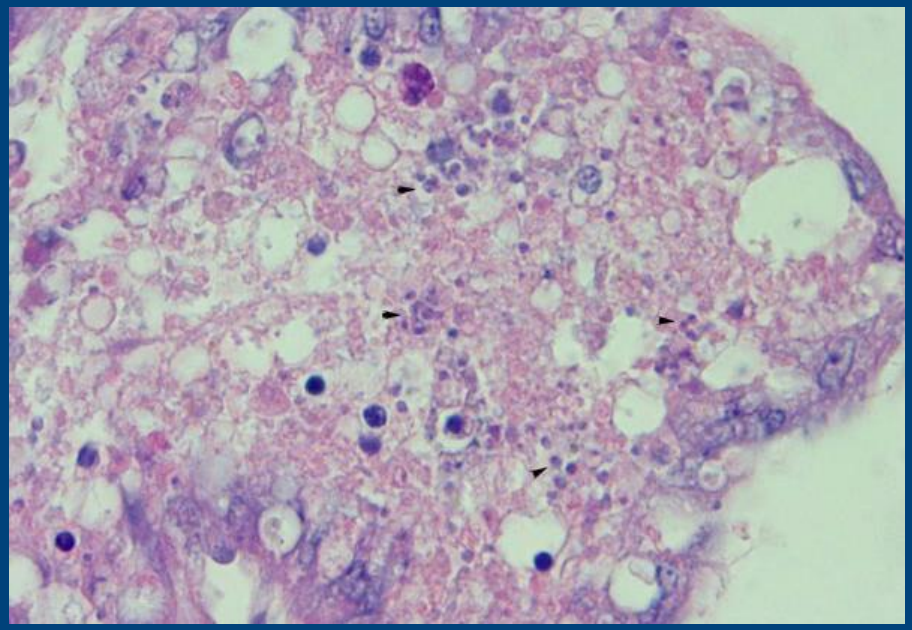


SARDI

Winter mortality of Sydney rock oysters

Cheryl Jenkins
Marty Deveney

7 August 2019

SOUTH AUSTRALIA

Government of South Australia
Primary Industries and Regions SA

SARDI
SOUTH AUSTRALIAN RESEARCH AND DEVELOPMENT INSTITUTE

Dr Cheryl Jenkins

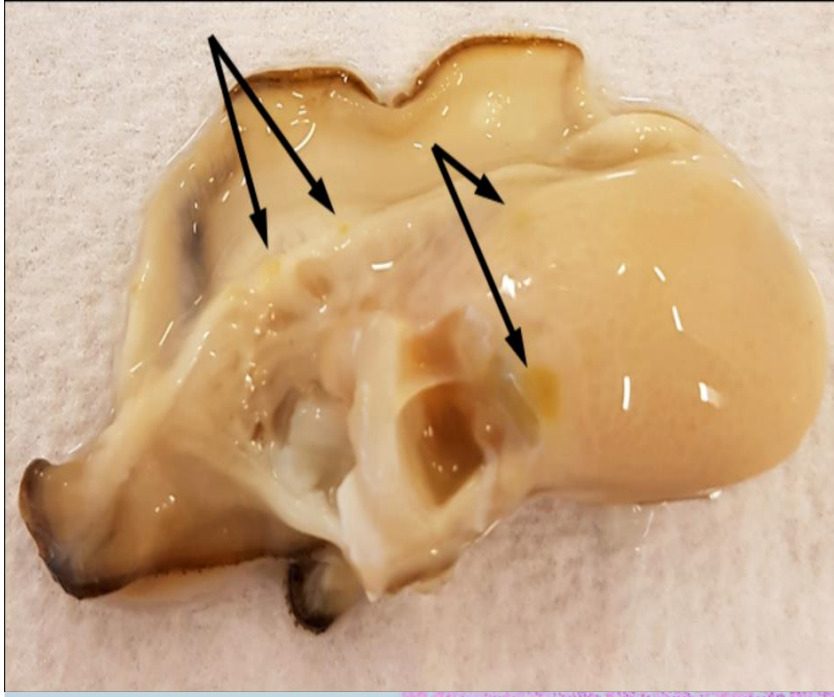
Winter mortality

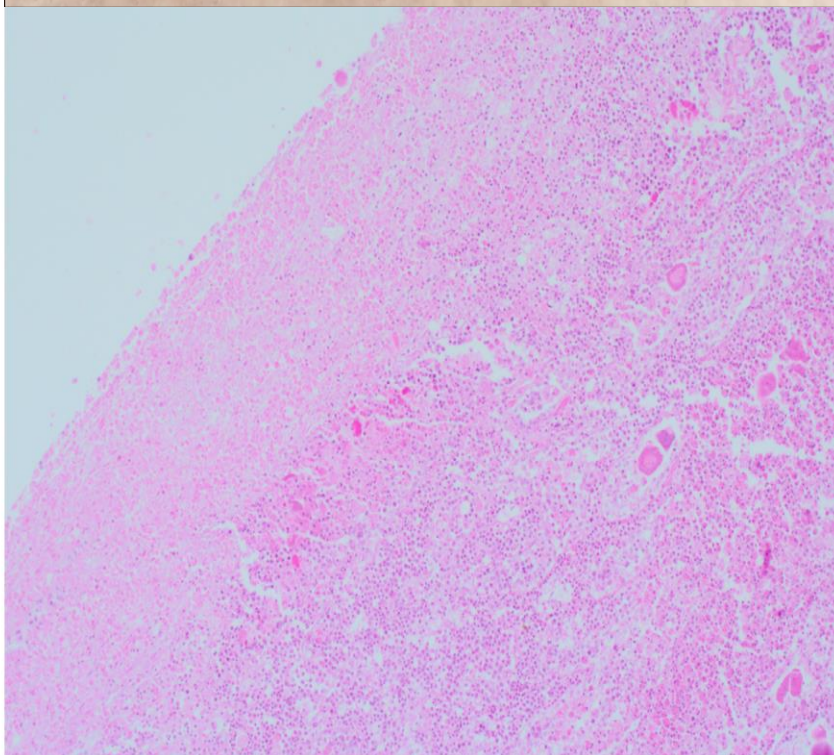
Case definition

Mortalities in adult *Saccostrea glomerata*
July to November
Port Stephens South
High salinity water
Gross focal lesions

Cause?

Microcells (*Bonamia roughleyi*?)
Bacteria





Submission	% mortality	Age	Submitter Comments	Gross lesions present?	Key histological findings	Meets case definition?
1 Crookhaven River	80%	<1.5 yr	Cool and dry conditions	No	No focal lesions.	Wrong age. No lesions.
2 Georges River	10-15%	2 yr	Routine submission	No	Not examined	No. No gross lesions observed.
3 Crookhaven River	80%	<1.5 yr	Cool and dry conditions	No	Not examined	Wrong age. No lesions.
4 Nelsons Lagoon	50%	(Spat) 0.5 yr		No	Alimentary duct hyperplasia. Non-specific infiltration.	Wrong age. No lesions.
5 Clyde River	15-20%	2 yr	No deaths in juvenile oysters on same lease	Yes	Focal lesions.	Yes.
6 Berrys Bay, Shoalhaven River	20%	1.5 yr	Recent frost High salinity	Yes	Focal lesions.	Yes
7 Shoalhaven River	5%	1-2 yr	Routine submission	No	Minimal pathology.	No lesions.

