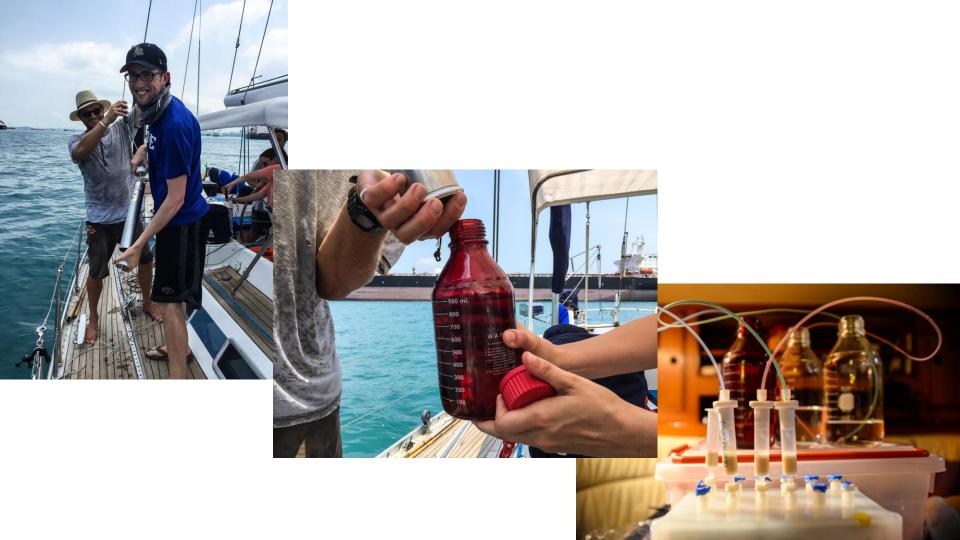


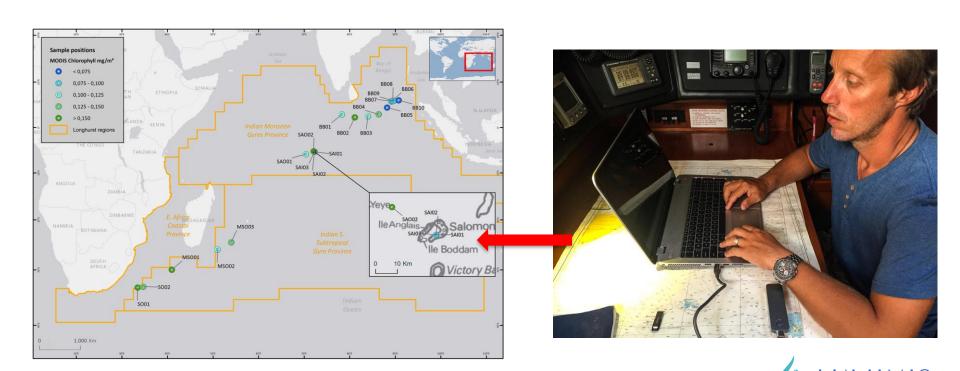
Decoding the microbiome

To solve the disease crisis in aquaculture



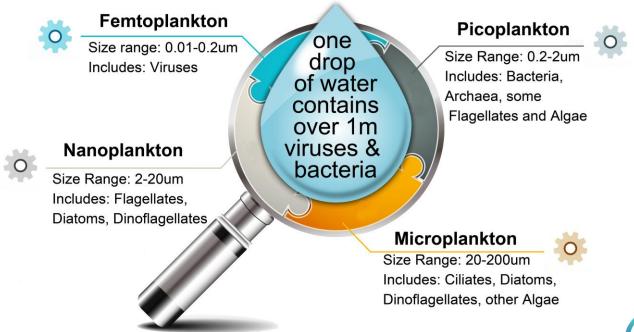


Established first microbiome baseline across the Indian Ocean and Chagos Archipelago (British Indian Ocean Territory)





What is the microbiome? Why is it gaining so much interest? Why is it important? And why haven't we looked at it before?







