

Integrating macro- & microbial ecology

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SYDNEY



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± HALF
OF THE WORLD'S
POPULATION LIVES
WITHIN 100 KM OF
THE COAST

+ 1 BILLION PEOPLE
LIVE IN POOR COASTAL
COMMUNITIES WITH
DIRECT CONNECTIONS
TO THE SEA

100 KM



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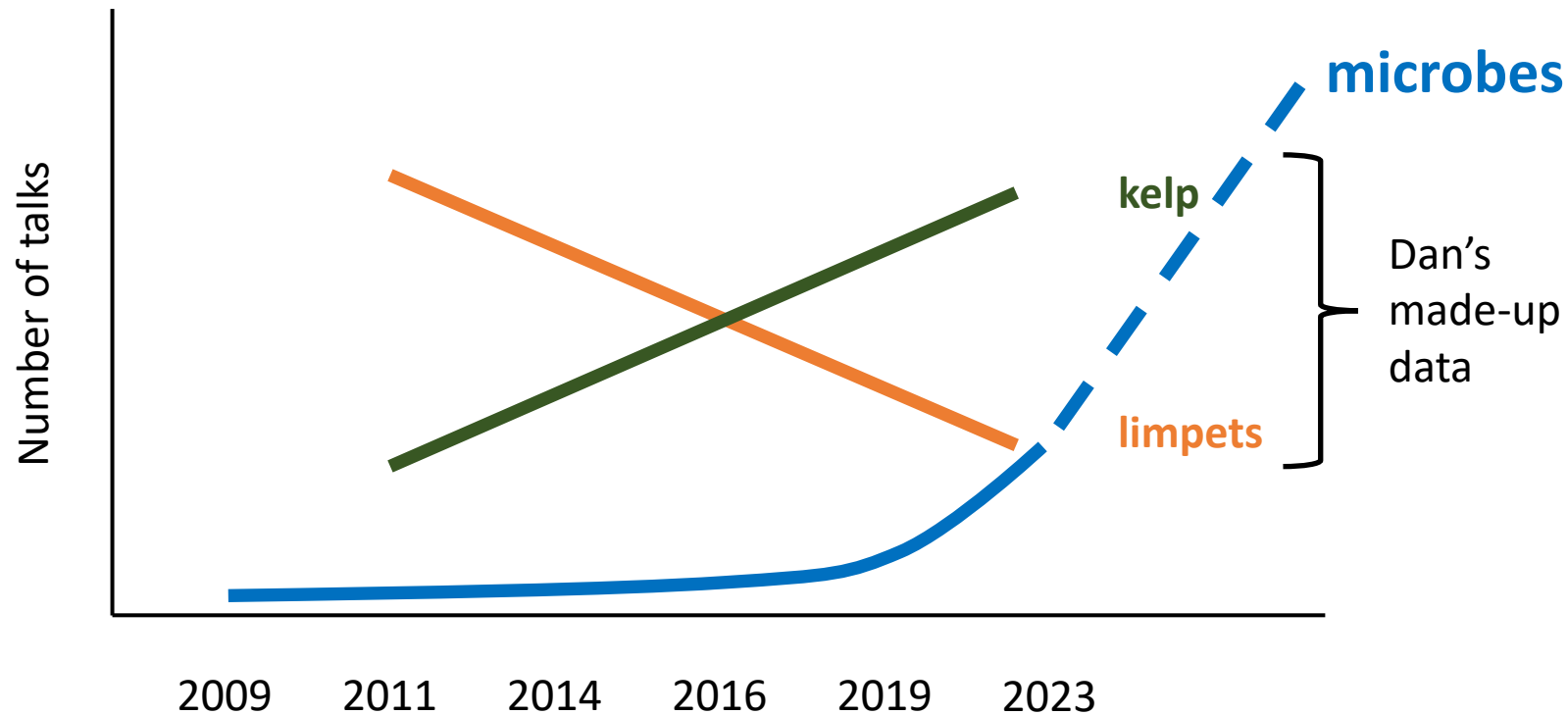
100 KM

An infographic with a white background and rounded corners. It features a teal globe icon, a teal house icon, and a teal distance marker labeled '100 KM'. The text is in teal and black. The background of the entire image is a collage of coastal and environmental scenes.

ITRS 2019 HK
(I think)



ITRS talks through time (according to us)



'Holobiont'



>50% of cells

>95% of genes

'Holobiont'



**Change in
environment,
diet**



**Shift / imbalance of
gut microbiota**



Disease

e.g. inflammatory bowel disease,
irritable bowel syndrome, asthma,
cardiovascular disease, etc.



Where/when...? How?

~~Do~~ changes in **microbiomes** matter?

What are the implications for **managing ecosystems**?

The 'omics' revolution

Ecology + Microbiology

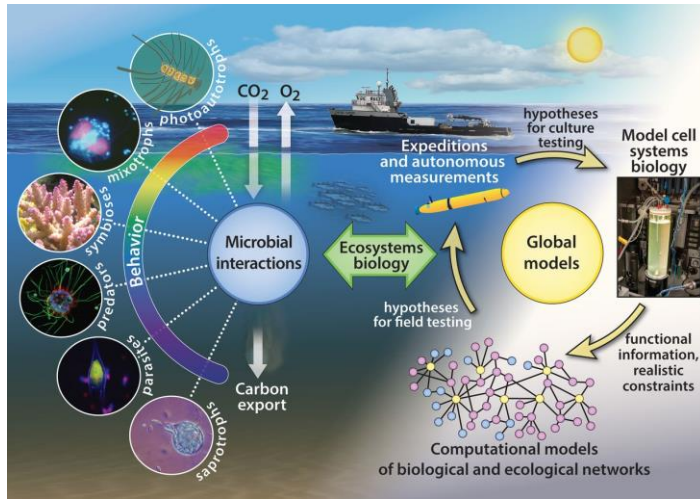


Molecular and computational tools

- 16S rRNA gene/ ITS/ 18S amplicon sequencing
 - Trimmomatic, DADA2
- Metagenomics
 - Trimmomatic, metaSPAdes, MetaBAT (MAGs)
- Metatranscriptomics
 - MetaTrans
- Metabolomics, etc.
- Data analysis
 - Distance-based, mGLM, networks

Marine systems

Open ocean



Worden et al. 2015 *Science*


Coastal habitat-formers??



