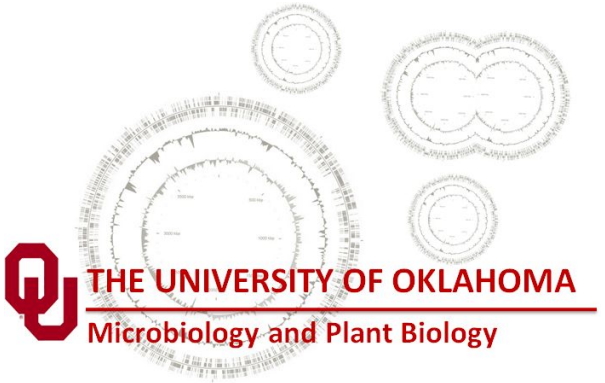
Metabolomics as a tool for corrosion diagnostics: Investigation of produced water samples from different oil field systems with varying rates of corrosion



AUTHORS **Vincent Bonifay**[1], Kathleen Duncan[1], Pierre Souquet[2], Jean Malinge, Iwona Beech[1], Jan Sunner[1]

AFFILIATION 1: University of Oklahoma, Department of Microbiology and Plan Biology, Norman, Oklahoma, 73019, USA.
2: Total SA, Pau, France

Metabolomics – like looking at the painting, not asking which colors were on the artist's palette

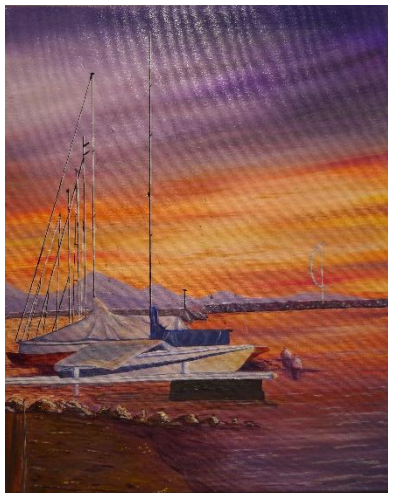
Genomics

What is in the catalog?

Transcriptomics / Proteomics

What parts are in use?

Metabolomics



What is the final product

Metabolomics – like looking at the painting, not asking which colors were on the artist's palette

Genomics

What is in the catalog?
Who is there?

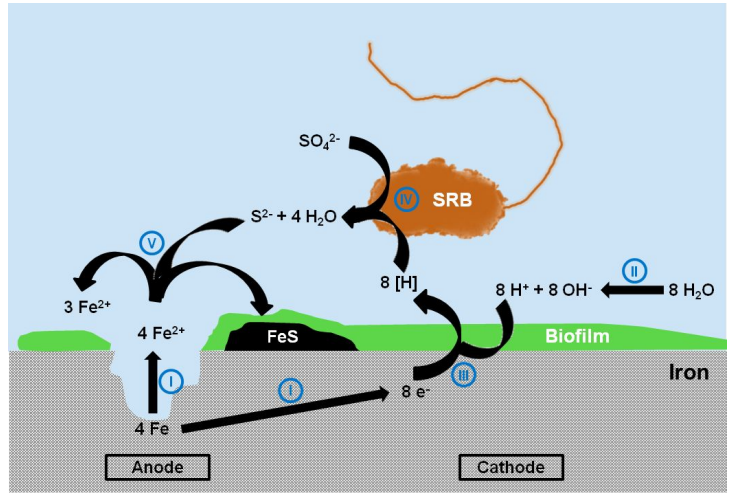
SRB, IOB, Shewanella
…

Transcriptomics / Proteomics

What parts are in use?
What are the capabilities?

BssA, AssA, RusA
…

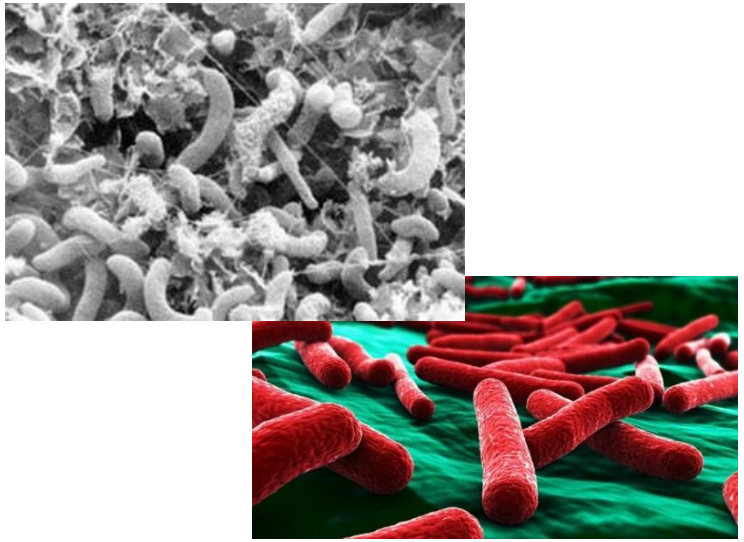
Metabolomics



What is the final product?
Corrosion or not?