Genomic complexity

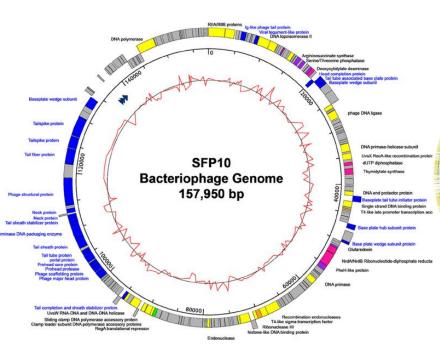
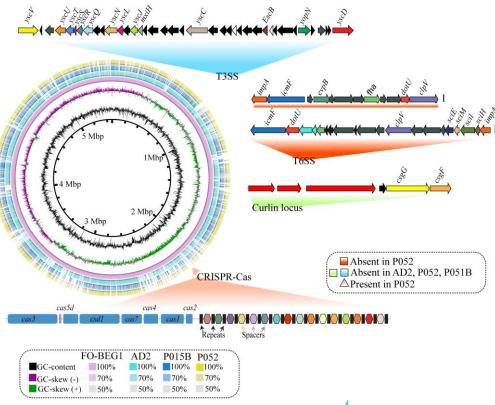


Fig 5

Genome-wide BLAST comparison of proposed minimal genomes of *P. axinellae* AD2, *P. stylochi* UST20140214-052, and *P. hongkongensis* UST20140214-015B with *Pseudovibrio* so. FO-BEG1.

Innermost circle represent the raw skeletal structure. Second, third, and fourth circles represent GC-content, GG-skew, and all predicted ORFs (open reading frames) of the reference genome FO-BEG1. Fifth, sixth, and seventh circles denotes similarity of predicted ORFs shared among AD2, UST20140214-052, and UST20140214-015B. Major gene clusters absent and detected in the genomes of AD2, UST20140214-052, and UST20140214-015B are indicated outside the circle. Absent gene clusters from top to clockwise direction- type 3 secretion systems (T3SSs), cluster I and cluster II of type 6 secretion system (T6SSs), and curlin locus. The only gene cluster, CRISPR-Cas detected in UST20140214-052 was represented at the bottom of the ring. Seven CRISPR associated genes (CAS)—cas3, cas5, cas7, cas7, cas4, cas1, and cas2 are shown in blue color. CRISPR locus detected downstream of CAS operon are represented by repeats (black) and soacers (colored diamond shapes).