Marzinelli et al. 2015 *Environ. Microbiol.*;
Thompson et al. 2017 *Nature*; Trevathan-Tackett et al. 2019 *Nature Eco. Evo.*



Kelp
Ecklonia radiata



Crayweed
Phyllospora comosa

Highly valuable

Highly threatened



Neptune neckless
Hormosira banksii



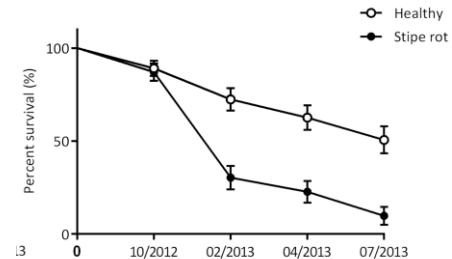
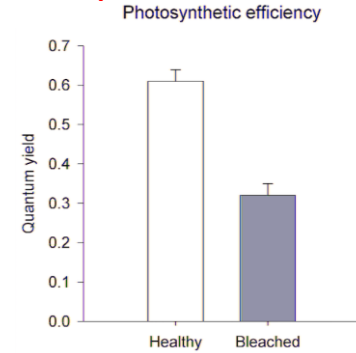
Seagrass
Zostera mulleri

Host-microbe interactions & environmental change

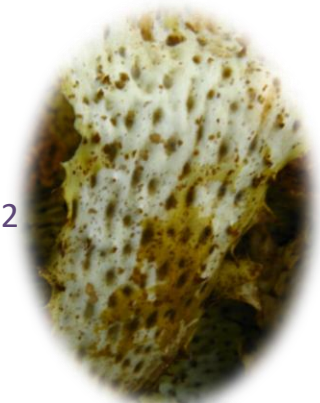
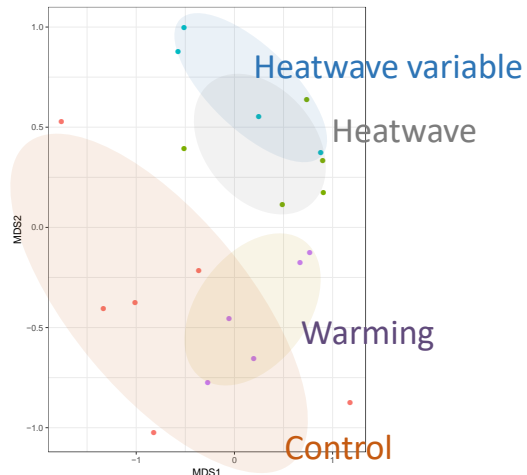
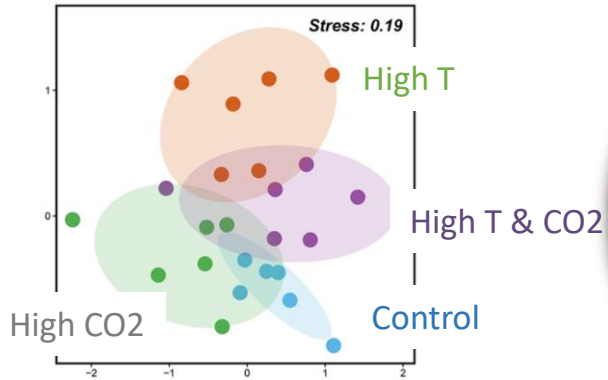
Warmer waters
and/or urban



Lower survival/
performance

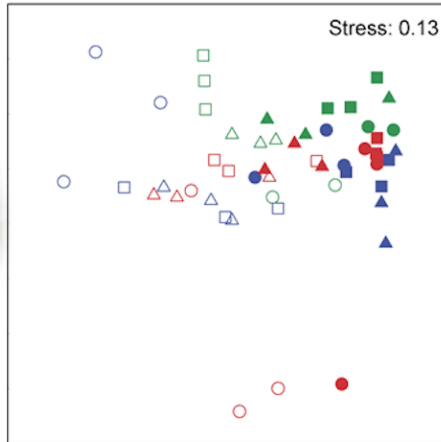


~ 10,000 ASV (= Amplicon Seq. Variants)

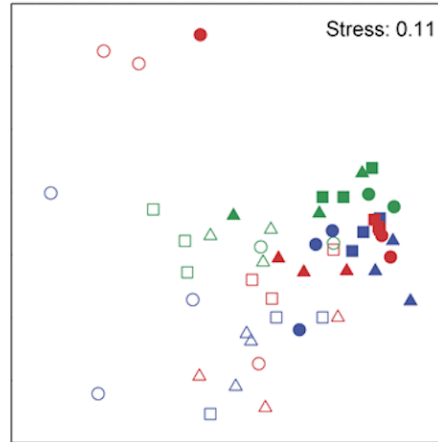


Cause-effect: thousands, but high redundancy

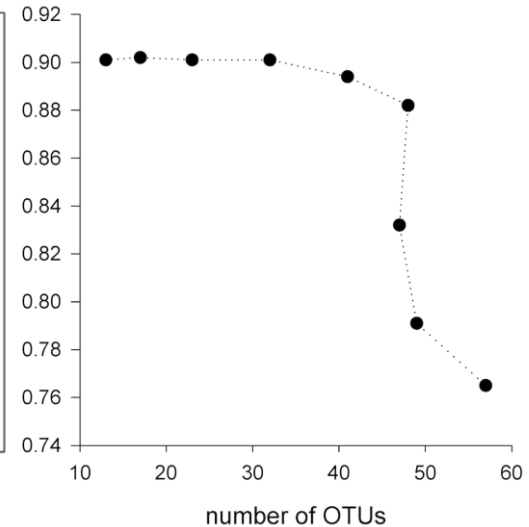
Microbial community structure
1,107 OTUs (bacterial taxa)