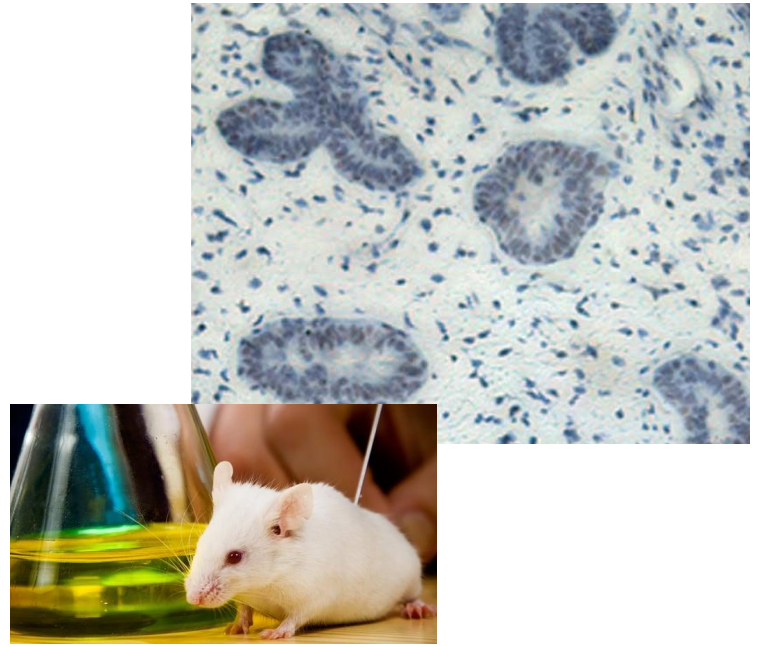
S. Kakooei, World Applied Sciences Journal 17 (4): 524-531, 2012

Many metabolomic pathways are widely shared, enabling species-independent analysis



Bacteria and arcaea
SRB, IOB, NRB, *E. coli* …

Yeast



Tissue culture

Goal: a powerful and affordable tool for mitigation and prediction of corrosion

Field: Gas, oil, fracking, off shore, or on shore

Samples analyzed:
Produced water, pigging debris

Ongoing or future corrosion?

Case study - background

3 production areas in 3 different countries separated in 8 fields:

- A1 and A3 are separate fields
- B1/B2/B3 -same field different sampling points
- B4 to B8 and B15 to B19 - same field different sampling and time points
- C11/12/13/14 : 4 are different fields.

3 areas, low MIC, fossil MIC and active MIC

A

Fossil MIC
Previously corroding but now under control due to strong biocide treatment
2 samples (A1 and A2)

From field/operator data

B

No MIC
Chemical corrosion
3 Samples (B1, B2, B3)

Strong MIC (December 2015)
5 Samples (B4 to B8)

Strong MIC duplicate (August 2016)
5 Samples (B15 to B19)

C

Known/possibility of MIC
3 samples:

- **C11, known MIC**
- **C12, presence of SRB**
- **C14, indication of MIC**

Low/No MIC
Biocide controlled
1 sample (C13)

3 areas, low MIC, fossil MIC and active MIC

A

Low cell count
Fermicutes
(halanaerobiales)
Genes:
anaerobic degradation of alkanes, BTEX and phenols

From metagenomics data

B

High cell counts
APB Fermicutes
(Caminicella)
Genes:

High cell counts
SRB/APB Fermicutes
(thermoanaerobacterales)

Genes:
methanogenesis (mcrA), sulfate reduction, anaerobic degradation of alkanes, BTEX and phenols

C

Known/possibility of MIC
3 samples:

- **C11, known MIC**
- **C12, presence of SRB**
- **C14, indication of MIC**

Low/No MIC
Biocide controlled
1 sample (C13)