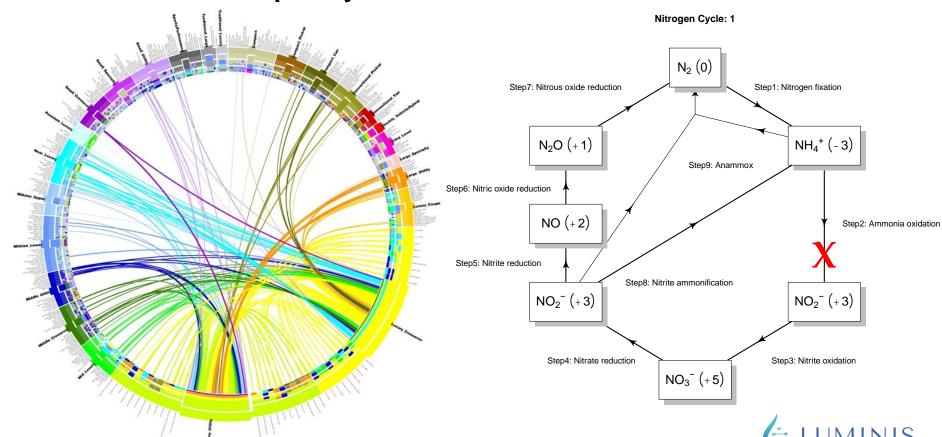
Pseudovibrio spp



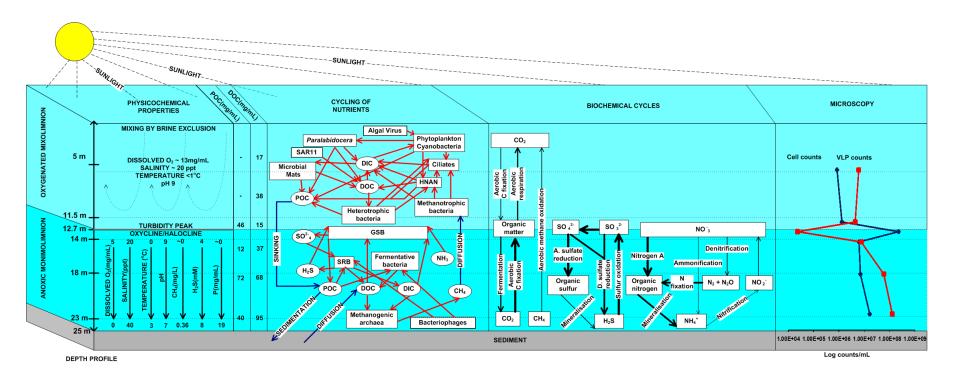
Source: Alex et al., 2018 Plos One



Functional complexity

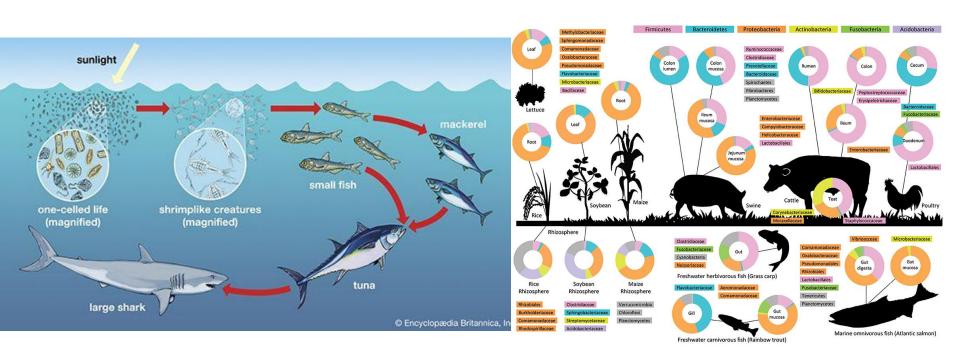


System complexity





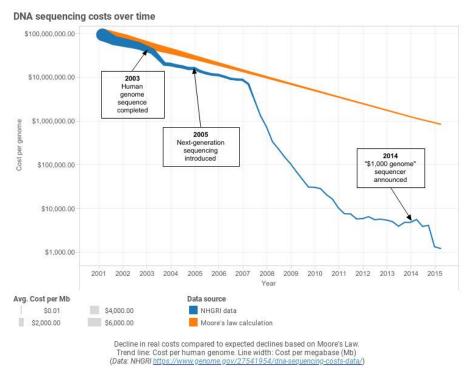
Why is the microbiome important?