Cases during CRC-P

Cases

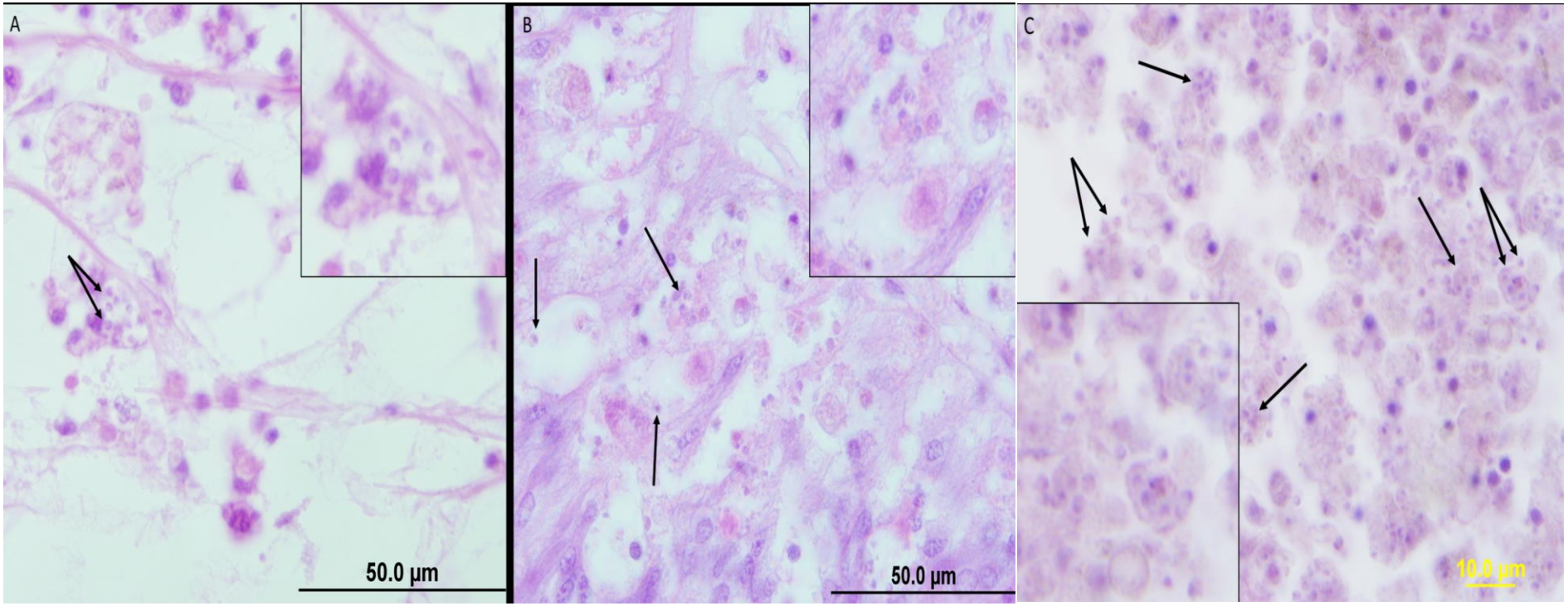
Few (7) submissions
2 meet case definition