Microbial community structure
13 OTUs only



Correlation



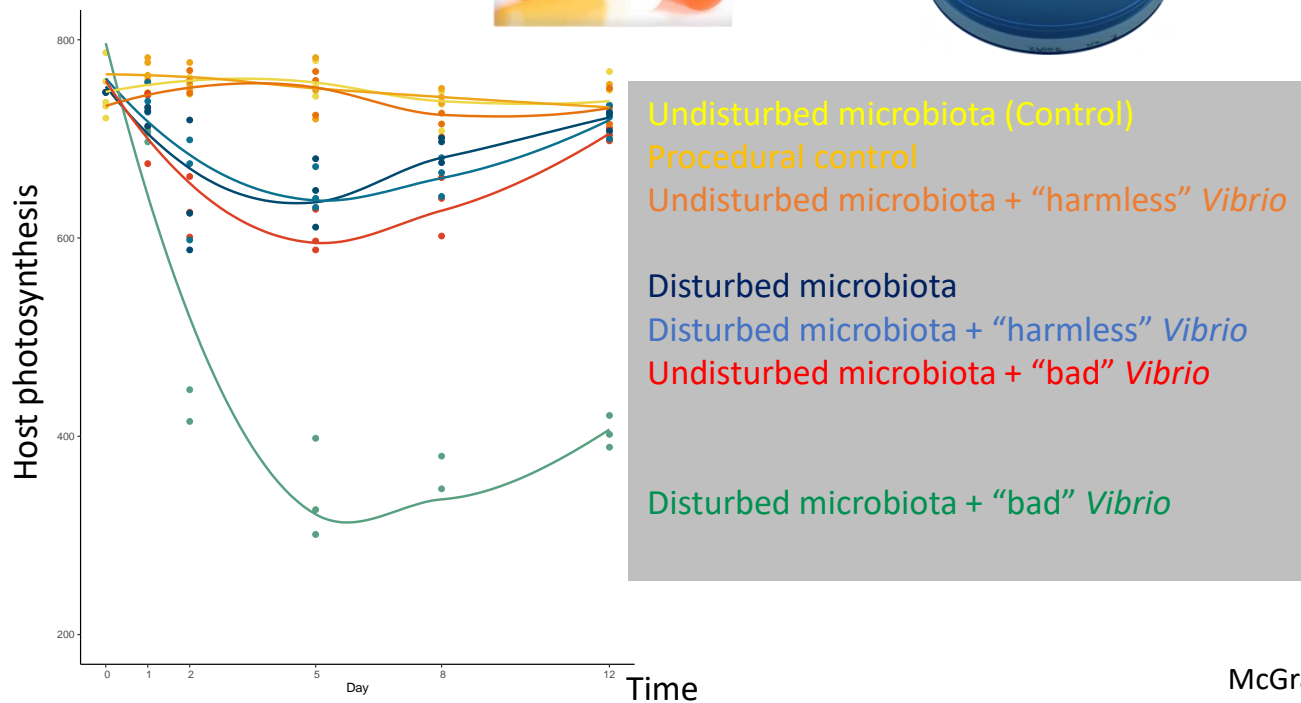
■ NSW
■ TAS
■ WA

Same for functional genes (e.g. nutrient transport, sugar and phlorotannin degradation, stress responses)

Cause-effect: removal/disturbance + inoculation

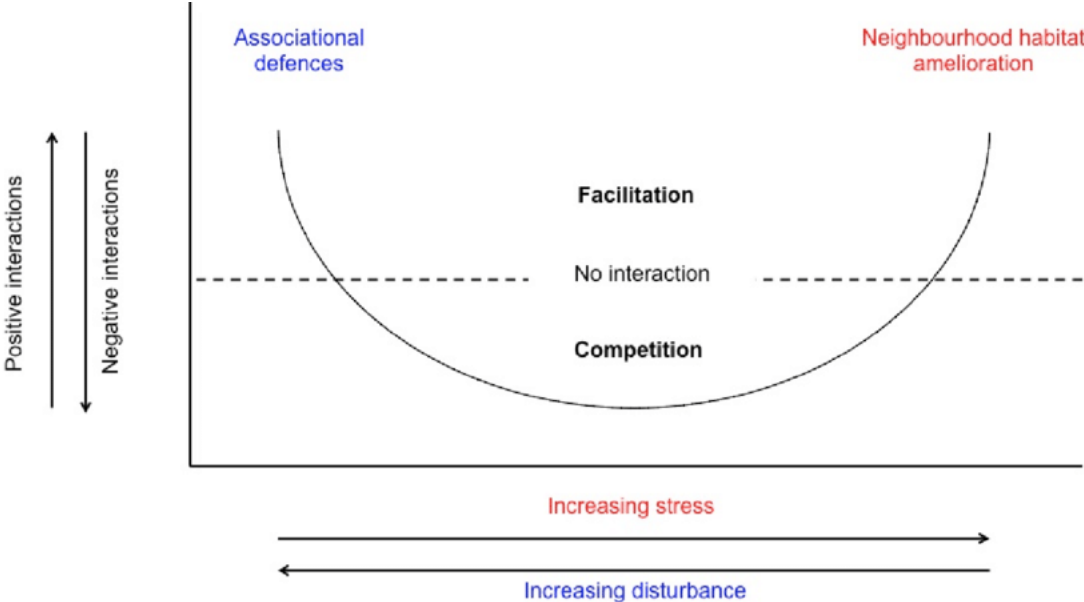


Alex McGrath



Where/when?