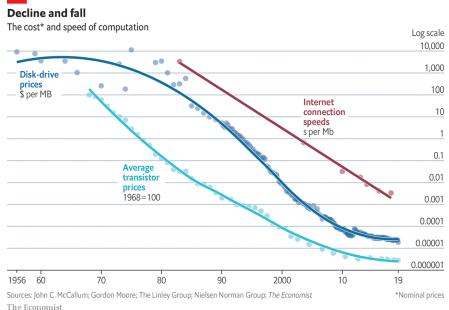


Underpins all life on planet earth



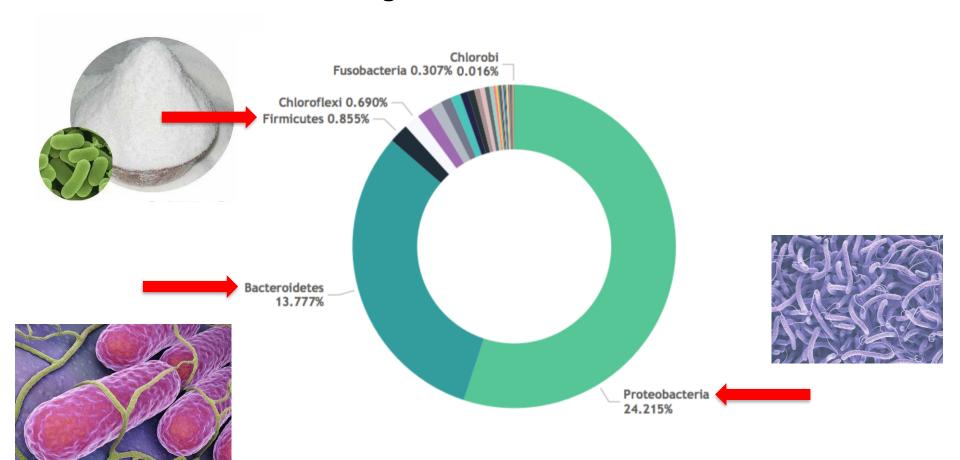
Why now?







Putting Faces to the Names



The Zen State of Balance = Free of Disease



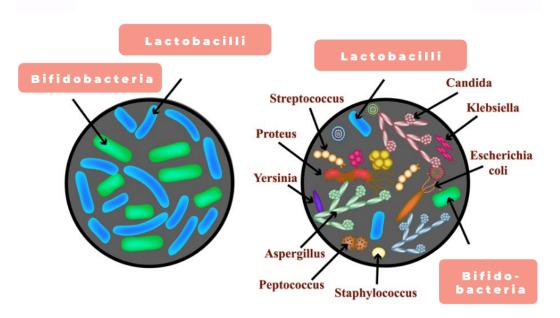


Loss of competitive pressure for resources The Two Step Mechanism of Disease

Step One: Reduced biodiversity

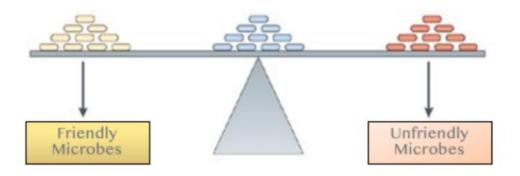
Step Two: A shift in the types of microbes present

