MDBfutures CRN
Biodiversity Project

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Biodiversity and Conservation

1. Biodiversity and bioregionalization of the MDB

2. Species distribution modelling

3. Genetic population structure

Top-Down study patterns of biodiversity

Bottom-Up study processes that affect biodiversity

Management recommendations
Sub-projects

Species Distribution Modelling (Bernd Gruber)

Bioregionalization of the MDB (Carlos E. González-Orozco)

Genetic population structure (Peter Unmack)

Ramsar Wetlands (Max Finlayson)
One of the main pitfalls in Biodiversity

Biodiversity isn’t just species

• Biodiversity is the *whole tree of life*, not just the named species
• There are clades smaller and larger than the traditional species level
• Species are not comparable between lineages in any manner, just an arbitrary cut-off somewhere along a branch tree of life
Species richness for eucalyptus in the MDB

Number of species per grid cell

31

1
New methods applied to our project

1. Multiple-taxon combinations (Summary maps for raw diversity, clusters of fuzzy logic, combine maps of significance)

2. Categorical Analyses of Neo- and Paleo- Endemism (CANAPE). Developed as part of software Biodiverse

3. CANAPE modelling under future climate change. Developed as part of software Biodiverse
Data Sources

1. Species distributions: Australia’s Virtual Herbarium, historical collections from museums

2. Phylogenies: Different universities, CSIRO

3. Climate change projections: Hadley global climate model (hadcm3) available from http://wallaceinitiative.org/
Multiple taxon combinations: Species richness for all taxon groups

- Acacias
- Eucalypts
- Plant genera
- Tree frogs
- Fishes
Categorical Analysis of Neo and Paleo Endemism (CANAPE)

Paleo-endemism

Wollemi Pine
(200 Mya, Araucariaceae)

Neo-endemism

Darwin’s Finches
(15-20 Mya, Galapagos)
What do we learn from the new methods? CANAPE

Need for hypothesis tests:
raw values do not tell us much, unless we understand how much to expect
Maps of CANAPE for five taxonomic groups in the MDB

<table>
<thead>
<tr>
<th>CANAPE</th>
<th>Acacia</th>
<th>Eucalyptus</th>
<th>Plant genera</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neo</td>
<td>![Map of Acacia Neo]</td>
<td>![Map of Eucalyptus Neo]</td>
<td>![Map of Plant genera Neo]</td>
</tr>
<tr>
<td>Paleo</td>
<td>![Map of Acacia Paleo]</td>
<td>![Map of Eucalyptus Paleo]</td>
<td>![Map of Plant genera Paleo]</td>
</tr>
<tr>
<td>Mixed</td>
<td>![Map of Acacia Mixed]</td>
<td>![Map of Eucalyptus Mixed]</td>
<td>![Map of Plant genera Mixed]</td>
</tr>
<tr>
<td>Super</td>
<td>![Map of Acacia Super]</td>
<td>![Map of Eucalyptus Super]</td>
<td>![Map of Plant genera Super]</td>
</tr>
<tr>
<td>Not sig</td>
<td>![Map of Acacia Not sig]</td>
<td>![Map of Eucalyptus Not sig]</td>
<td>![Map of Plant genera Not sig]</td>
</tr>
<tr>
<td>No data</td>
<td>![Map of Acacia No data]</td>
<td>![Map of Eucalyptus No data]</td>
<td>![Map of Plant genera No data]</td>
</tr>
</tbody>
</table>

No common phylogenetic patterns across the studied taxon groups.

Phylo-bioregions for acacias and eucalyptus in the MDB

“Phylo-Jaccard index express the proportion of lineage diversity that is shared between two set of locations”

Some conservation applications: acacias and eucalyptus in the MDBA as an example

Example of the impact of climate change on phylogenetic diversity of eucalyptus

• Spatial data

• Phylogenetic tree

• Modelling species shifts under current and future scenarios

• Incorporation of phylogenetic approaches under current and future climate change scenarios
Eucalypt species are shifting under climate change by 2085

Phylogenetic diversity of eucalypts on the move

Disappearance of areas with paleo and neo-endemism of eucalypts by 2085 due to climate change

Losses of unique branches from the eucalypt tree under climate change by 2085


Paleo-endemism 2014/2085
Australia

240
(21.7%) 52
4

both loss new
Number of branches present in paleo-endemic grid cells (N= 240)

Eucalyptus (5 sp.)
southwest Western Australia

MDB futures
Collaborative Research Network
Aquatic Biogeography MDB

M. adspersa
Goal

Are there common phylogeographic patterns within MDB aquatic species?
Should we manage parts of MDB separately?
Goal

The MDB is surrounded by more basins (22) than any other in Australia

This provides a convoluted and dynamic biogeographic setting with different fishes having relationships with many surrounding basins.
Outline

• Within basin biogeographic patterns
• Within basin genetic patterns
• Next generation sequence data

G. bispinosus
MDB contains

36 obligate freshwater fishes

3 diadromous fishes

at least 5 estuarine spp
MDB has relatively few narrow range species (9/36)