Relative abundance SRB/APB + IR: B > C > A

Heatmap

A Strong biocide treatment

B CO_2 corrosion

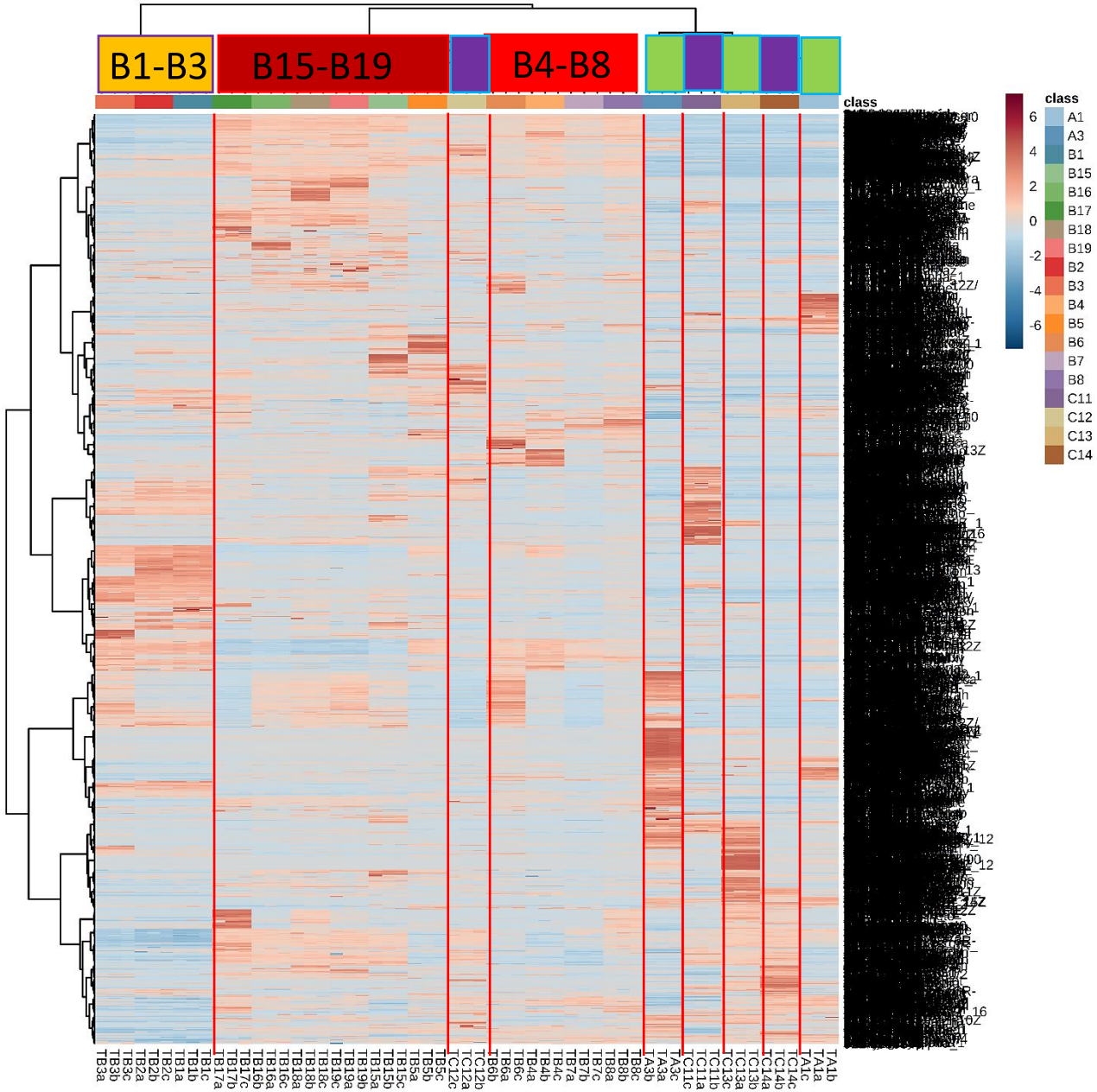
C Low MIC

B High MIC – sampling 2015

B High MIC – sampling 2016