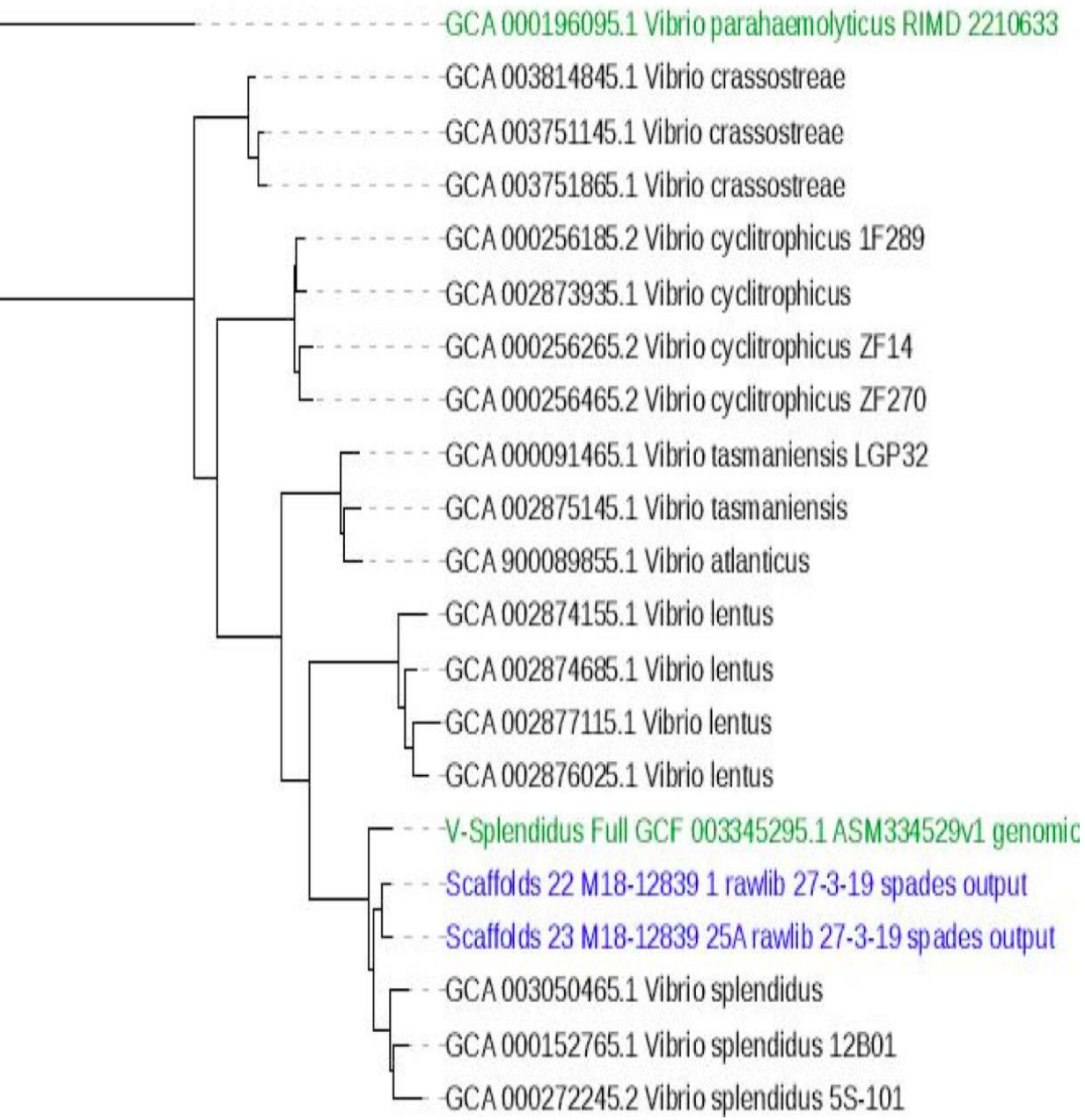
Investigations

Histology
Microcells (*Bonamia*, *Mikrocytos*, *Perkinsus*)
Bacteria – culture, PCR, microbiomics

Microcells

Inconsistent occurrence
PCR negative:
Bonamia assay: Marty et al. 2006
Mikrocytos assay: Garcia et al. 2018
Perkinsus assay: Gauthier et al. 2006





