# Rocking the cradle of life: predicting and responding to climate change threats in Shark Bay microbialites

**Brendan Burns**

**The University of New South Wales**

**Shark Bay Ecosystem Workshop,**
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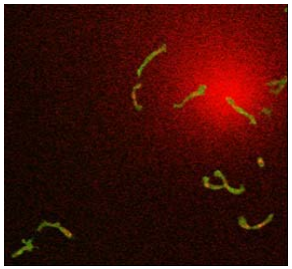
# Our research interests

- Microbial stress response
- Microbial communication
- Human impacts on microbial systems
- Microgravity and human health
- Functional complexity of Early Earth ecosystems



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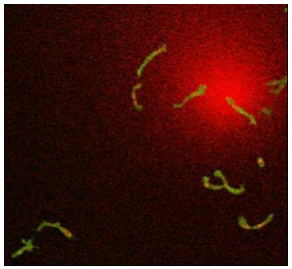
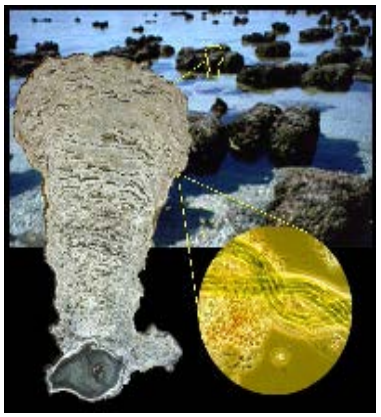
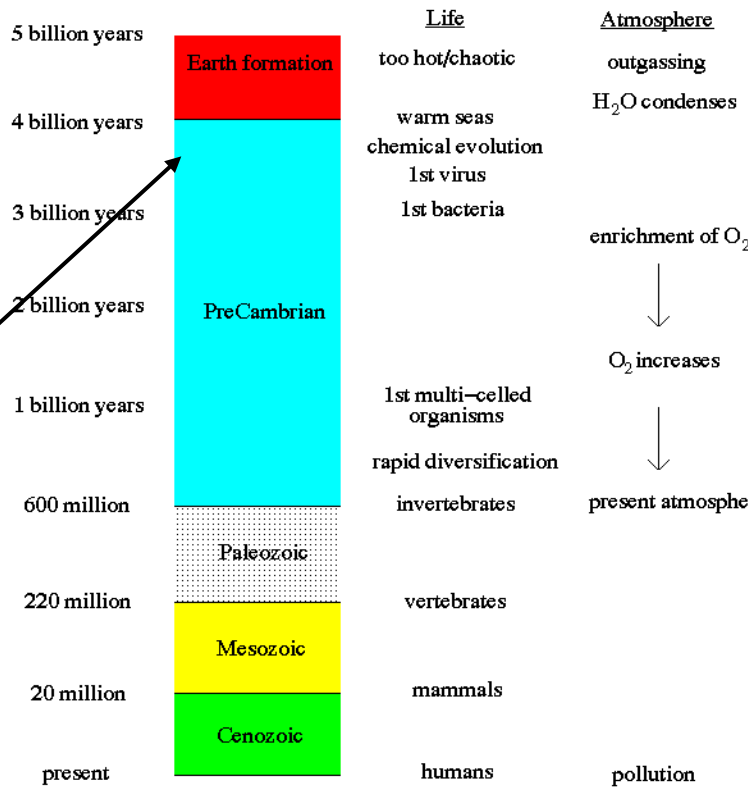


# Microbialites

- Geobiological ecosystems produced by activity of microorganisms
- Present on Earth > 3.5 billion years….
- Linked to oxygenation of early atmosphere
- Fossil microbialites earliest record of life on Earth