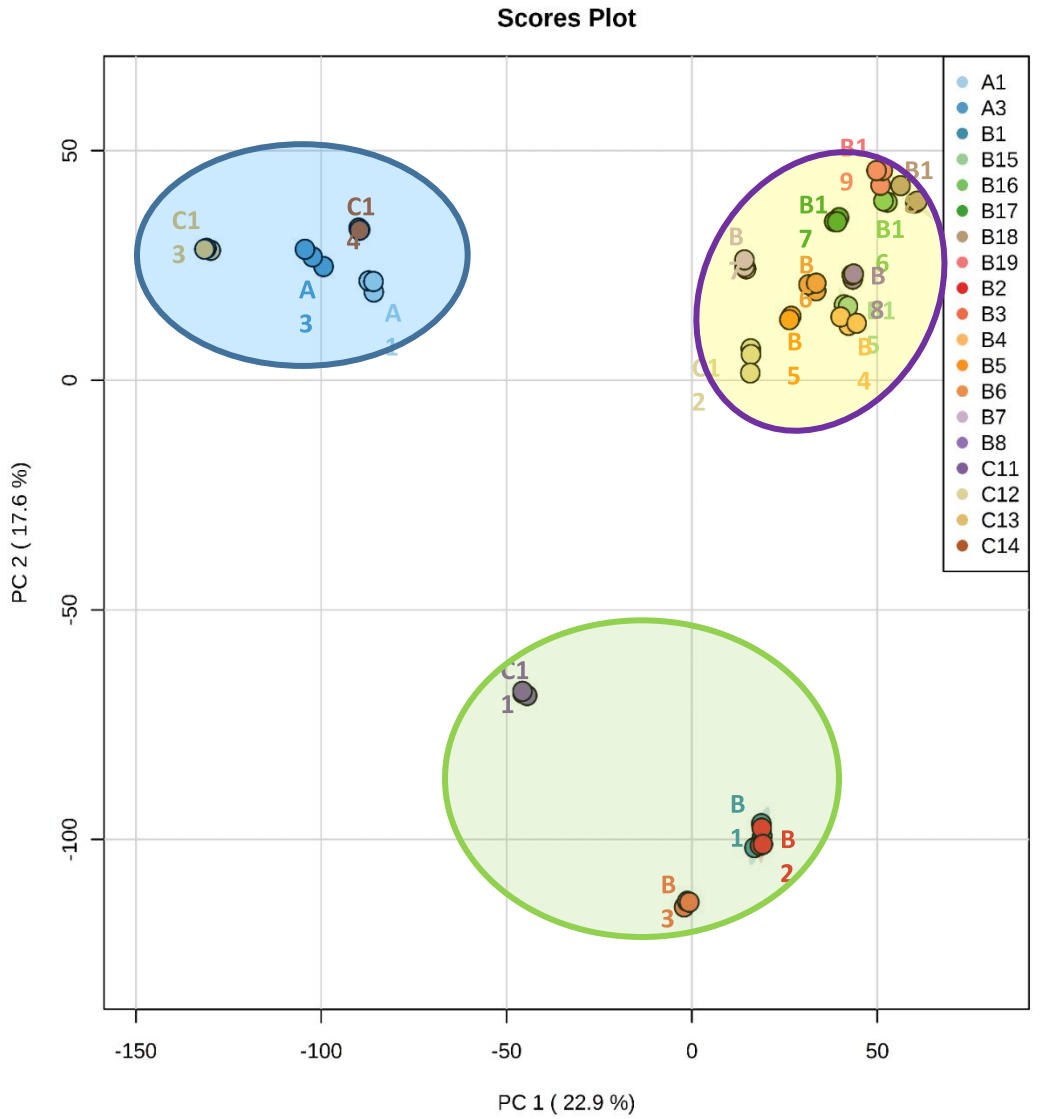
- Grouping corresponding to the
- Each group shows a different metabolome

- The duplicate (B15-B19) show some differences with the original (B4-B8)= time differences