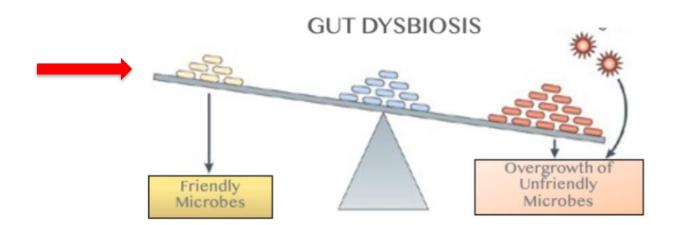
DYSBIOSIS





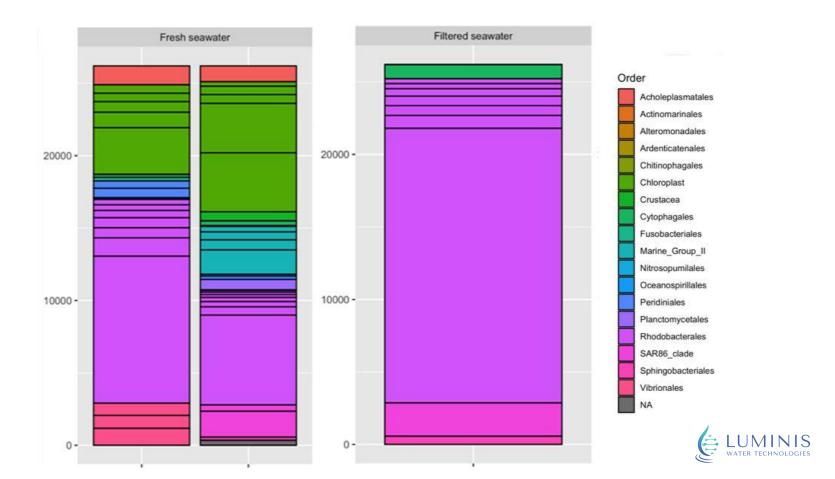
BALANCED GUT MICROBIOTA

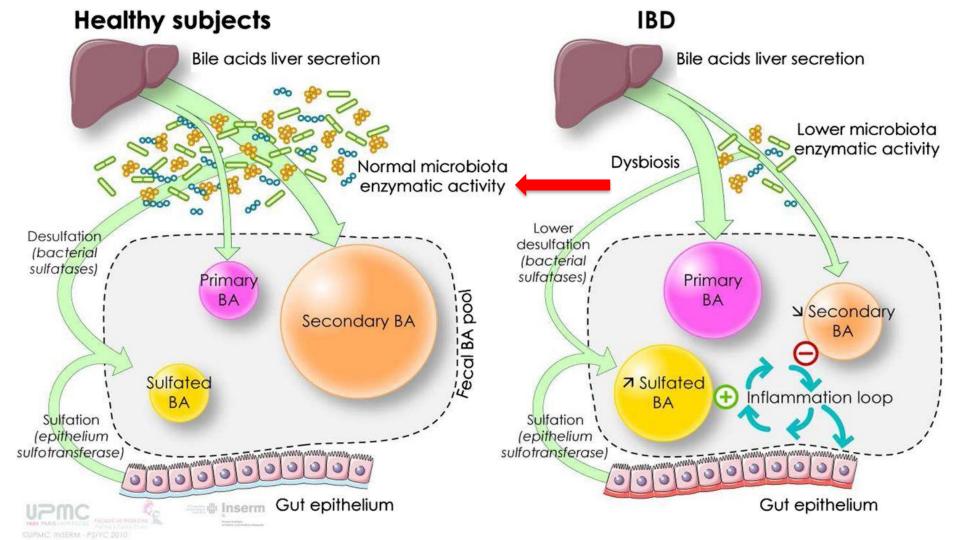






Good vs Bad Biodiversity in Recirculated Aquaculture System (RAS)





Toxin Removal Dysfunction

Function	Altoromonoo	Phaeobacter	Kanaialla	Marivita
			Kangiella	6.8
C-S-01:Organic carbon oxidation - CO oxidation	0	6	0	
C-S-01:Organic carbon oxidation - amino acid utilization	18	2.1		2.4
C-S-01:Organic carbon oxidation - aromatics degradation	3.3	0	0.2	0
C-S-01:Organic carbon oxidation - complex carbon degradat	ior 1.9	0	0	2.5
C-S-01:Organic carbon oxidation - fatty acid degradation	1.9	2.2	0	2.5
C-S-01:Organic carbon oxidation - formaldehyde oxidation	9.4	11.2	0	12.6
C-S-01:Organic carbon oxidation - formate oxidation	9.8	19.8	0	22.3
C-S-01:Organic carbon oxidation - methanol oxidation	0	47	0	53
C-S-02:Carbon fixation - CBB cycle (Rubisco)	0	80.2	0	0
C-S-03:Ethanol oxidation	1.8	3.6	0	4
C-S-04:Acetate oxidation	1.1	0	0.1	0
C-S-05:Hydrogen generation	0	0	0	0
C-S-06:Fermentation	1.9	2.2	0	2.5
C-S-08:Methanotrophy	5.3	10.6	0	0
C-S-09:Hydrogen oxidation	22.4	0	0	0
N-S-04:Nitrate reduction - napAB	0	0	0	0
N-S-04:Nitrate reduction - narGH	47.9	0	0	76.4
N-S-05:Nitrite reduction - nirKS	0	0	0	0
N-S-07:Nitrous oxide reduction	0	0	0	0
N-S-08:Nitrite ammonification - nirBD	97.8	48.4	0	0
N-S-08:Nitrite ammonification - nrfADH	2.2	0	0	0
O-S-01:Iron reduction	1.2	0	0	0
O-S-02:Iron oxidation:	10.2	12.1	0.2	0
S-S-01:Sulfide oxidation - sqr	11.6	0	0	0
S-S-03:Sulfur oxidation - sdo	0.8	2.3	0	2.6
S-S-04:Sulfite oxidation	0	0	0	43.5
S-S-05:Sulfate reduction	0	0	0	43.5
S-S-07:Thiosulfate oxidation	0	26.1	0	29.4