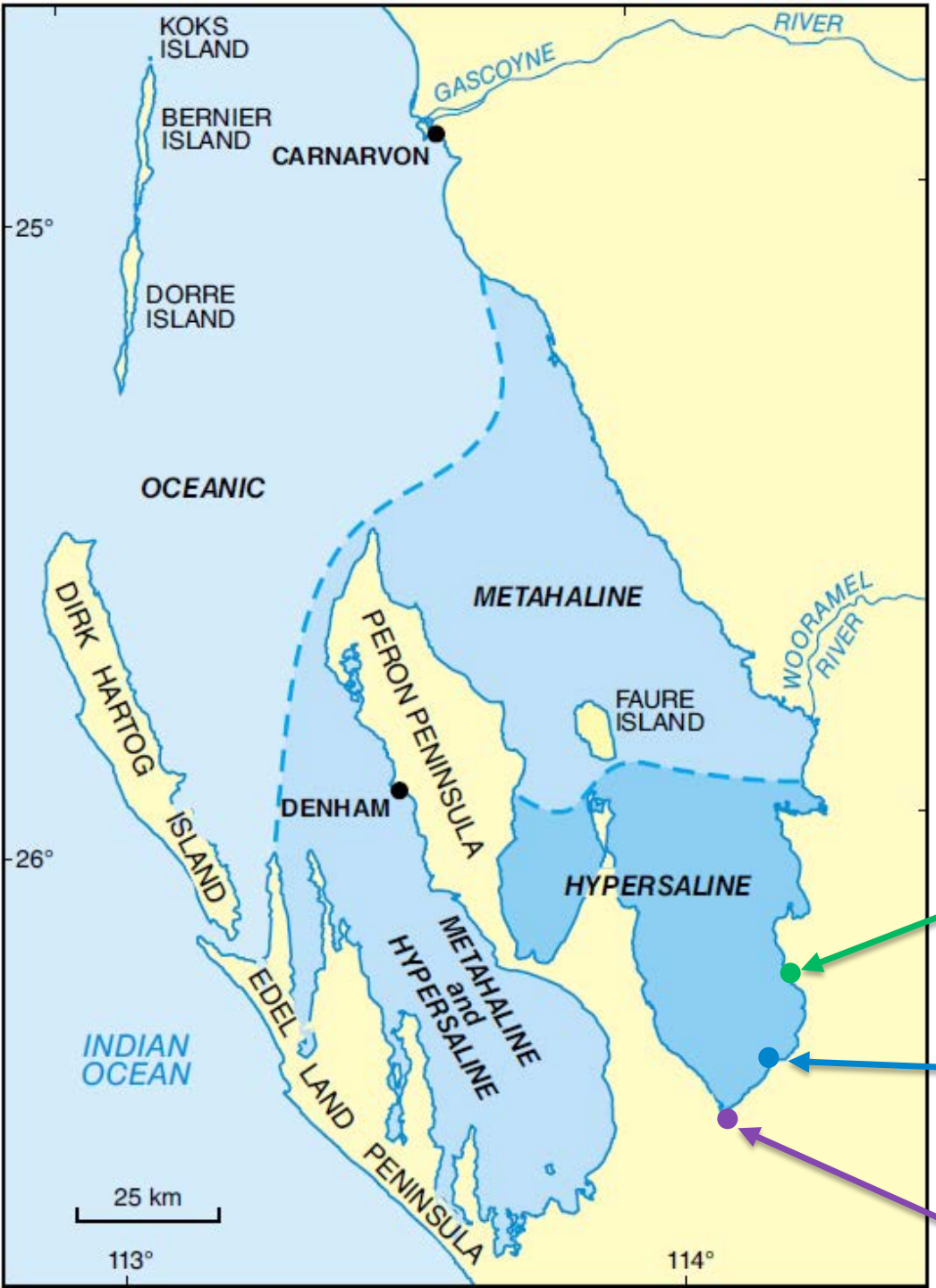
# Shark Bay microbialites

- One of the best examples on earth of living marine stromatolites/microbial mats – very extensive, diverse systems
- Ca. 300 $km^2$ various formations
- Surrounding seawater at least twice as saline as normal seawater (fluctuates); high UV, desiccation
- Higher salinity in early oceans?
- Key to understanding the past

  is to study the present…

# Shark Bay….and me

- Began working in Shark Bay ca. 15 years ago
- Initially with Malcolm Walter, Brett Neilan
- More recently with Pieter Visscher, Therese Morris, Lindsay Collins, Tony Larkum
- My background….microbial physiology, ecology, molecular genetics
- Several ARC grants and numerous publications
- Work on Shark Bay microbialites recognised in 2005 with Eureka prize for Interdisciplinary Research




# Our study area - Hamelin Pool

Carbla Point

Telegraph Station

Nilemah

# Shark Bay microbialites

- Despite their evolutionary significance, little was known about their specific associated microbial communities
- Thought it was mainly cyanos driving these systems
- Enhance our understanding of survival in high salt, UV, temp, dessication
- Exposed to increasing temperatures, rising sea levels, and urban/agricultural development
- Characterising the microorganisms present is intrinsic to microbialite conservation

**Garnaut Climate Change Review**

# Impacts of climate change on Australia's World Heritage properties and their values

Prepared by
Lance Heath, ANU Institute for Environment, The Australian National University

June 2008

"…..Australia's World Heritage property at Shark Bay contain 'outstanding examples representing major stages of earth's history, including the record of life, significant on-going geological processes in the development of landforms, or significant geomorphic or physiographic features….'

….."Shark Bay will face a more immediate threat from further sea level rise causing an increase in flooding of low lying areas."

# Our overarching premise

Microorganisms drive Earth's biogeochemical cycles, and microbialites in Shark Bay are model systems to delineate how essential processes of nutrient cycling and adaptive response are influenced by perturbations in the environment

Focus on drivers of ecosystem function – microbial diversity, adaptation to stress, nutrient cycling, novel pathways and activities

# Established research platform

Analysis of microbial community structure at a discrete millimeter scale in Shark Bay microbial mats

How:

- High throughput sequencing of microbial community DNA
- *in situ* biogeochemical measurements
- Elemental analyses

Facilitates community wide dynamic and predictive modeling

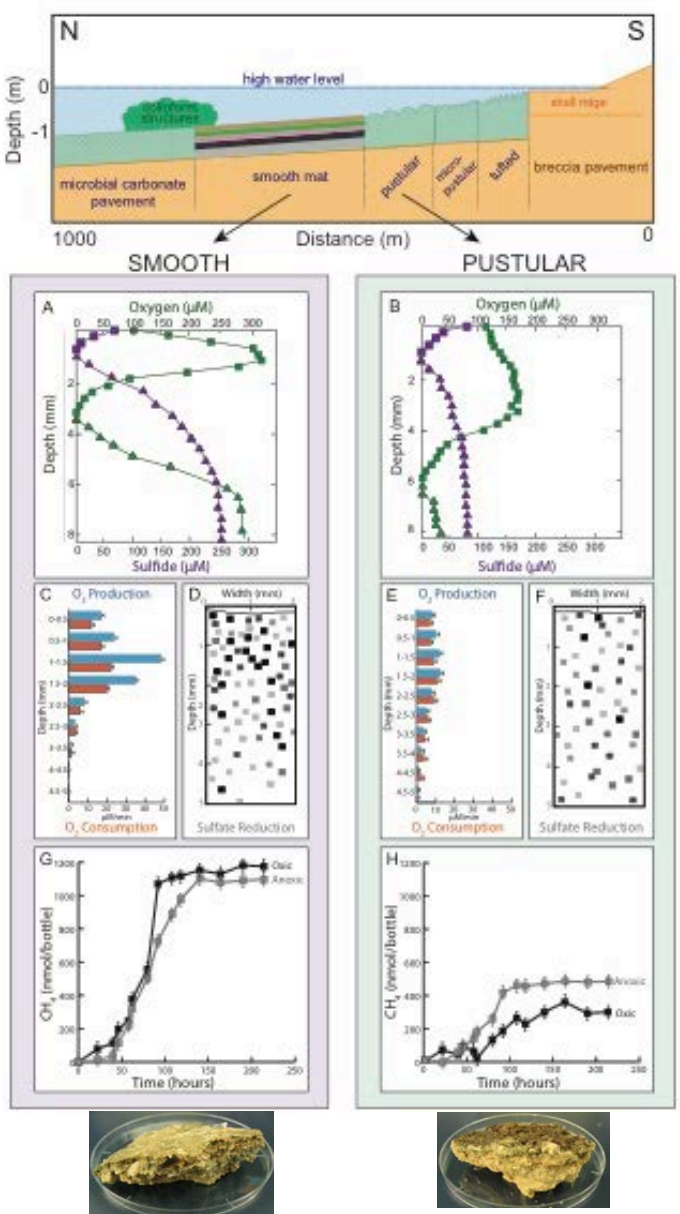
# What will mm-scale analyses tell us?

