological and evolutionary responses of natural microbial communities to fire. Ultimately, these outcomes will contribute to improving predictions of the impacts of changes in fire regimes on global biodiversity.
2.30 – 3.00	**Afternoon Tea**
3.00 – 4.30	**Discussion – National Biodiversity Genomics Strategy for Australia**

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