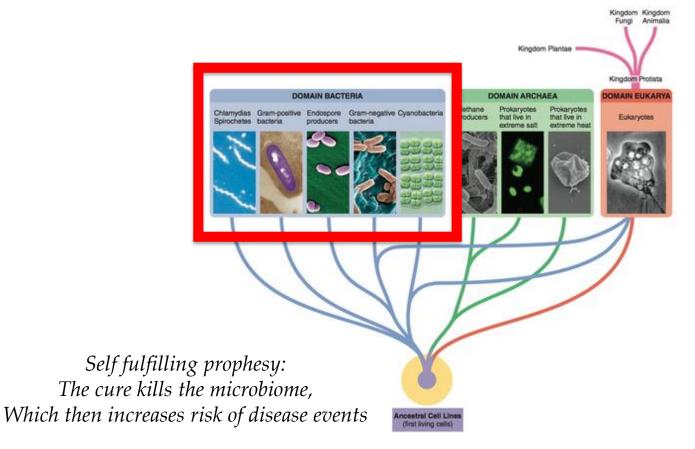
How Is Dysbiosis Induced?

Reason 1. Disinfection & Use of Antibiotics

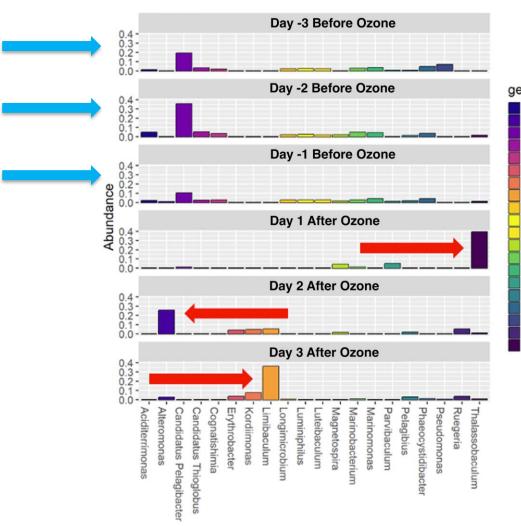
Reason 2. Protocols are not optimized



Antibacterial Catch 22: Kill off some pathogens, but also lose biodiversity

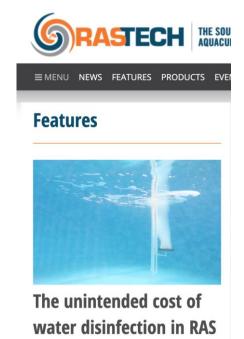






genus

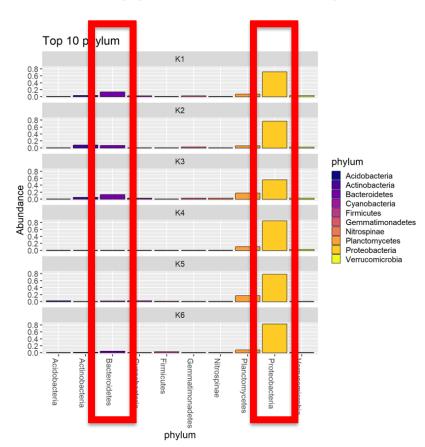
Aciditerrimonas Alteromonas Candidatus Pelagibacter Candidatus Thioglobus Cognatishimia Erythrobacter Kordiimonas Limibaculum Longimicrobium Luminiphilus Luteibaculum Magnetospira Marinobacterium Marinomonas Parvibaculum Pelagibius Phaeocystidibacter Pseudomonas Ruegeria Thalassobaculum



Water in this state of chaos is not capable of productive farming.