Bacteriology

Species

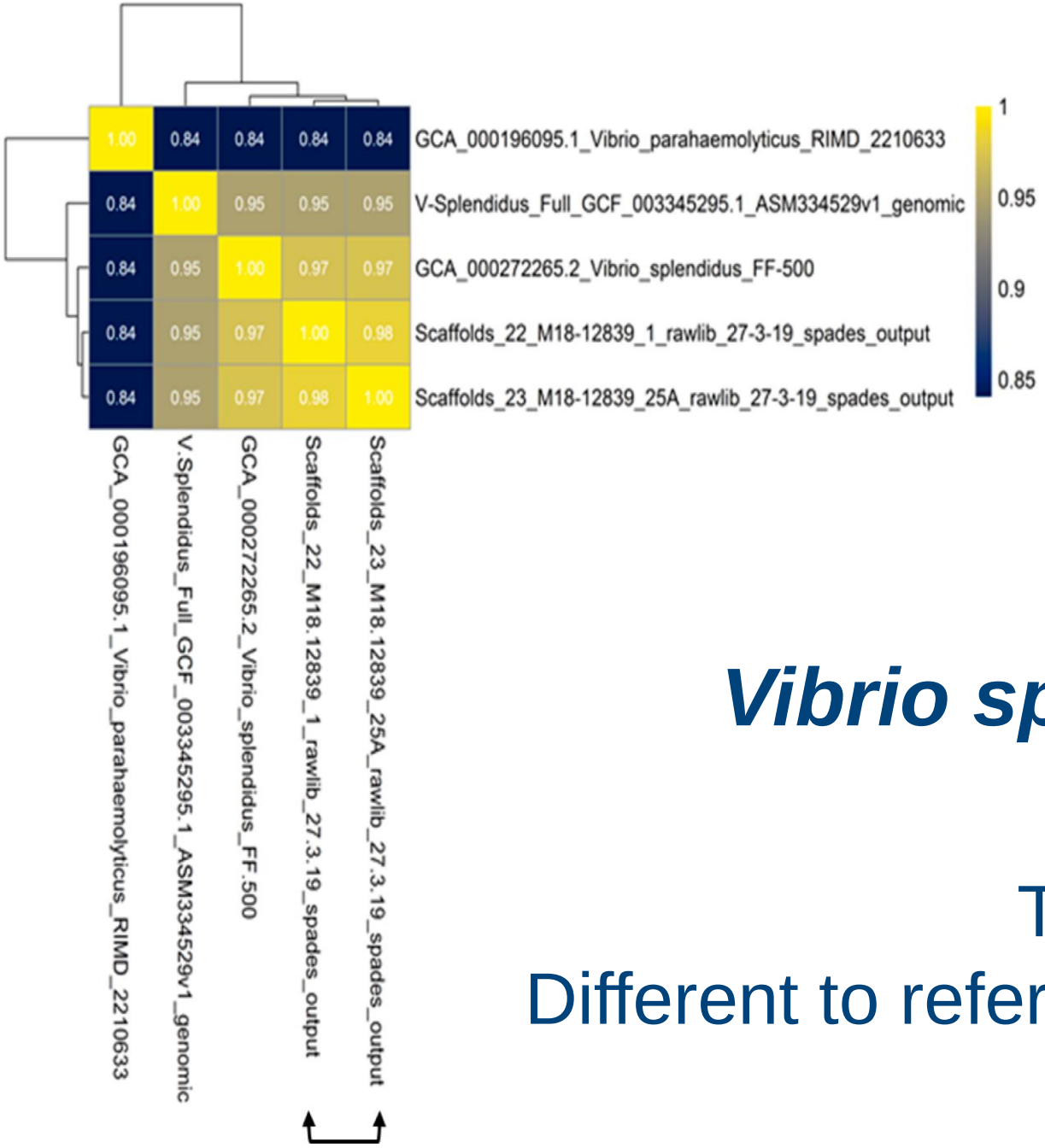
Vibrio splendidus

Characteristics

Known pathogen

Toxin-producing genes

Inconsistent presence

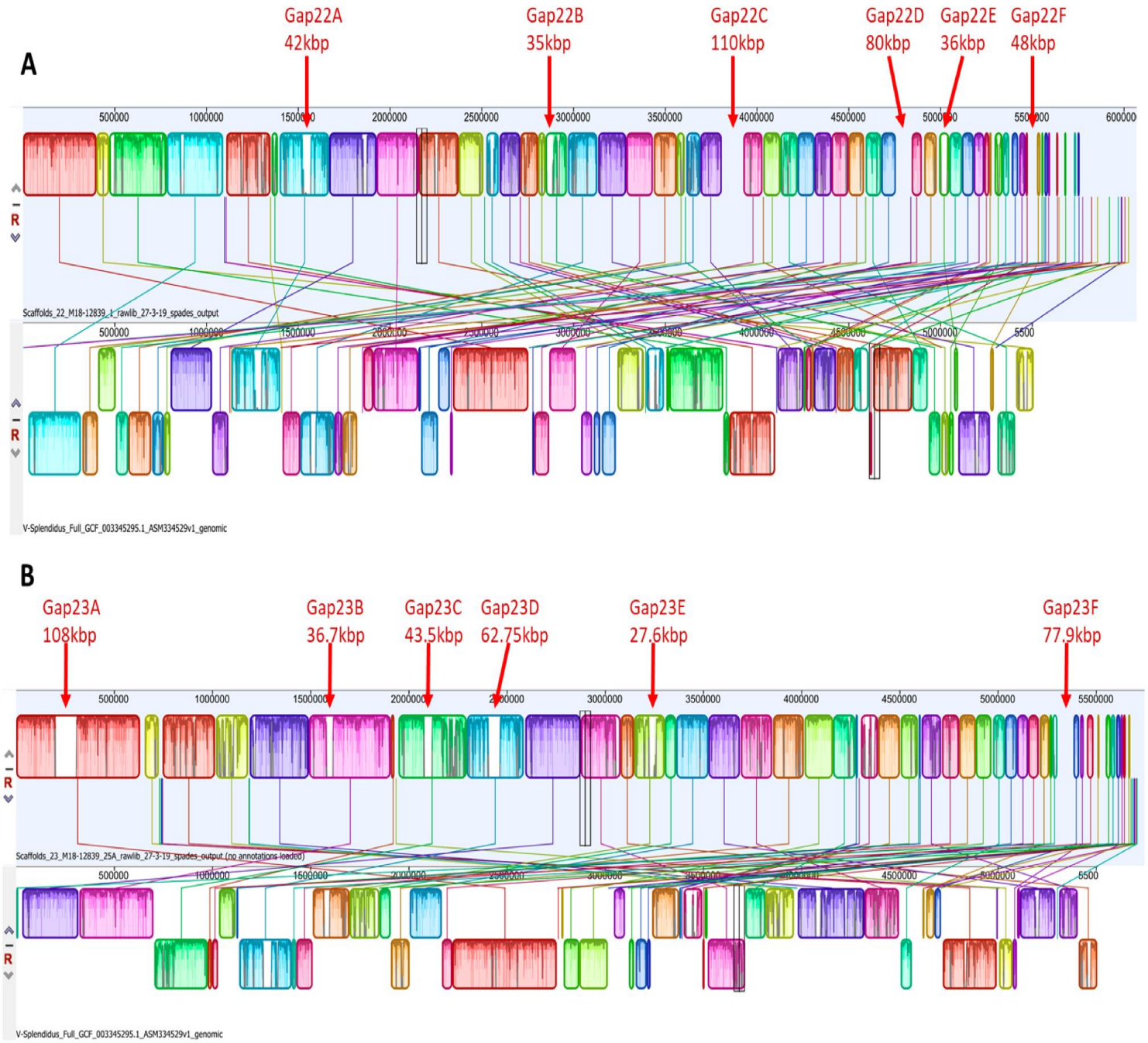


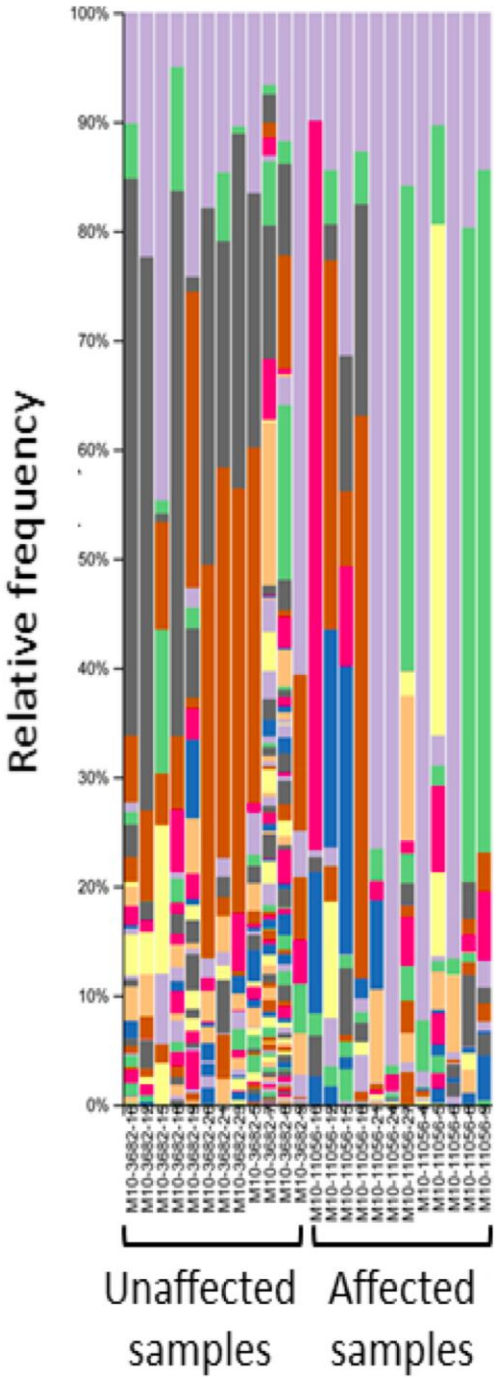
Vibrio splendidus

NGS

Toxin genes

Different to reference strain


A
Gap22A
42kbp
Gap22B
35kbp
Gap22C
110kbp
Gap22D
80kbp
Gap22E
36kbp
Gap22F
48kbp
Scaffolds_22_M18-12839_1_rawlib_27-3-19_spades_output
V-Splendidus_Full_GCF_003345295.1_ASM334529v1_genomic
B
Gap23A
108kbp
Gap23B
36.7kbp
Gap23C
43.5kbp
Gap23D
62.75kbp
Gap23E
27.6kbp
Gap23F
77.9kbp
Scaffolds_23_M18-12839_25A_rawlib_27-3-19_spades_output (no annotations loaded)
V-Splendidus_Full_GCF_003345295.1_ASM334529v1_genomic