- Microbes will likely position themselves according to the availability of a given nutrient (or away from a toxic one)
- Close physical association – infer interactions (with each other and environment)
- Identifying spatial distribution of microorganisms with mat depth facilitates a greater understanding of specific niches
- Adaptive response to environmental change
- ‘Next generation’ sequencing facilitates unprecedented access

# Microelectrode profiling

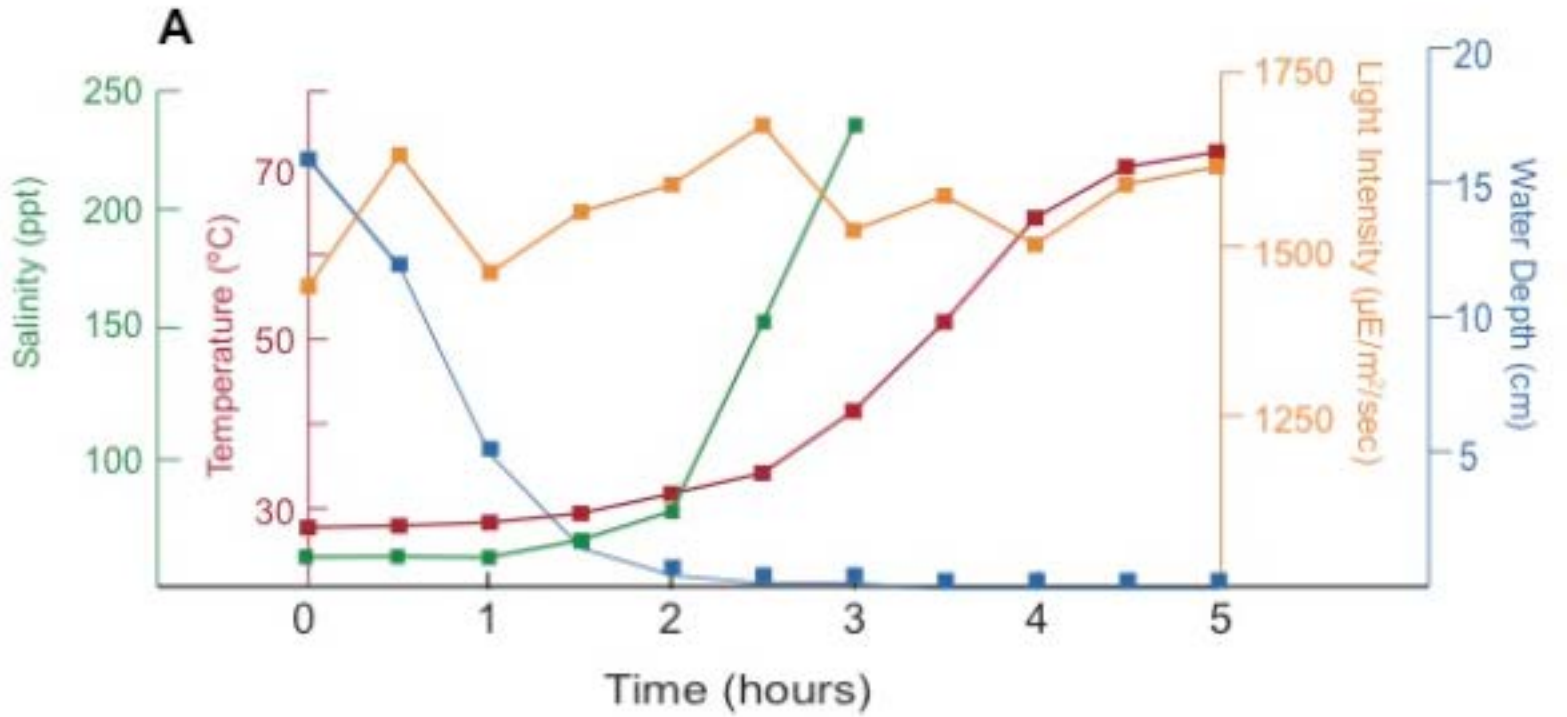
- Measure changes in O and S turnover every 0.2 mm depth over diel cycle
- Photosynthesis, respiration, and sulphur metabolism
- Show productivity (day/night), relate to specific organismal groups and spatial location within microbialites
- Can facilitate measures of ecosystem health