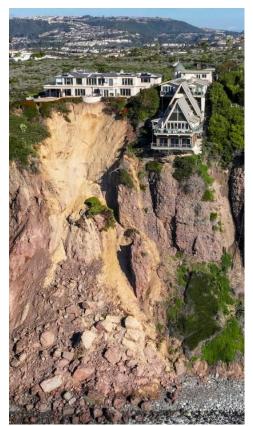
Reason 2. Protocols Are Not Optimised (disinfection is too aggressive, dosing is wrong, etc)





Typical State of Water Health During Growout



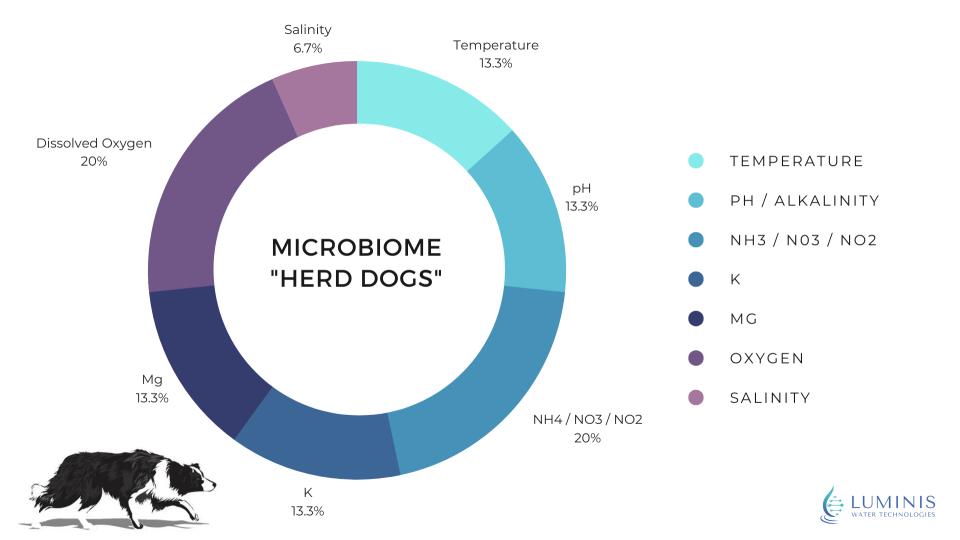




Next Gen Sequencing based Microbiome Engineering

Solution:





NGS-Guided Precision Probiotics

and Targeted Inoculants



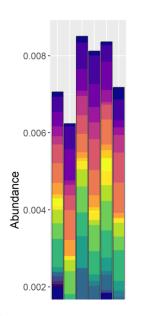
Personalised Medicine for Ponds and Tanks







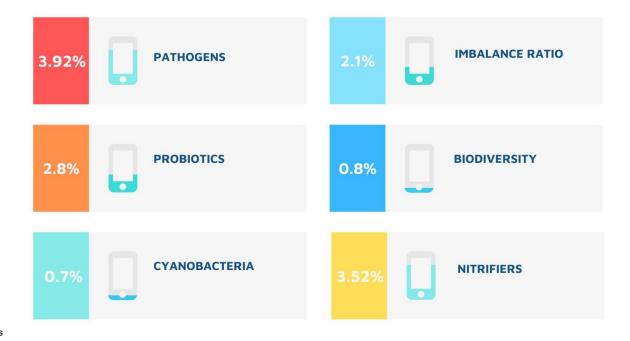
Six Key Aspects of Water Health





Bacillus amyloliquefaciens
Bacillus cereus
Bacillus coagulans
Bacillus licheniformis
Bacillus marisflavi
Bacillus pumilus
Bacillus subtilis
Bifidobacterium adolescentis
Bifidobacterium animalis
Bifidobacterium bifidum
Bifidobacterium breve
Bifidobacterium longum
Enterococcus faecalis