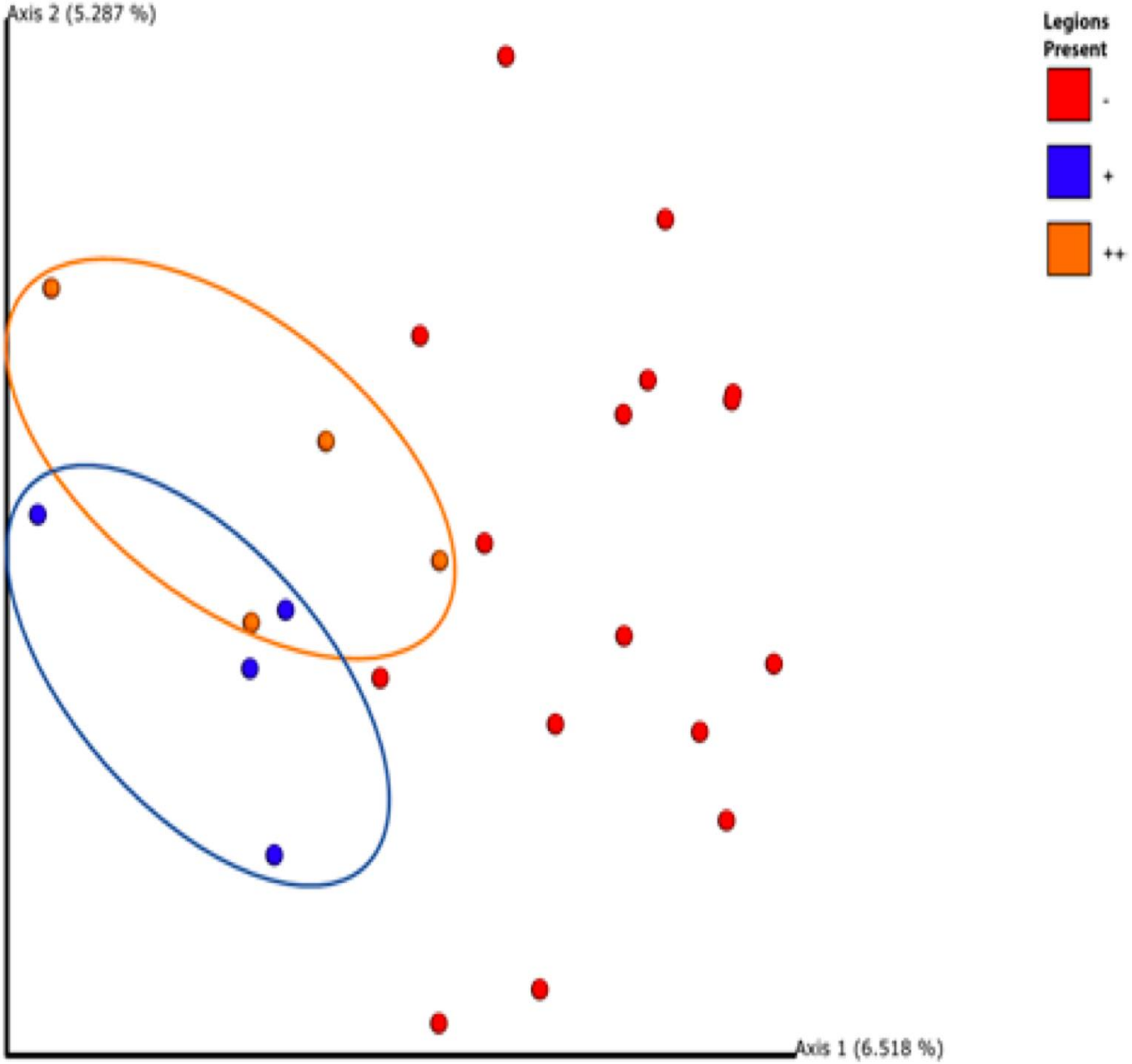


Microbiomics

Community diversity loss

Characteristics

Similar communities in WM cases

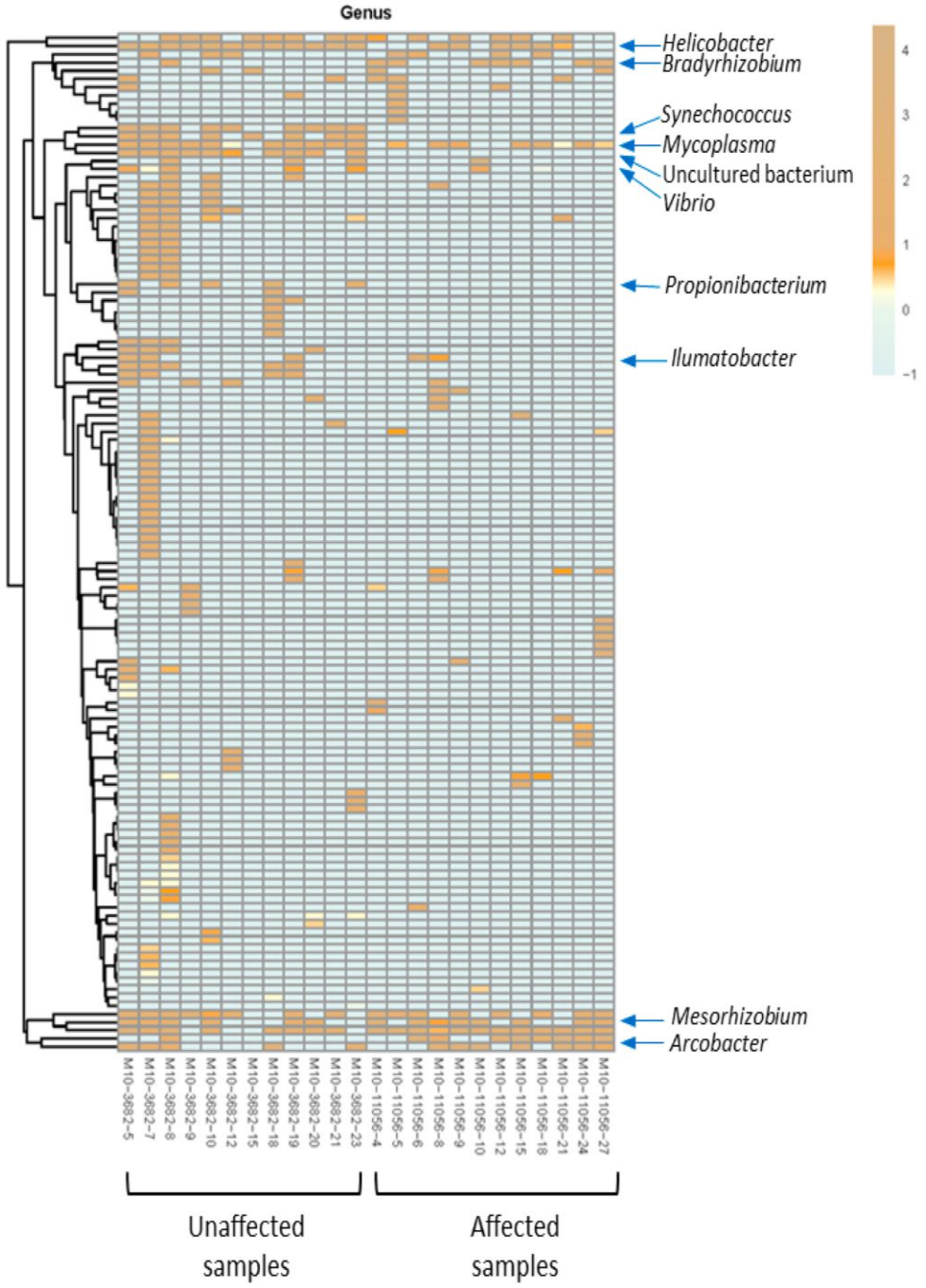

Axis 2 (5.287 %)
Legions Present
-
+
++
Axis 1 (6.518 %)

Bacterial community shifts

Taxa

Bradyrhizobium, *Mesorhizobium* and *Arcobacter* increased

Helicobacter, *Synechoccocus*, *Mycoplasma*, *Propionibacterium*, *Ilumatobacter*, *Vibrio* and unidentified uncultured bacteria decreased



Conclusions

Developed case definition

Investigated 7 events

2 met case definition

Microcells not causative

Definite shifts in bacterial communities

Cause unclear but multifactorial

Acknowledgements

CRC-P, DIIS, Steven Clarke, Xiaoxu Li, Tim Ward, Gavin Begg

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Jenkins, EMAI staff. Cheryl Jenkins, EMAI staff.

When biosecurity works nothing happens