# Metabolic measurements



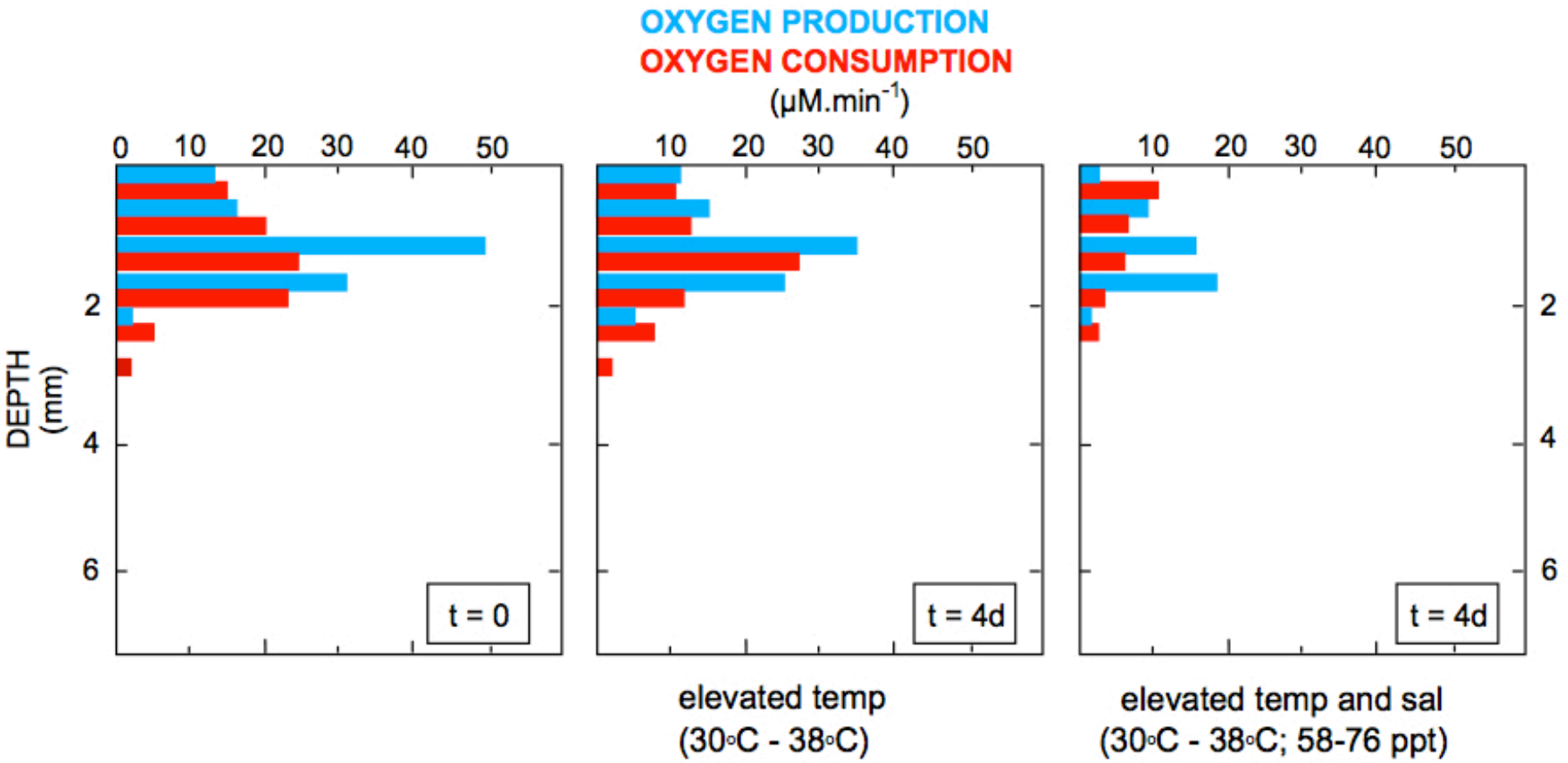

- Measures of rates of $O_2$ production/ consumption, sulphate reduction, methane turnover
- High rates of SR even in oxic zones
- Very efficient, adapting systems
- Changes over a diel cycle
- Different metabolisms likely dominate depending on level of stress

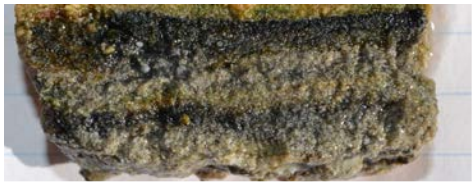
Measurements of water depth, salinity, temperature, light intensity taken during the transition from high tide to low tide in Shark Bay mats



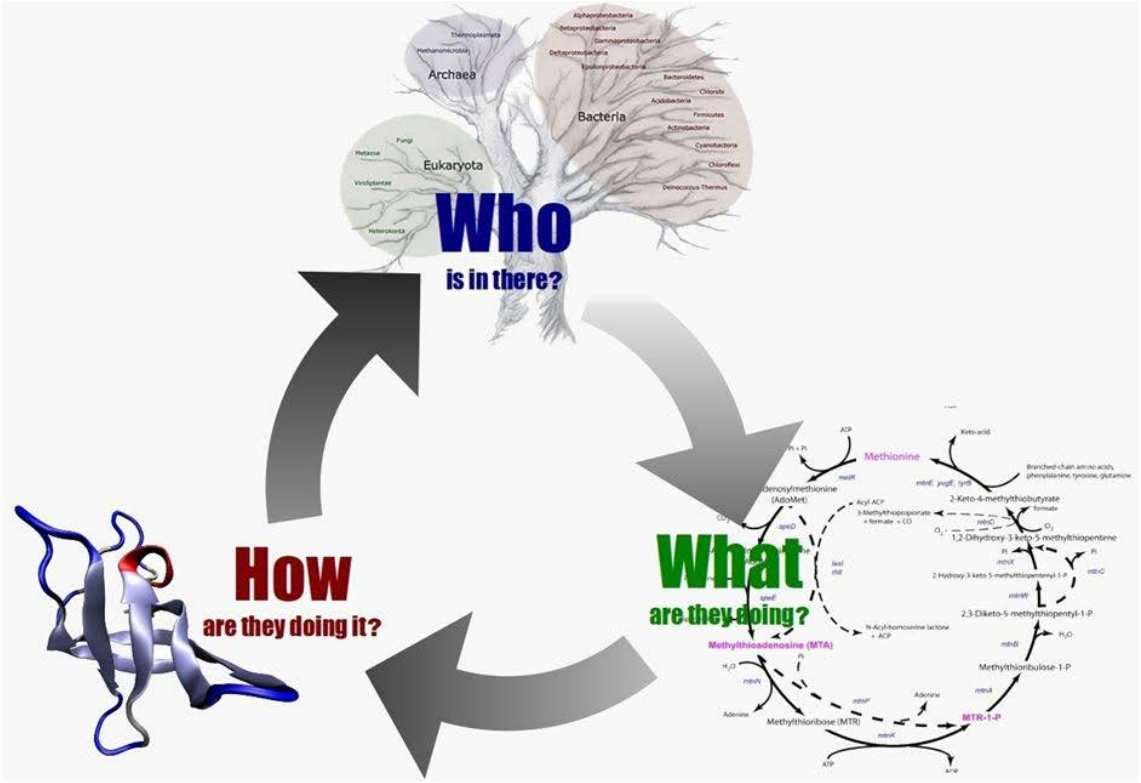

At low tide mats subjected to salinity/desiccation stress… have to evolve adaptation strategies