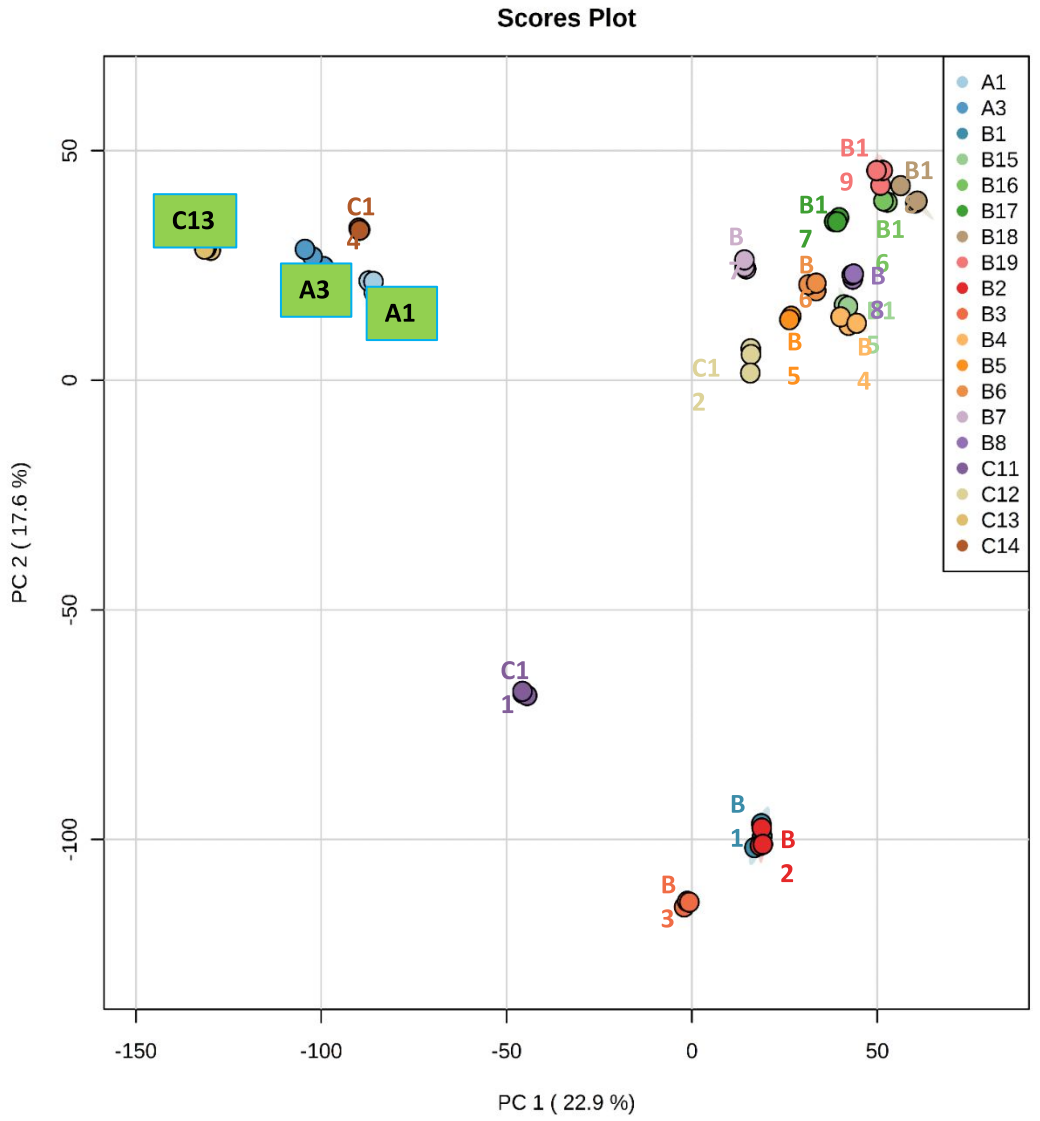
Principal component analysis shows a separation into 3 groups