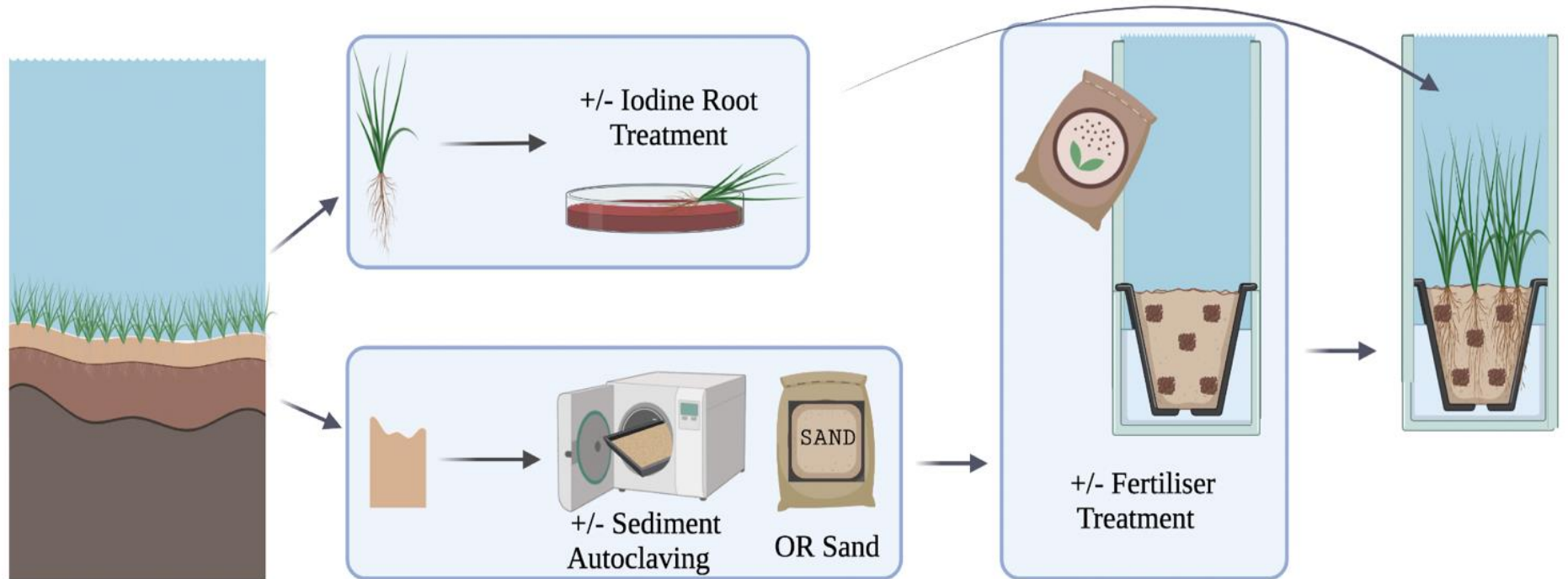
Stress gradient model



Where/when? Plant-sediment interactions



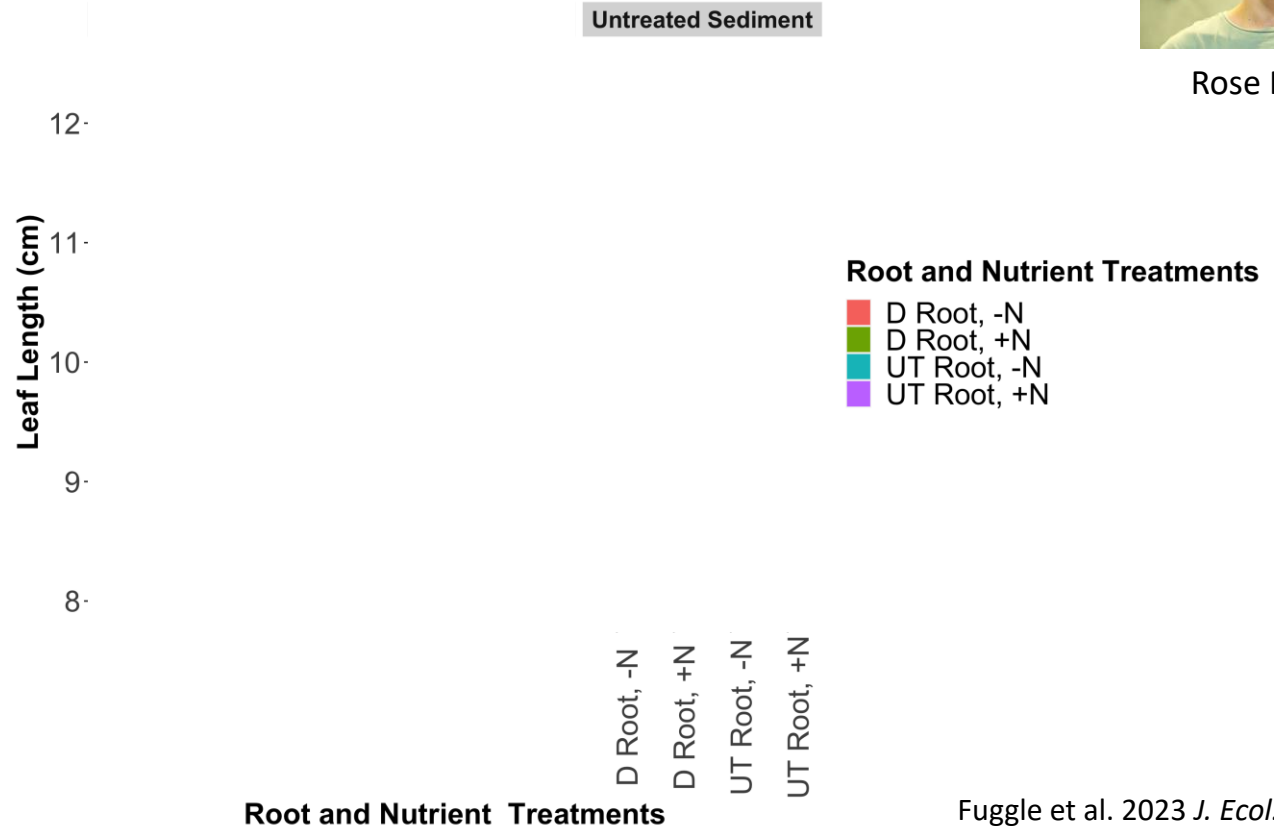
Where/when? Plant-sediment interactions



Where/when? Plant-sediment interactions



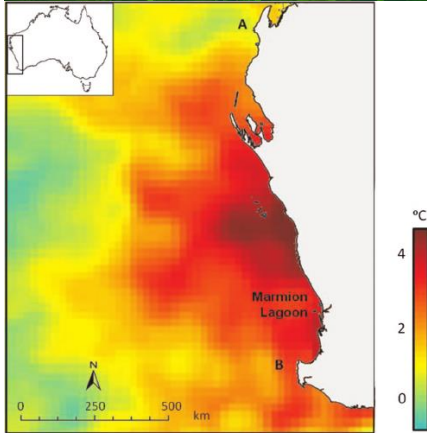
Rose Fuggle



High N ->
anoxia, sulphides ->
Enrichment of
sulphide oxidising &
denitrifying bugs
(e.g. *Beggiatoaceae*
Candidatus thiopilula)