# Stress/climate change effects on ecosystem health

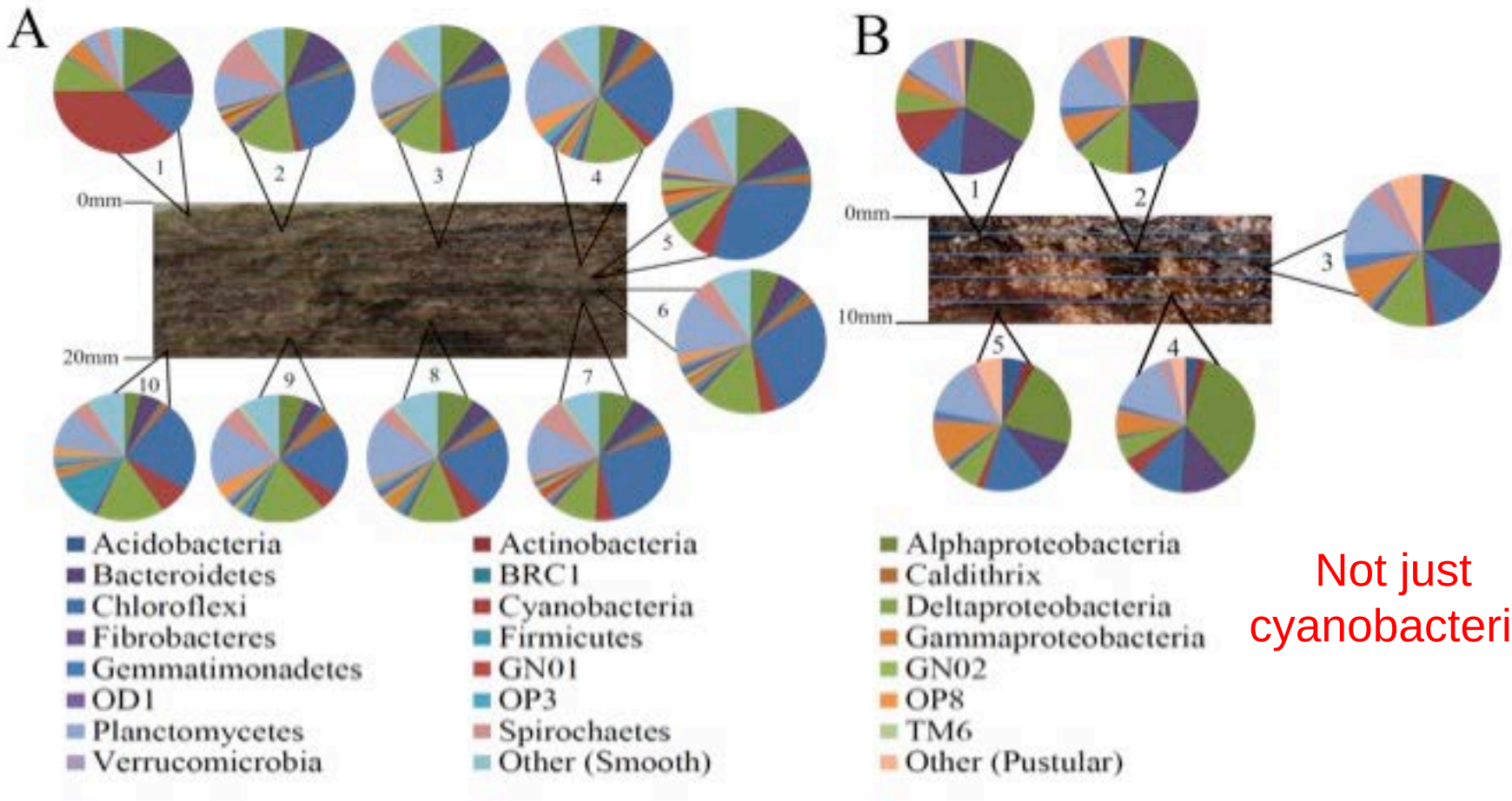


Can now couple these metabolic measurements to *what* microbes are *where* and their metabolic potential through various ‘omic’ analyses…..