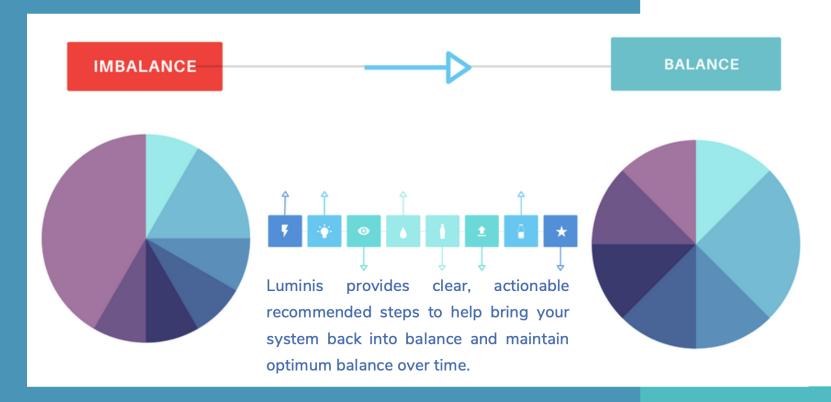
Enterococcus faecium
Lactobacillus crispatus
Lactobacillus gasseri
Lactobacillus pensenii
Lactobacillus jensenii
Lactobacillus jensenii
Lactobacillus kefiranofaciens
Lactococcus lactis
Pediococcus acidilactici
Pediococcus pentosaceus
Saccharomyces cerevisiae
Streptococcus thermophilus



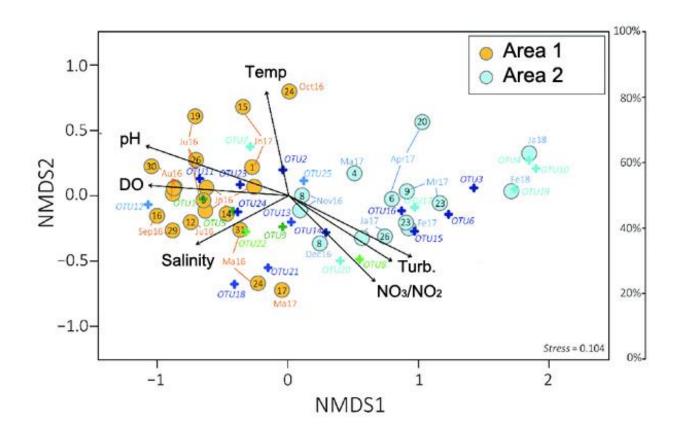


Optimised Protocols

CLEAR STEPS TO CORRECT IMBALANCES



How Do We Identify The Right Parameter?





Luminis Optimised Microbiome Unlocks 56% More Growth





Luminis

Control





Our Mission

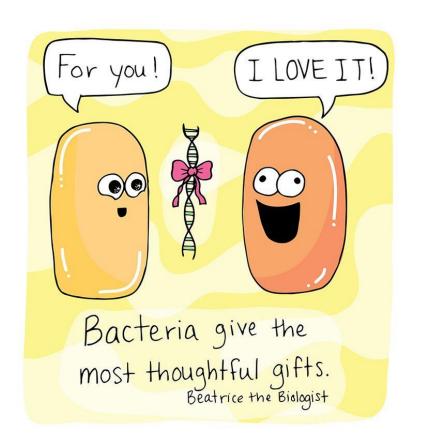
To solve the disease crisis in aquaculture

To underpin sustainability

For a food secure future



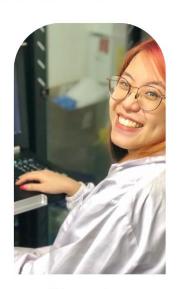




KEY TEAM



Rachelle Jensen CEO & FOUNDER



Simone Low BIOINFORMATICS



Farah Azrini
NEXT GEN SEQUENCING

ADVISORY BOARD



Prof Federico Lauro, NTU SCIENTIFIC ADVISOR



Ayan Desai, Nalanda Capital MARKET EXPANSION



Ian Browne, On Piste BUSINESS DEVELOPMENT



Thank you

WEBSITE

www.luministech.com

CONTACT

rachelle@luministech.com