How? Ecological interactions

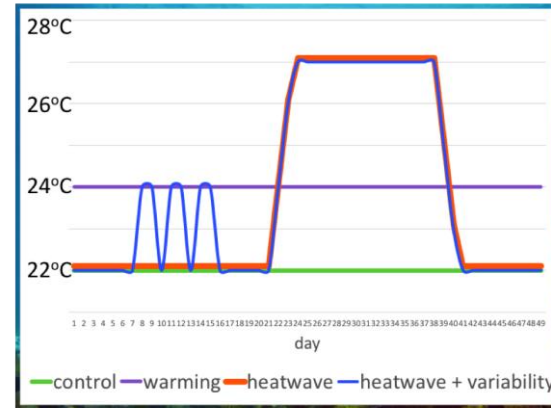
How? Ecological interactions



Wernberg et al. 2016 *Science*



Temperature treatments

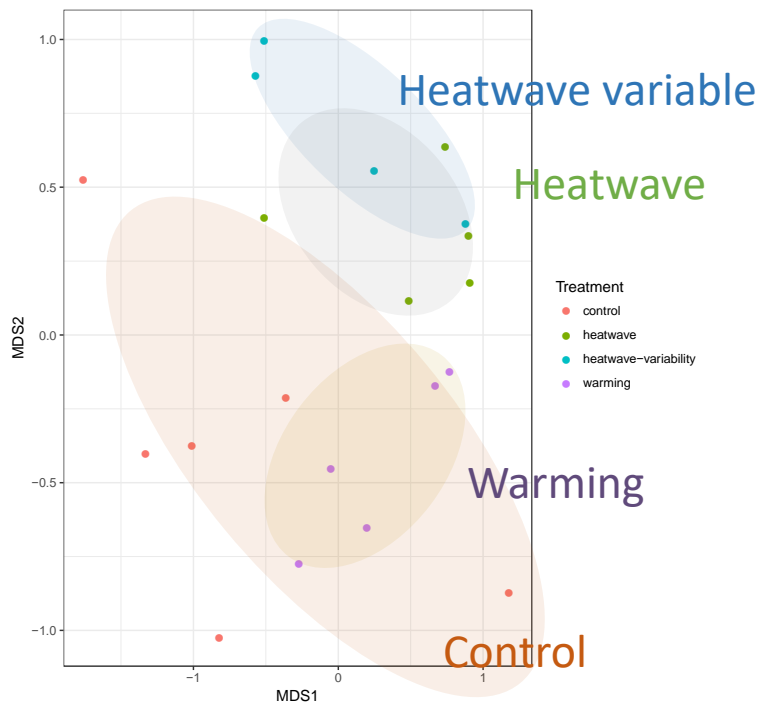


Straub et al. 2022 *J. Phycol.*; Castro et al. in rev. *Molecular Ecology*

How? Ecological interactions

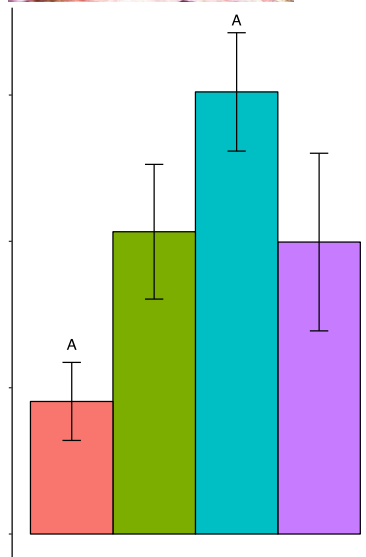
Kelp

Microbial community structure



Sea-urchin

Tripneustes gratilla



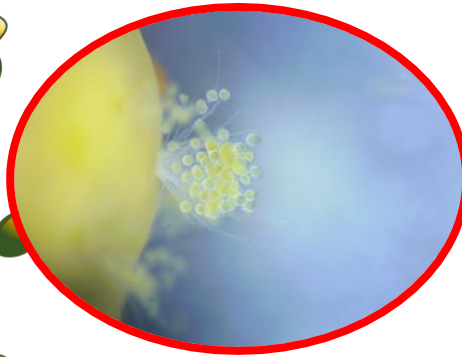
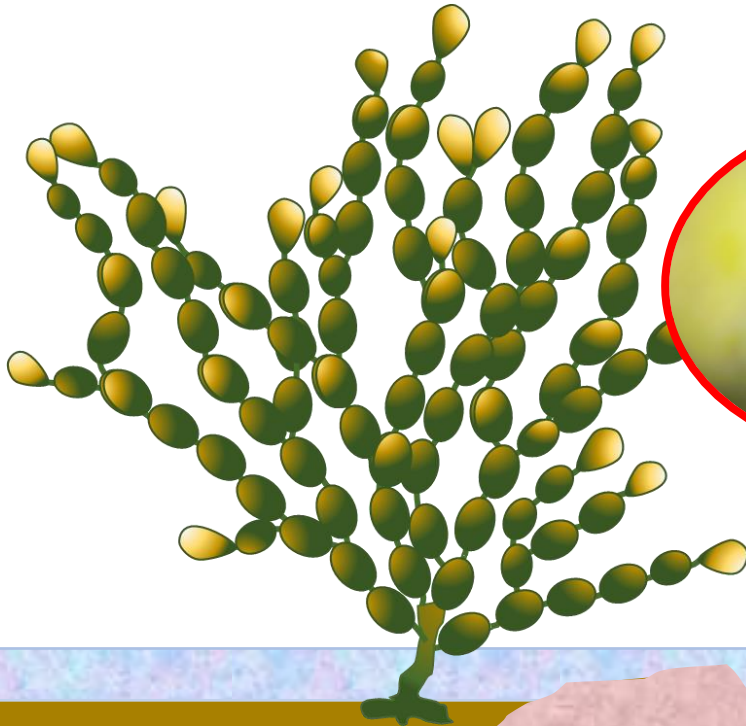
No effects on
C, N, chem. def.