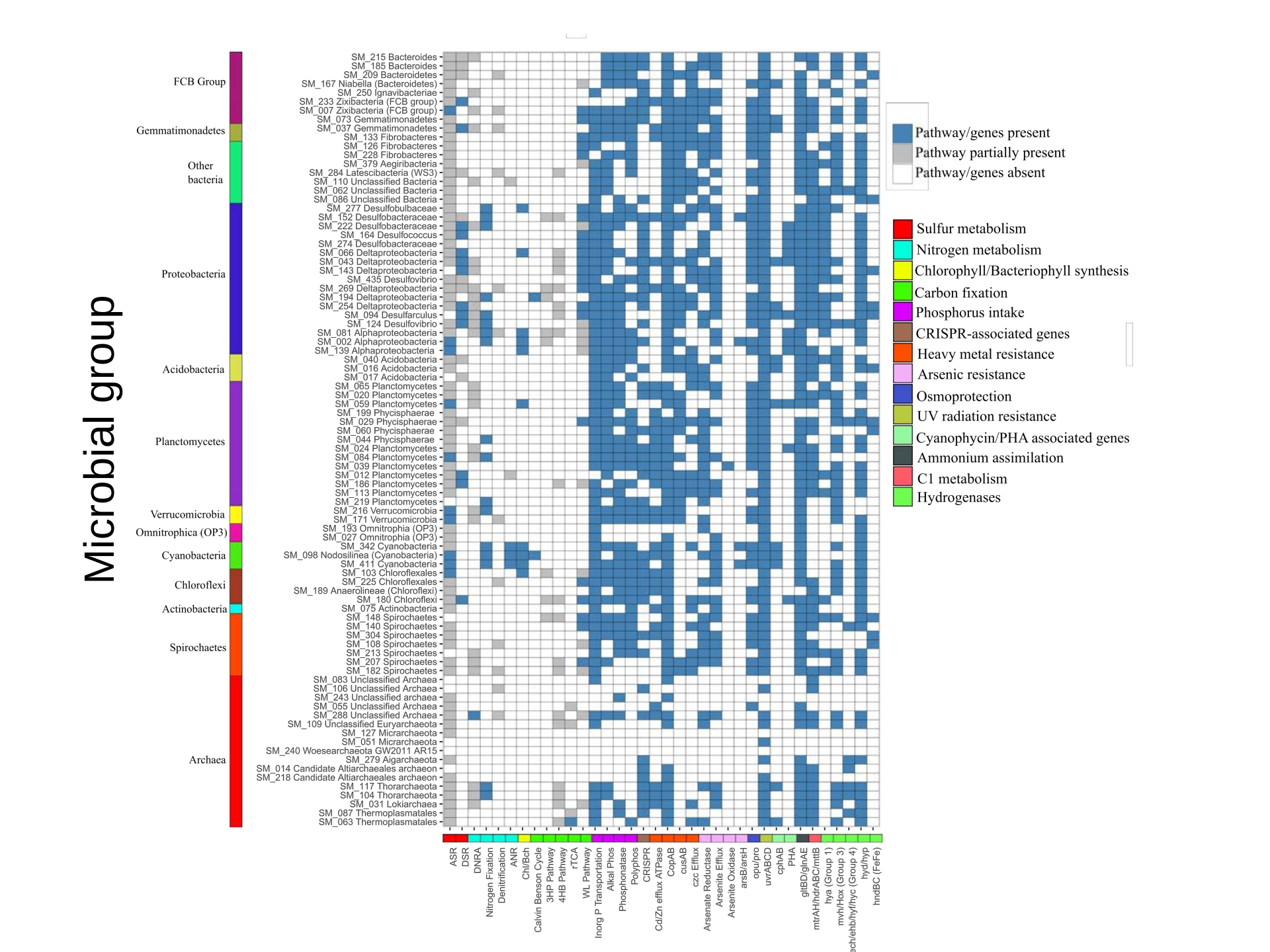


# Bacterial distribution in Shark Bay mats with depth

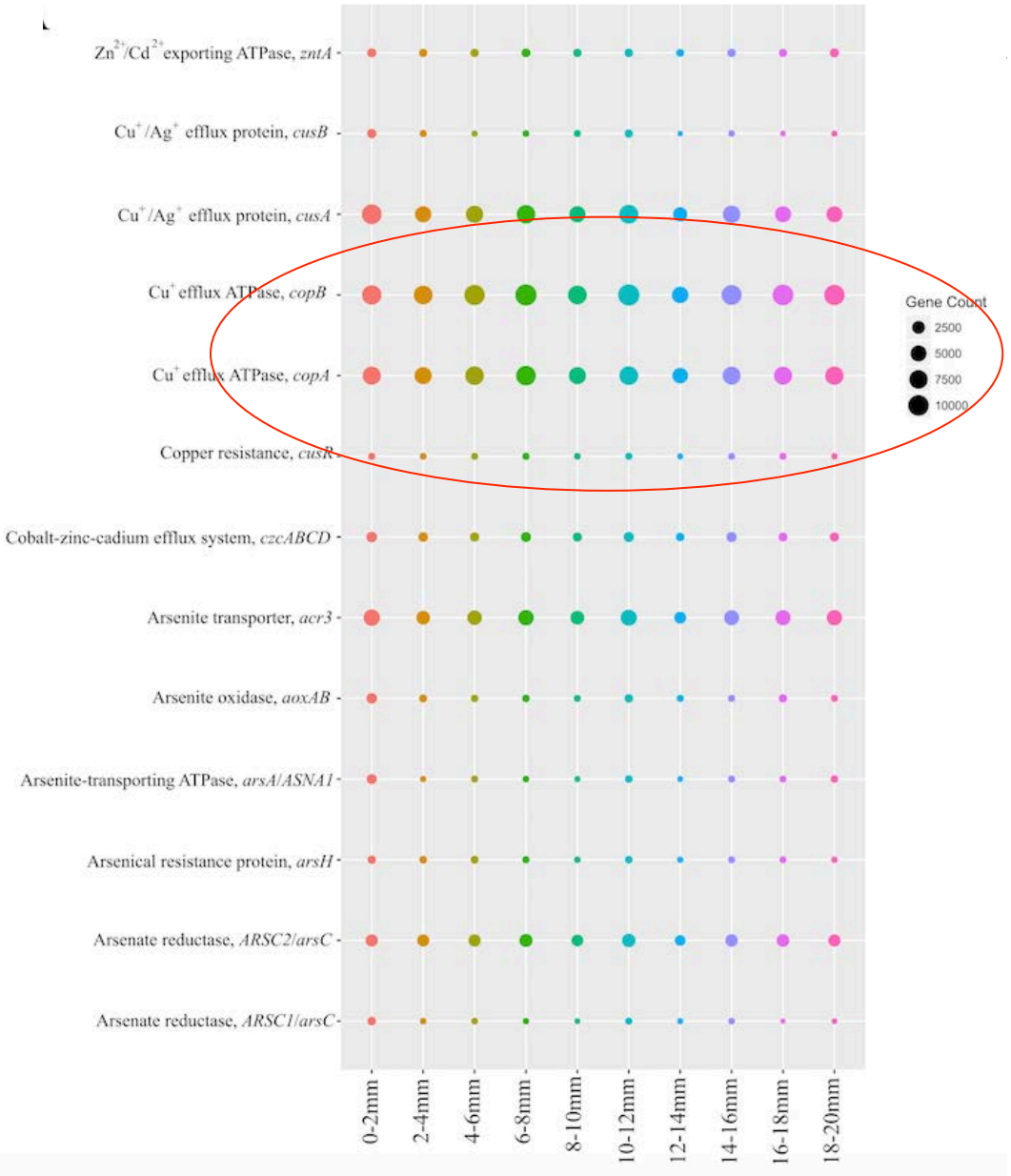



Not just cyanobacteria!

Long term aim to measure changes in abundance of different groups as a result of environmental change/stress


Microbial group
FCB Group
Gemmatimonadetes
Other bacteria
Proteobacteria
Acidobacteria
Planctomycetes
Verrucomicrobia
Omnitrophica (OP3)
Cyanobacteria
Chloroflexi
Actinobacteria
Spirochaetes
Archaea
SM_215 Bacteroides
SM_185 Bacteroides
SM_209 Bacteroidetes
SM_167 Niabella (Bacteroidetes)
SM_250 Ignavibacteriae
SM_233 Zixibacteria (FCB group)
SM_007 Zixibacteria (FCB group)
SM_073 Gemmatimonadetes
SM_037 Gemmatimonadetes
SM_133 Fibrobacteres
SM_126 Fibrobacteres
SM_228 Fibrobacteres
SM_379 Aegiribacteria
SM_284 Latescibacteria (WS3)
SM_110 Unclassified Bacteria
SM_062 Unclassified Bacteria
SM_086 Unclassified Bacteria
SM_277 Desulfobulbaceae
SM_152 Desulfobacteraceae
SM_222 Desulfobacteraceae
SM_164 Desulfococcus
SM_274 Desulfobacteraceae
SM_066 Deltaproteobacteria
SM_043 Deltaproteobacteria
SM_143 Deltaproteobacteria
SM_435 Desulfovibrio
SM_269 Deltaproteobacteria
SM_194 Deltaproteobacteria
SM_254 Deltaproteobacteria
SM_094 Desulfarculus
SM_124 Desulfovibrio
SM_081 Alphaproteobacteria
SM_002 Alphaproteobacteria
SM_139 Alphaproteobacteria
SM_040 Acidobacteria
SM_016 Acidobacteria
SM_017 Acidobacteria
SM_065 Planctomycetes
SM_020 Planctomycetes
SM_059 Planctomycetes
SM_199 Phycisphaerae
SM_029 Phycisphaerae
SM_060 Phycisphaerae
SM_044 Phycisphaerae
SM_024 Planctomycetes
SM_084 Planctomycetes
SM_039 Planctomycetes
SM_012 Planctomycetes
SM_186 Planctomycetes
SM_113 Planctomycetes
SM_219 Planctomycetes
SM_216 Verrucomicrobia
SM_171 Verrucomicrobia
SM_193 Omnitrophia (OP3)
SM_027 Omnitrophia (OP3)
SM_342 Cyanobacteria
SM_098 Nodosilinea (Cyanobacteria)
SM_411 Cyanobacteria
SM_103 Chloroflexales
SM_225 Chloroflexales
SM_189 Anaerolineae (Chloroflexi)
SM_180 Chloroflexi
SM_075 Actinobacteria
SM_148 Spirochaetes
SM_140 Spirochaetes
SM_304 Spirochaetes
SM_108 Spirochaetes
SM_213 Spirochaetes
SM_207 Spirochaetes
SM_182 Spirochaetes
SM_083 Unclassified Archaea
SM_106 Unclassified Archaea
SM_243 Unclassified archaea
SM_055 Unclassified Archaea
SM_288 Unclassified Archaea
SM_109 Unclassified Euryarchaeota
SM_127 Micrarchaeota
SM_051 Micrarchaeota
SM_240 Woesearchaeota GW2011 AR15
SM_279 Aigarchaeota
SM_014 Candidate Altiarchaeales archaeon
SM_218 Candidate Altiarchaeales archaeon
SM_117 Thorarchaeota
SM_104 Thorarchaeota
SM_031 Lokiarchaea
SM_087 Thermoplasmatales
SM_063 Thermoplasmatales
ASR
DSR
DNRA
Nitrogen Fixation
Denitrification
ANR
Chl/Bch
Calvin Benson Cycle
3HP Pathway
4HB Pathway
rTCA
WL Pathway
Inorg P Transportation
Alkal Phos
Phosphonatase
Polyphos
CRISPR
Cd/Zn efflux ATPase
CopAB
cusAB
czc Efflux
Arsenate Reductase
Arsenite Efflux
Arsenite Oxidase
arsB/arsH
opu/pro
uvrABCD
cphAB
PHA
gltBD/glnAE
mtrAH/hdrABC/mtrB
hya (Group 1)
mvh/Hox (Group 3)
ach/ehb/hyf/hyc (Group 4)
hyd/hyp
hndBC (FeFe)
Pathway/genes present
Pathway partially present
Pathway/genes absent
Sulfur metabolism
Nitrogen metabolism
Chlorophyll/Bacteriophyll synthesis
Carbon fixation
Phosphorus intake
CRISPR-associated genes
Heavy metal resistance
Arsenic resistance
Osmoprotection
UV radiation resistance
Cyanophycin/PHA associated genes
Ammonium assimilation
C1 metabolism
Hydrogenases

