Two Jump Start Project for the Global Ecosystem Assessment Initiative (GEAI)

There is a growing effort at local, regional, State and Federal levels to address the challenges facing Australia's biodiversity through improvements in conservation and stewardship. However, governments and an emerging philanthropic sector have all found it hard to target their interventions because of a lack of real-time indicators of biodiversity status and trends. Urgent action is needed to accelerate the scale and depth at which biodiversity assessments can be conducted, as well as the analysis, synthesis and modelling of data needed to better understand the structure-function and threat-response relationships in our ecosystems, assess the relative merits of different interventions, and improve on them. The emergence of high throughput DNA seqencing technologies provides an opportunity for an unprecedented scale and depth of analyses of diversity, pattern and process. We can move from small-scale, somewhat siloed studies towards a greater integration of knowledge and understanding across landscapes. This fusion of expertise in ecology, taxonomy, and systematics, with genomics, bioinformatics, and imaging tools and techniques, has led to the creation of the term "ecogenomics". Ecogenomics is viewed as a means to better quantify and predict the impacts from current and future environmental drivers at population, species, community and ecosystem scales across landscapes.

Two "jump start projects" were initiated with **SIEF** funding to serve as the scientific foundations of the **Global Ecosystem Assessment Initiative (GEAI)**. The overarching objective for GEAI is to produce a suite of innovative tools and approaches in ecogenomics that can be employed to improve environmental decision-making in Australia and internationally; thereby positioning Australian scientists as global leaders in biodiversity science and policy making.

The First Jump Start Project: DNA sequencing

The first "jump start" project was designed to develop approaches based on DNA sequencing of samples that can improve the efficiency of environmental impact assessment (EIA) for resource projects in Australia. Industry has demonstrated a willingness to conduct intensive biological surveys of prospective sites – but the distribution and abundance of the invertebrate species identified in the EIA surveys are often unknown, making it difficult to assess impacts in the context of biodiversity conservation. A goal of this first project was to rapidly examine how insect species identified by DNA "barcodes" varied in their abundance and distribution across a landscape known to possess biodiversity values. The project focused on patches of rainforest, or vine thickets, in the coastal Kimberley region of Western Australia for two reasons:

(1) The flora and vertebrate fauna in these rainforest pockets have already been well-characterised in previous surveys, and

(2) as isolated patches of rainforest spread across a large distance and a rainfall gradient, the composition of insect species was expected to vary between the rainforest patches.

Sampling was conducted in collaboration with Wunambal Gaambera and Dambimangari landholders during January 2013. A total of 36 rainforest patches were accessed by helicopter, with four sites (two rainforest, one edge, one savannah) sampled per patch. Over a half million invertebrate specimens were collected using various sampling techniques. Half of the samples were targeted for DNA sequencing, while the other half were designated for standard morphological taxonomy. The 288 taxonomic subsamples, containing over 180,000 specimens, were first taxonomically sorted to Order or Family, and were then sent to international experts to determine the number and identify of

species present – and thereby construct a set of material identified using traditional methods against which the DNA results could be compared.

Two samples from each of 24 sites have been analysed using DNA sequencing. Much of the research effort in the project has been focused on developing effective methods of analysis of the resulting DNA sequence data, because standard methods would take months to analyse the DNA sequence data from just one sample. A new measure of biodiversity has also been developed specifically to analyse the novel data emerging from this project.   This new biodiversity measure has been applied to the data from the Kimberley for samples to examine how invertebrate biodiversity is distributed among these rainforest patches. Unique biodiversity values associated with individual sites are being identified, and the existing dataset will form the basis for future studies aiming to determine what environmental factors affect the distribution of invertebrate communities. Discussions have been initiated with the mining industry in Western Australia to apply the methods developed in this project to biodiversity assessments required for new resource projects.

The Second Jump Start Project: BASE

The second "jump start" project, entitled Biomes of Australian Soil Environments (BASE), is a collaborative effort to investigate and build a database that stores all the available information on microbial diversity in Australian soils. The organisms that live in soil are the main drivers of ecosystem function, largely by providing the nutrients that feed plants, animals and humans. As such, soil is not merely a passive player; it hosts communities of microbes (bacteria and fungi) that drive ecological processes, as well as acting as symbionts and pathogens of many plant species.

BASE targets all three domains of life, and provides information about soil bacterial and fungal communities. In this SIEF project, DNA sequence data was generated from all the microorganisms in the soil collected across a range of different sites in order to create a reference map of Australia's soil microbial biodiversity. This DNA sequence data is complemented in the BASE database with geo-referenced data on the climate, the flora, and the physical properties of the soil. The first data collected and entered into BASE came from Australia's national park system, some of the most pristine ecosystems in Australia and therefore providing the best indication of Australian soil microbial diversity in its most natural state. This information is being used to investigate what environmental variables are the best indicators of soil microbial diversity, in order to help us better assess the potential impacts of future land-use and climate change on soil microbial services. The datasets are being made publicly available so that the information in BASE can be linked with other measurements and data such as overland surveys, meteorological data and geological information to enhance the ecological knowledge of the Australian continent and contribute to land management strategies.

The framework dataset will be also be fully compatible with current global efforts to provide soil microbial diversity information (e.g., the Earth Microbiome Project).