3 distinct groups were first noticed during the principal component analysis



Principal component analysis support the field information

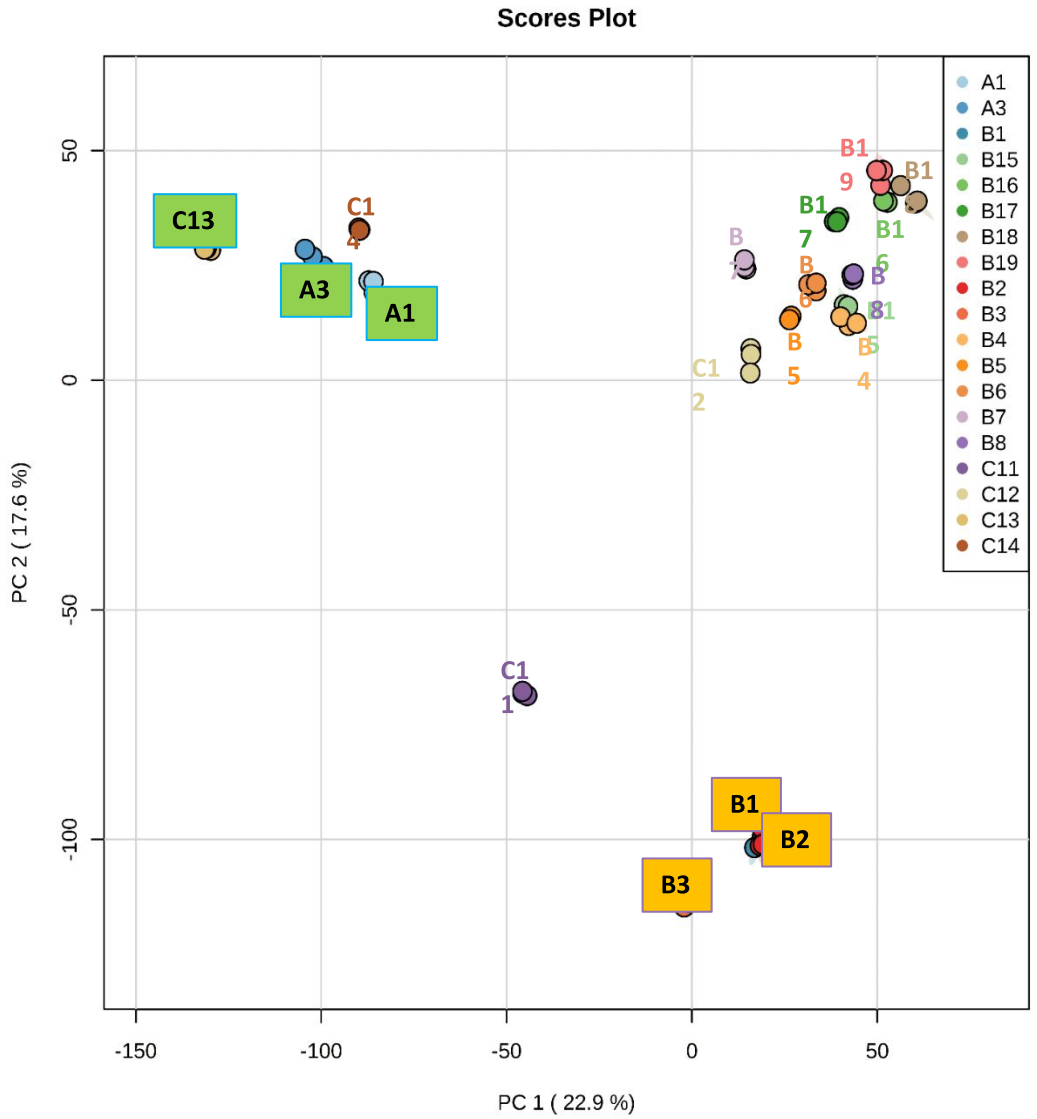
A Strong biocide treatment



Principal component analysis support the field information

A Strong biocide treatment

B CO_2 corrosion

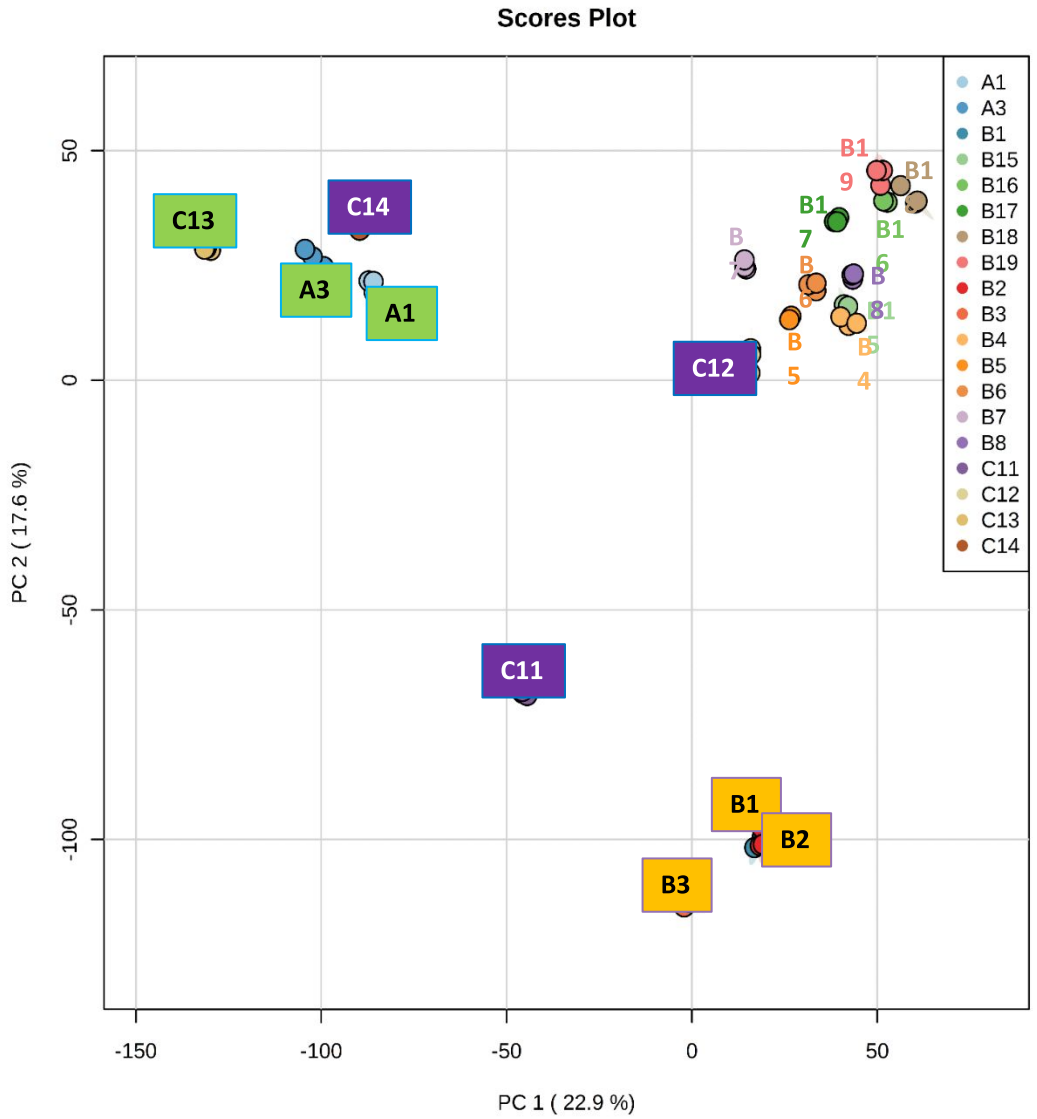


Principal component analysis support the field information