Louise Castro

How? Ecological processes?

How? Ecological processes?

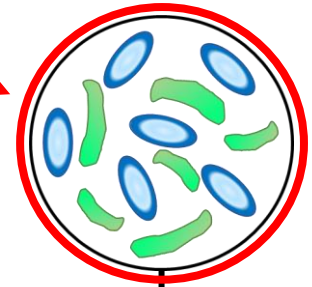


Alex McGrath



Seb Vellido

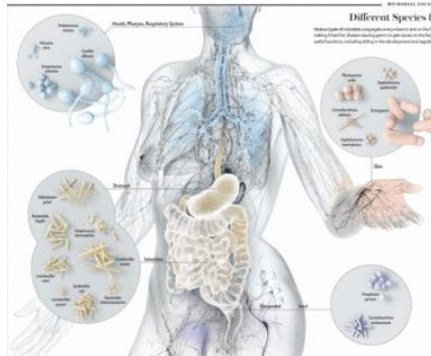
recruitment ?



Host-microbiome interactions & management

How does this new perspective change the way we would manage systems now and into the future?

- Diagnosis/prognosis
- Intervention: rehabilitation & resilience

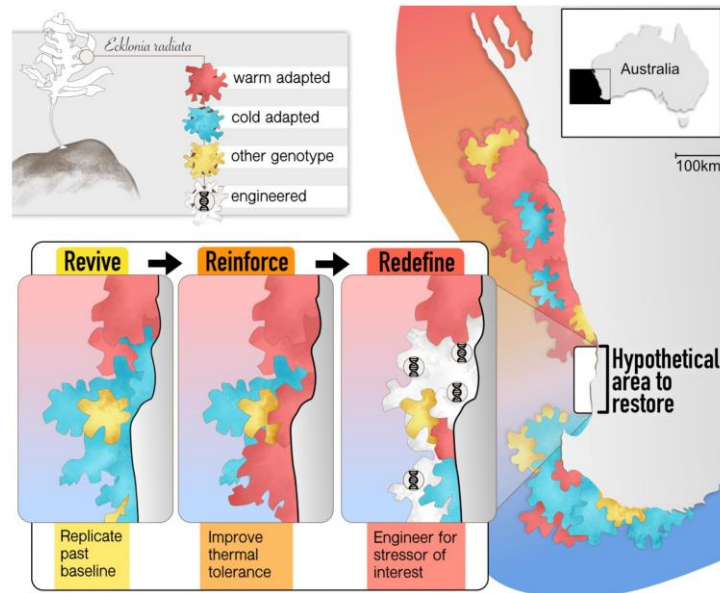




Future-proofing -> Host genotype

Restore or Redefine: Future Trajectories for Restoration

Melinda Ann Coleman^{1,2,3*}, Georgina Wood^{4,5}, Karen Filbee-Dexter^{3,6},
Antoine J. P. Minne³, Hugh Douglas Goold^{7,8}, Adriana Vergés^{4,5},
Ezequiel Miguel Marzinelli^{5,9,10}, Peter David Steinberg^{4,5,10} and Thomas Wernberg^{3,11}



'Holobiont'



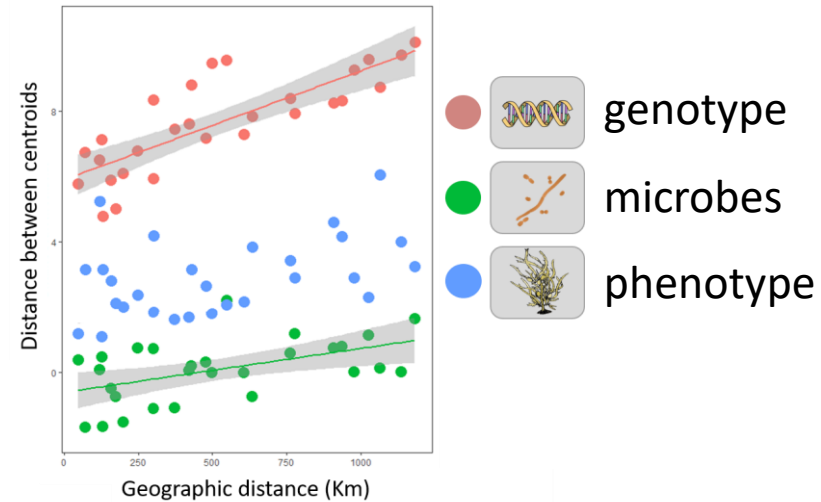
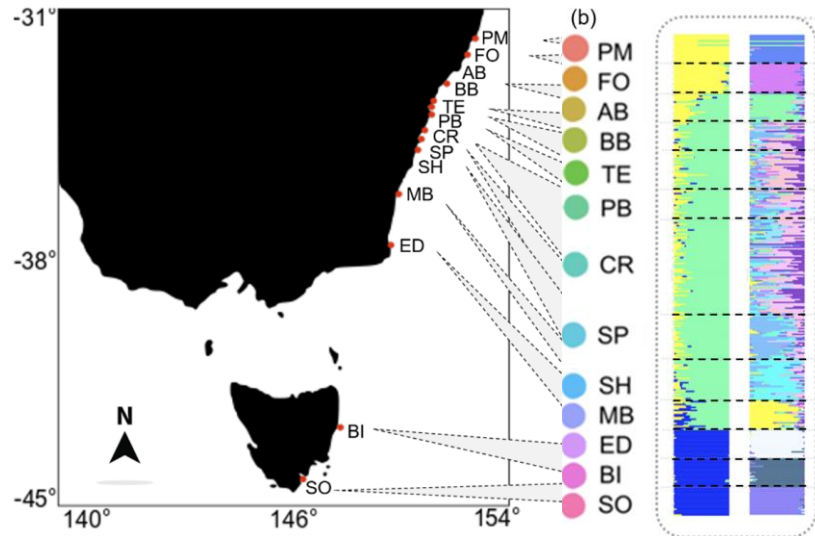
>50% of cells

>95% of genes

Future-proofing -> Host genotype + microbiome?