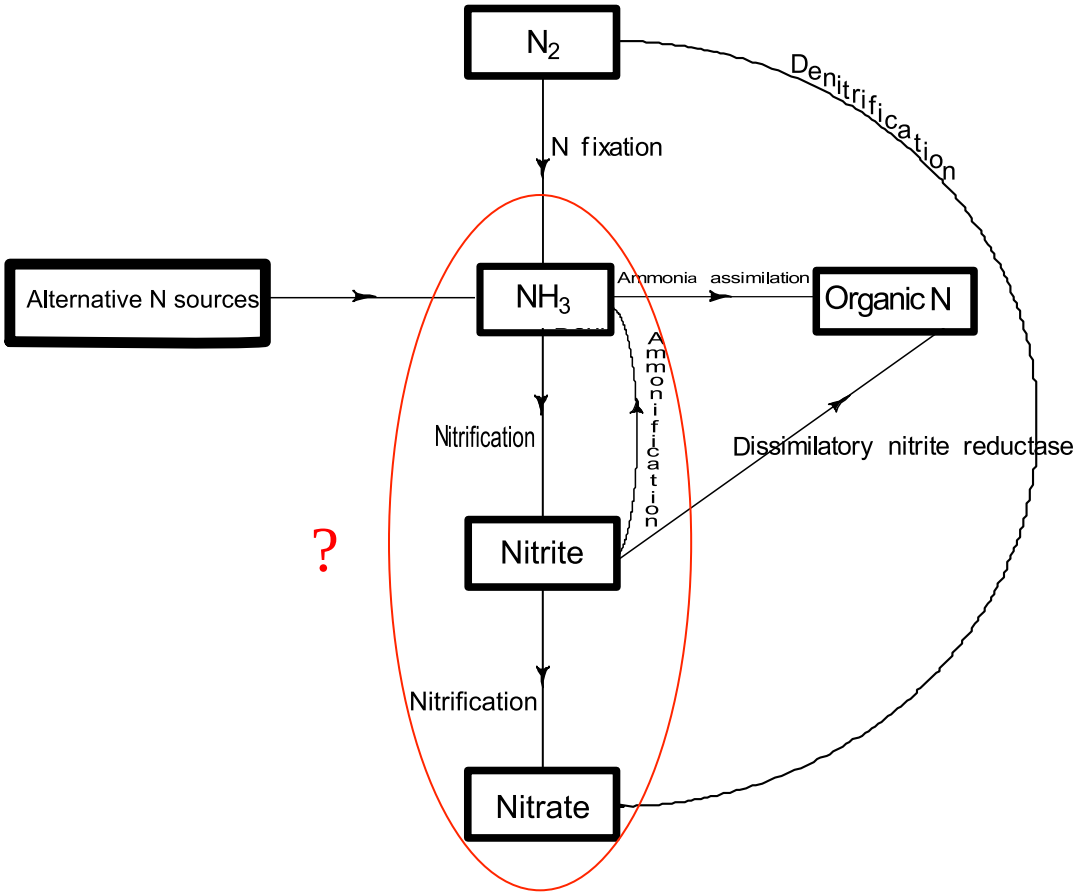
# Adaptive response mechanisms




- Multiple mechanisms to expel Cu present in microbialites
- Slightly increased [Cu] levels in Hamelin Pool water overlying microbialites
- Microbialites seem to be coping…but higher organisms?
- Ocean acidification as a result of climate change suggested to increase Cu toxicity even further*

*Lewis et al (2016) 6:21554 | DOI: 10.1038/srep21554

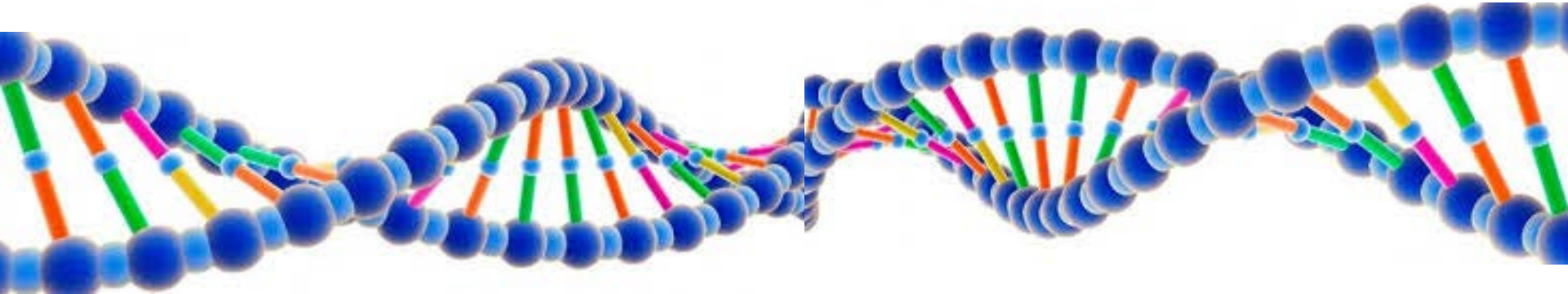
# Incomplete N cycle?