<table>
<thead>
<tr>
<th>Species</th>
<th># Basins</th>
<th>Basin</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Porochilus rendahli</em></td>
<td>1</td>
<td>Condamine</td>
</tr>
<tr>
<td><em>Galaxias Tantangara</em></td>
<td>1</td>
<td>Murrumbidgee</td>
</tr>
<tr>
<td><em>Galaxias fuscus</em></td>
<td>1</td>
<td>Goulburn</td>
</tr>
<tr>
<td><em>Gadopsis bispinosus II</em></td>
<td>1</td>
<td>Goulburn</td>
</tr>
<tr>
<td><em>Gadopsis marmoratus II</em></td>
<td>1</td>
<td>Wimmera</td>
</tr>
<tr>
<td><em>Nannoperca australis B</em></td>
<td>1</td>
<td>Wimmera</td>
</tr>
<tr>
<td><em>Nannoperca obscura</em></td>
<td>1</td>
<td>Lower Murray tribs</td>
</tr>
<tr>
<td><em>Melanotaenia splendidia</em></td>
<td>2</td>
<td>Warrego-Paroo</td>
</tr>
<tr>
<td><em>Craterocephalus amniculus</em></td>
<td>3</td>
<td>Border, Namoi, Gwydir</td>
</tr>
</tbody>
</table>

15 species are essentially found across most of the MDB (>16/24 sub-basins)
MDB contains 14/36 (39%) endemic fishes

- Maccullochella peelii (22)
- Gadopsis marmoratus I (21)
- Melanotaenia fluviatilis (20)
- Macquaria ambigua (20)
- Galaxias rostratus (12)
- Maccullochella macquariensis (12)
- Macquaria australasica (11)
- Craterocephalus fluviatilis (7)
- Galaxias Riffle (5)
- Gadopsis bispinosus I (5)
- Macquaria ambigua (20)
- Galaxias rostratus (12)
- Maccullochella macquariensis (12)
- Macquaria australasica (11)
- Craterocephalus amniculus (3)
- Galaxias fuscus (1)
- Galaxias Tantangara (1)
- Gadopsis bispinosus II (1)

G. rostratus
MDB UPMGA faunal similarity based on Jaccard’s Index

Murray

Darling

Warrego-Paroo

Wimmera-Avoca

UMU
KIE
OVE
BRO
CAM
LOD
MUR
GOU
MBI
LMU
LAC
MAC
LMT
BOR
GWY
NAM
CAS
MOO
DAR
CON
WAR
PAR
AVO
WIM

Murray-Darling-Warrego-Paroo-Wimmera-Avoca

0.0 0.2 0.4 0.6 0.8
Outline

• Within basin biogeographic patterns

• **Within basin genetic patterns**

• Next generation sequence data
mtDNA Data

Most fishes in the basin have been examined

Most species show low haplotype numbers, diversity and structure (no multiple ESUs identified within MDB)

Some rivers are slightly distinct, especially Warrego-Paroo

Four species show higher within basin differences which should be considered as MUs

- *Craterocephalus amniculus*
- *C. fluviatilis*
- *Nannoperca australis*
- *Gadopsis marmoratus*
Microsatellite Data

Few species examined

Similar to mtDNA, but more resolution

*M. peelii* Lachlan, Macquarie, Gwydir (Rourke et al. 2011)
*M. ambiguа* Macquarie, Paroo (but only slight) (Faulks et al. 2010)
*M. australasica* unclear given massive decline (Faulks et al. 2011)
*N. obscura* no diffs within MDB (Brauer et al. submitted)
*N. australis* most sub-basins distinct (Cole et al. in prep)
*G. marmoratus* most sub-basins distinct (Lean et al. in prep)

Next-gen SNP datasets are now being gathered for several species
Outline

• Within basin biogeographic patterns
• Within basin genetic patterns
• Next generation sequence data
Study Groups

Our genetic work is focused on four taxonomic groups:

- Australian Smelt *Retropinna semoni*
- River turtle *Emydura macquarii*
- River shrimp *Macrobrachium australiense*
- Yabby *Cherax destructor*

All are widespread, lack quirks such as hybridisation or cryptic species
Genetic Methods

Samples preserved in the field in liquid nitrogen

DNA extractions

Diversity Arrays Technology conducts the DNA sequencing using “double-digest restriction-site associated DNA sequencing” or ddRadSeq for short
Genetic Methods

**ddRadSeq**

Genomic DNA is “digested” using two enzymes which cut DNA at specific sites (e.g., AATTCC)

This creates lots of different length fragments

Fragments ~78 base pairs long get saved and sequenced

This produces approximately 2,500,000 reads per sample, or about 20 gigabases of sequence (seven human genomes)

Data is then cleaned up bioinformatically, but is time and computationally intensive

From DNA submission to data is around 3 months
Genetic Methods

DArT produces data file with around 30-40,000 variable loci (locus = unique place within the genome)

Because this data type is new, only a few methods are available

Complicated by the massive size of data files

Bernd is developing new pipeline using R package for analyses
Turtle Genetic Patterns

RAxML, 400 reps
76 otus, 1246416 bp!
1230818 characters are constant
1896 variable characters are pars-uninformative

Pars-informative characters = 13702
Shrimp Genetic Patterns

 MDB - Tooh

 MDB - Ashf

 MDB - Bour

 MDB - Goon

 MDB - Goul

 MDB - Laan

 MDB - Oven

 MDB - Pall

 MDB - Wagg

 MDB - Umur

 MDB - Vyeh

 MDB - Umur

 MDB - Tooh

 MDB - Wilc

 MDB - Wagg

 d = 5
Yabby Genetic Diversity

MDB-Tooh
MDB-Ashf
MDB-Bour
MDB-Goon
MDB-Laan
MDB-Naga
MDB-Oven
MDB-Pall
MDB-Toon
MDB-Umur
MDB-Wagg
MDB-Wilc
MDB-Canb
Yabby Genetic Diversity

Paroo  Sth MDB  Nth MDB
ARC Linkage Grant

Drivers of fine scale genetic spatial structuring in aquatic organisms
Conclusions

MDB, at least for turtles has high levels of genetic diversity

Paroo River consistently sticks out, although possibly for different reasons

Some north-south separation in shrimp and yabby

Severn River tends to stand out as being a little different
Thank You

M. splendida