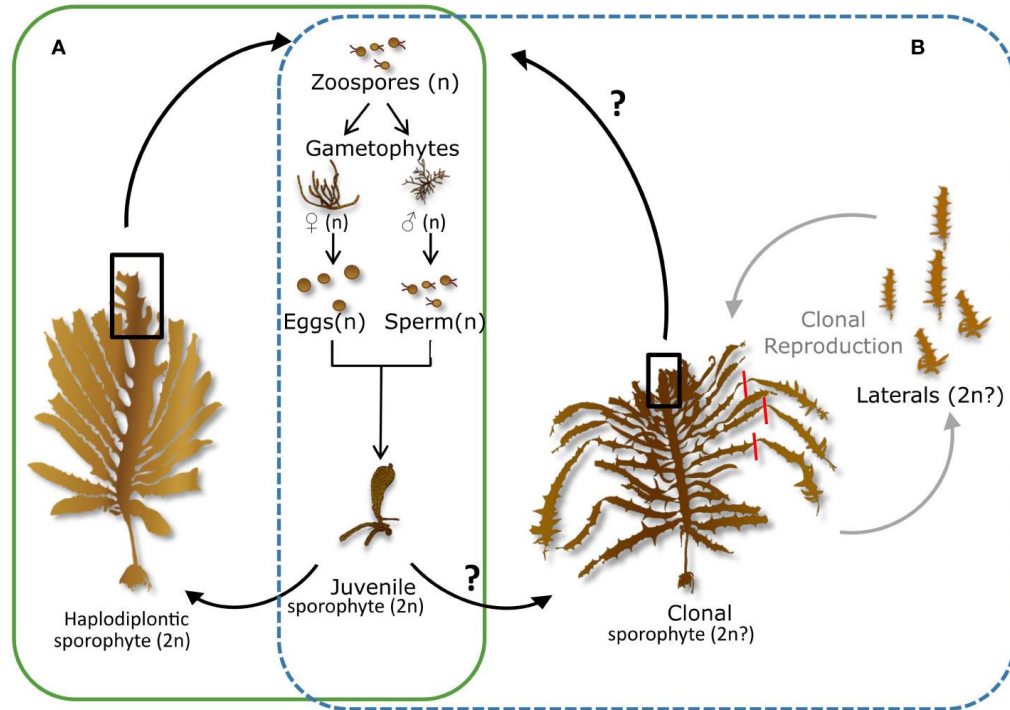


George Wood



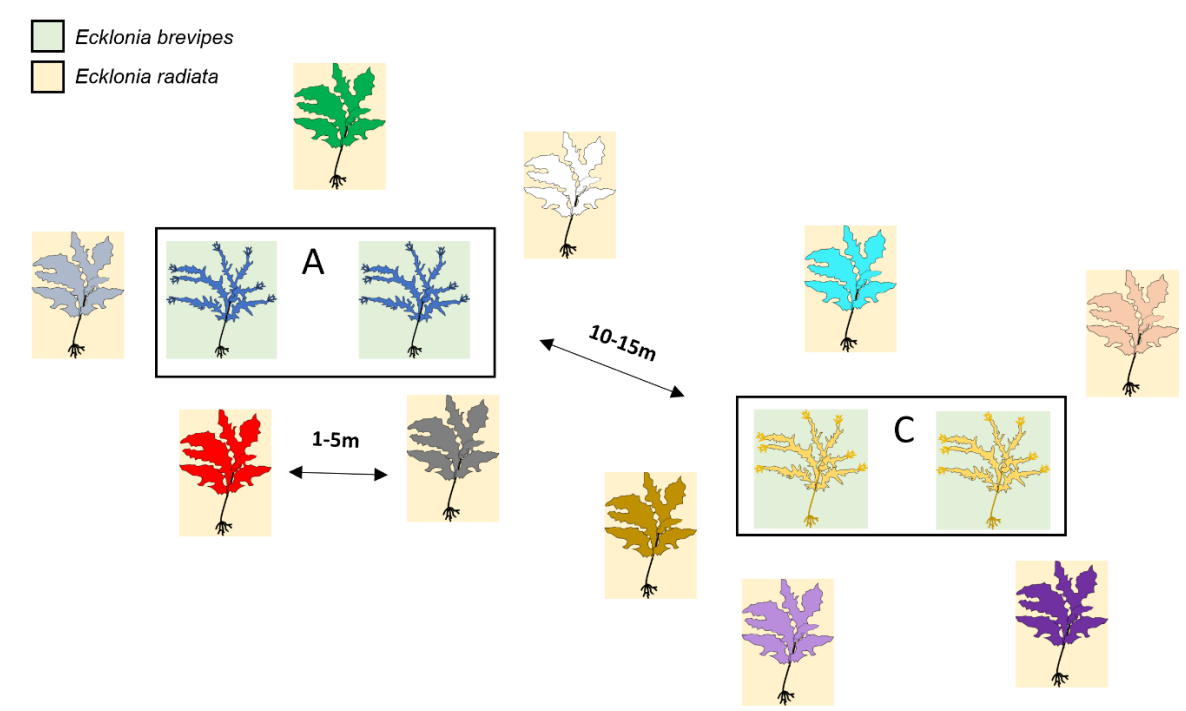
Kelp clones vs unique genotypes vs diff. morphs in same environment