- No known nitrification pathways….ammonia could build up
- High salt inhibiting nitrifying bacteria?
- Potential bottleneck…..could this affect other systems (e.g seagrasses)?

# ‘Omic’ analyses very powerful but…

- Any bias needs to be reduced – expt design, replication
- May not be catching everything, snapshot, how representative
- How deep to sequence, where do you stop?
- Important not to sequence for sequencing sake - need rational, focused questions to address
- Still a need to combine with in situ metabolic data, defined culture expts etc, to tell the *whole* story

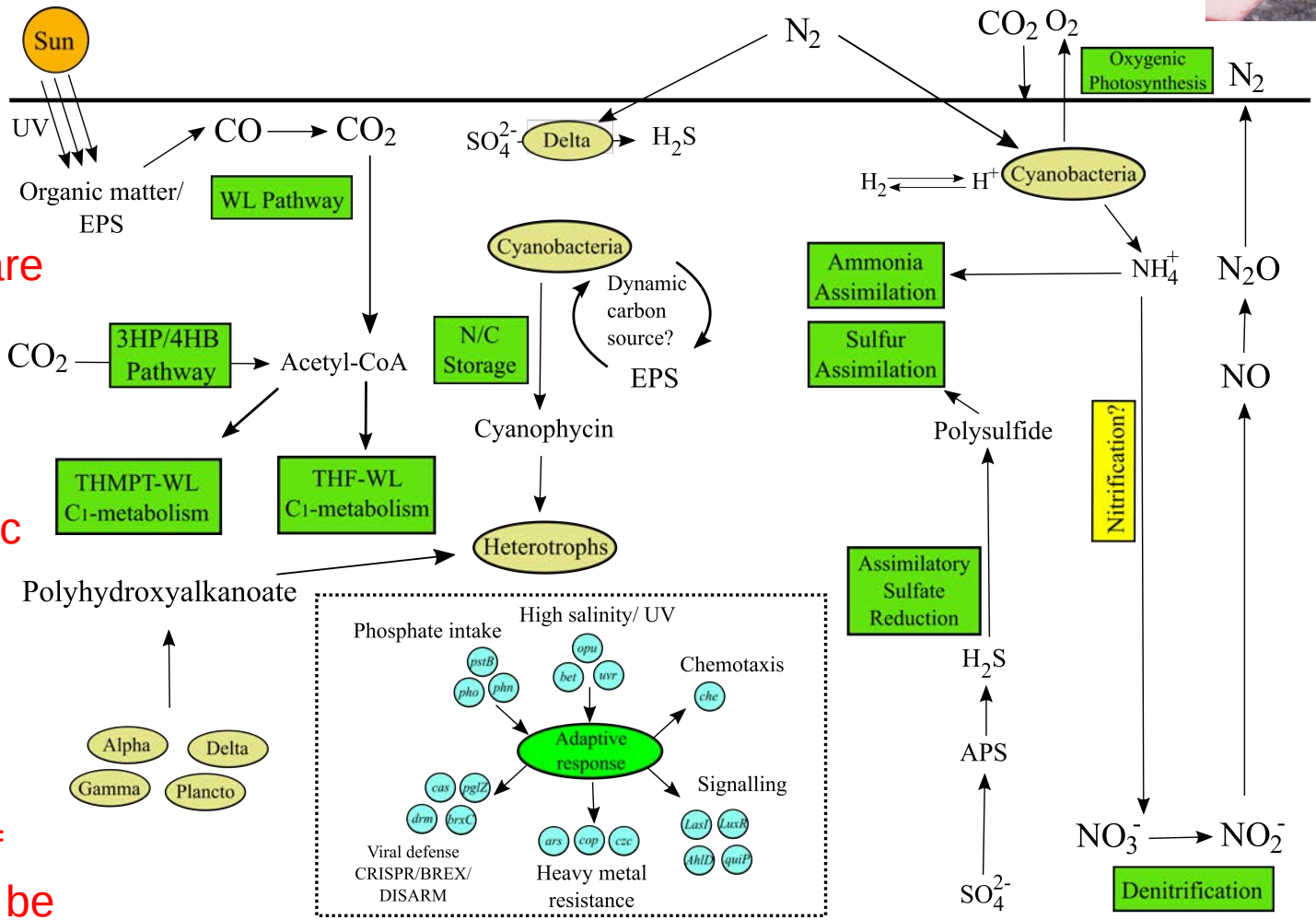


# What is going on in a Shark Bay mat ….

Interactions are *key*…

Opportunistic niches

Coupling of activities may be linked adaptation, survival, resilience




Microbialites are the original social network ☺

Microorganisms exploit every energetic opportunity

# Ongoing/future work

- Delineate impact of extreme stressors on critical pathways in threatened microbialites
- Critical to ascertain before any irreversible ecosystem tipping points are reached
- Disentangle drivers of adaptation and stress response in Shark Bay mats
- Assess impacts of environmental fluctuations
- Ability of a system to retain critical structure and feedbacks after disturbance will depend on community composition and inherent resistance capabilities
- Identify key population shifts, changes in gene/metabolite expression patterns to predict responses under the threat of environmental change
- Establish short and long term monitoring programs

# Microbialite conservation and Shark Bay - summary

- Several heritage values in Shark Bay (environmental, Aboriginal)
- Conservation of microbialites significant drive of our research
- Microbialites very vulnerable to human impact
- Temporal reduction in microbial diversity can indicate detrimental impact
- Microbialites are excellent markers to the health of Shark Bay
- Need to effectively manage these ecosystems in the face of environmental challenges
- AND link coherently with management practices for other systems in Shark Bay (dolphins, seagrasses, etc)…..i.e why we are here today! ☺

# Acknowledgements


- Pieter Visscher
- Alan Wong
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- Tony Larkum
- Rick White
- Therese Morris
- Lindsay Collins