Ecklonia radiata
sexual reproduction

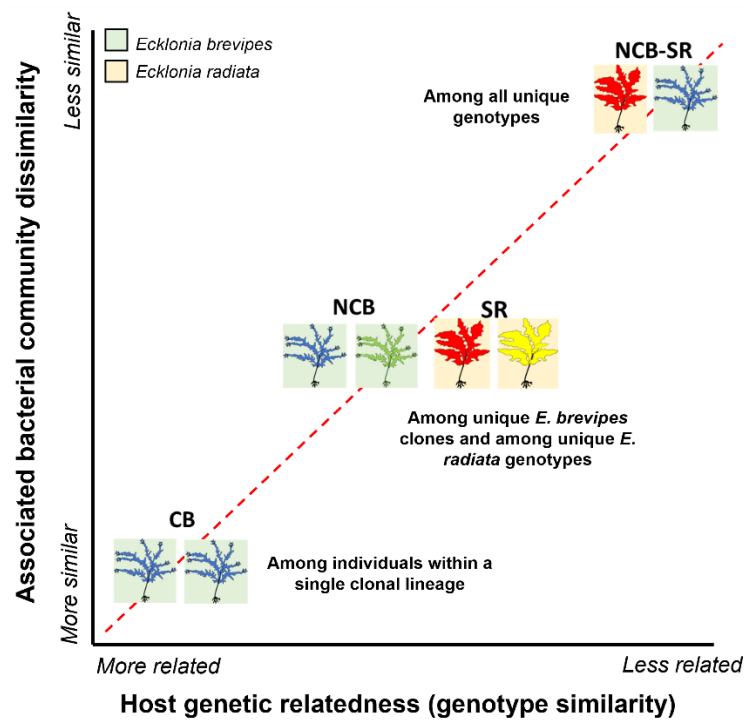


Ecklonia brevipes
sexual +
clonal reproduction

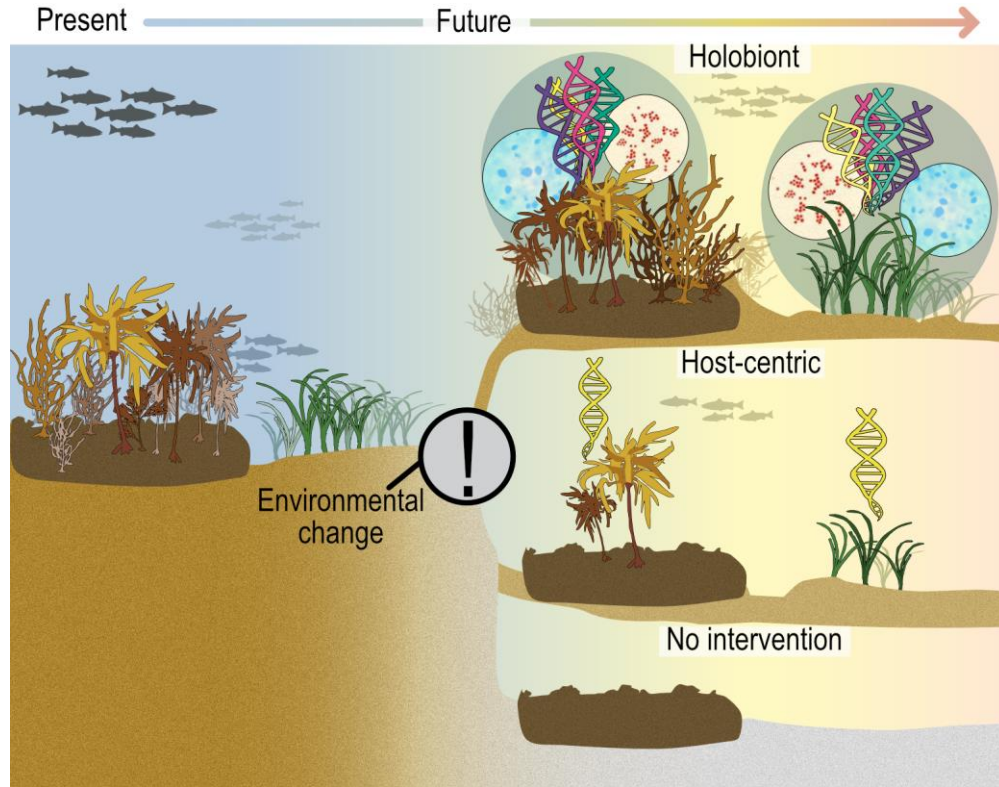
Kelp clones vs unique genotypes vs diff. morphs in same environment



Kelp clones vs unique genotypes vs diff. morphs in same environment



Future-proofing -> Host genotype + microbiome



The Super Coral



 PERSPECTIVE

Building coral reef resilience through assisted evolution

Madeleine J. H. van Oppen^{a,1}, James K. Oliver^a, Hollie M. Putnam^b, and Ruth D. Gates^b

^aAustralian Institute of Marine Science, Townsville MC, QLD 4810, Australia; and ^bHawaii Institute of Marine Biology, ,

 GLOBAL CHANGE

Coral microbiome dynamics, functions and design in a changing world

Madeleine J. H. van Oppen^{1,2*} and Linda L. Blackall¹



Conclusion and future directions

- **Integrating ecology and microbiology**
 - Role of microbes in ecosystem function
 - New tools for management
- **Enhancing resilience into the future**
 - Host genotype + microbiome (and life-stage)
 - Mediating macro-macro interactions, e.g. invasion, herbivory
 - Phase-shifts: host-associated vs “habitat-associated” microbiomes
 - Links to animal and human health



Collaborators, students, volunteers:

Peter Steinberg, Torsten Thomas, Mel Coleman,
Suhelen Egan, Adriana Vergés, Paul Gribben, Alex
Campbell, Thomas Wernberg,
Kim Lema, George Wood, Alex McGrath, Seb Vadillo,
Sandra Straub, Sofie Vranken, Louise Castro,
Rose Fuggle, Renske Jongen

Lim-Sutton



Recreational
Fishing Trusts



Department of
Primary Industries

SCELSE

Singapore Centre for Environmental Life Sciences Engineering



Australian Government

Australian Research Council