A Strong biocide treatment

B CO_2 corrosion

C Low MIC



Principal component analysis support the field information

A Strong biocide treatment

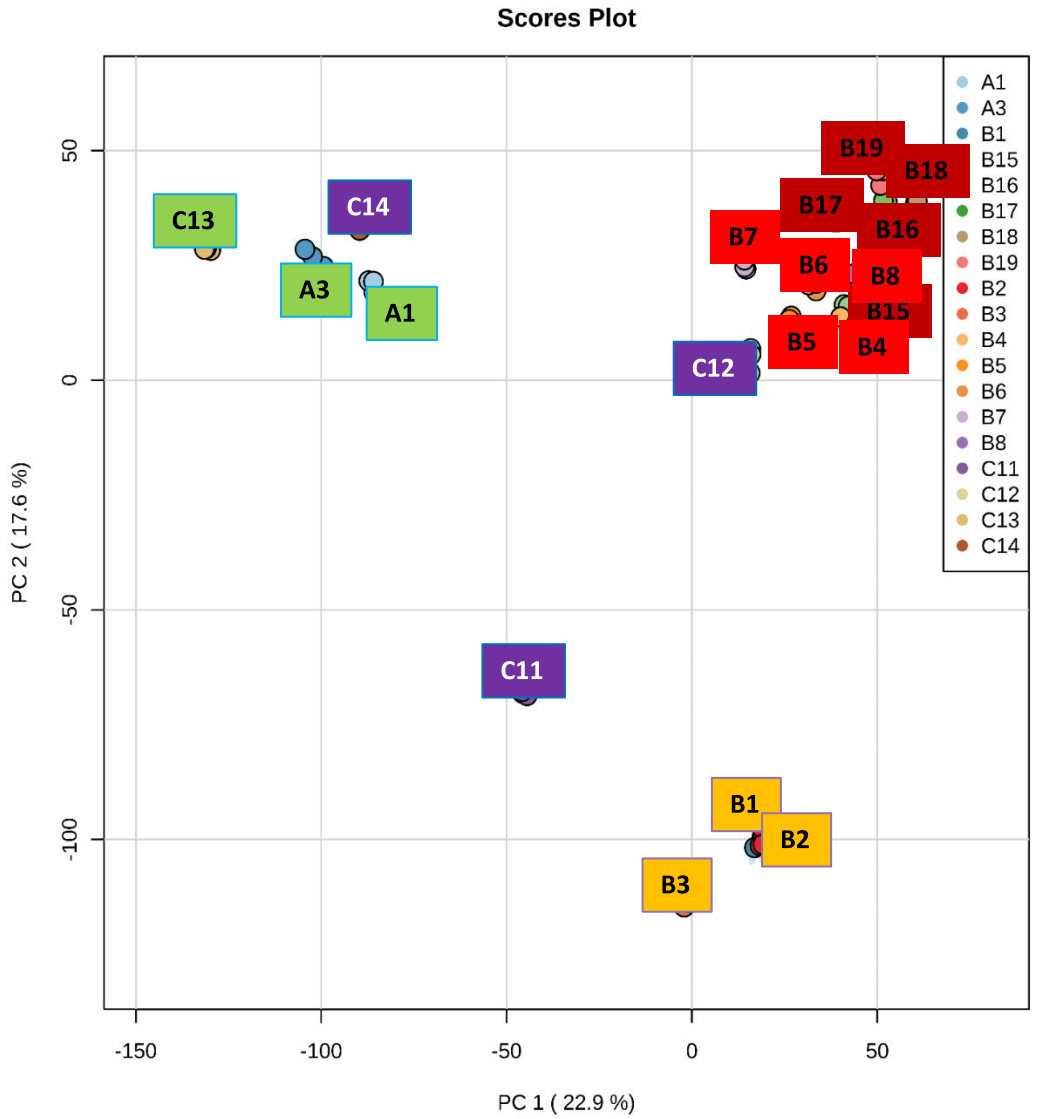
B CO_2 corrosion

C Low MIC

B High MIC – sampling 2015

B High MIC – sampling 2016

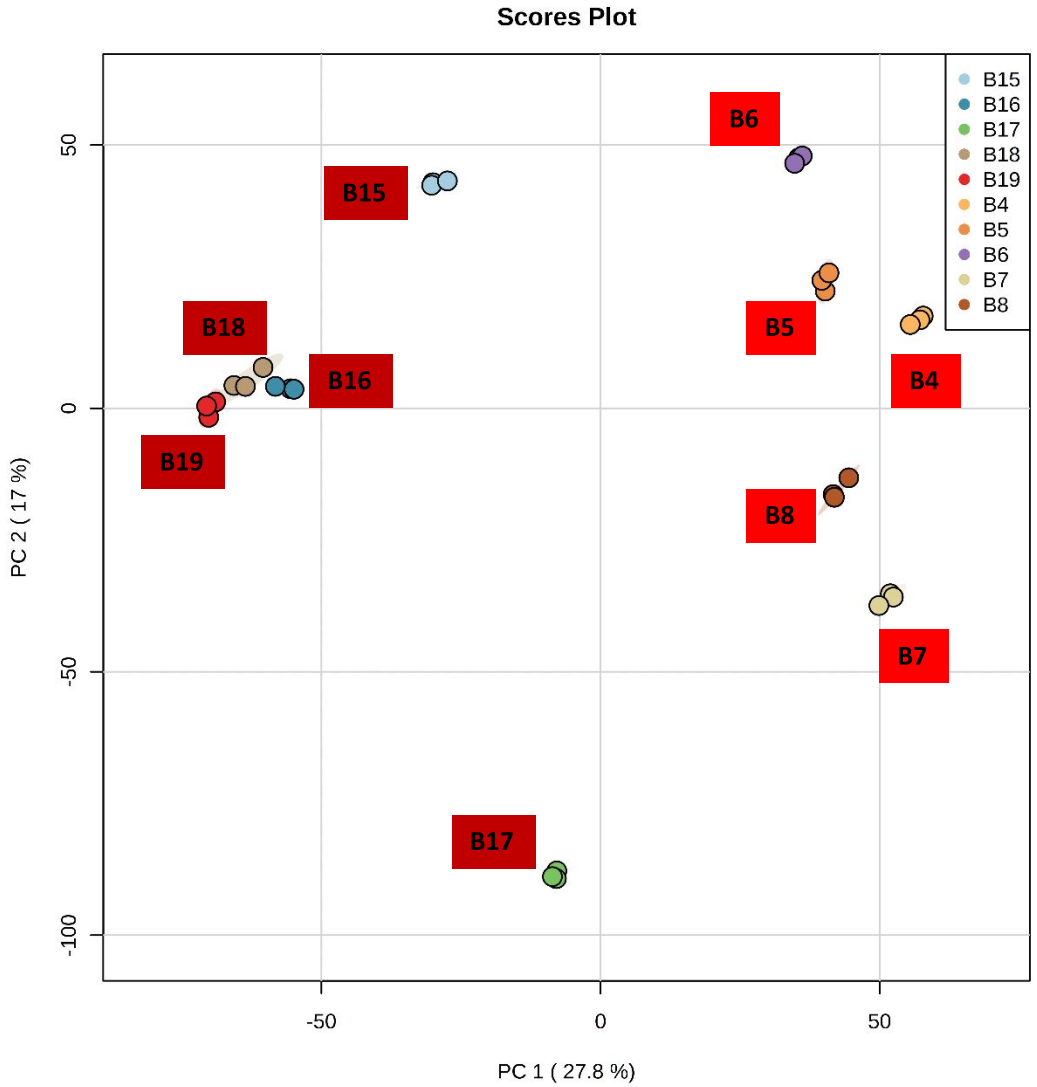
- PC1 is separating biocide treated vs others
- PC2 is separating CO_2 corrosion from MIC and no MIC



High MIC samples separate by potential severity of corrosion

From metagenomics and field data:

- Sample 8 contains the highest abundance of organism with capability to induce corrosion
- Metagenomic data show a higher possibility of corrosion for the later set of samples (august 2016)



B High MIC – sampling 2015

B High MIC – sampling 2016

Principal component analysis: summary of observations

A Strong biocide treatment

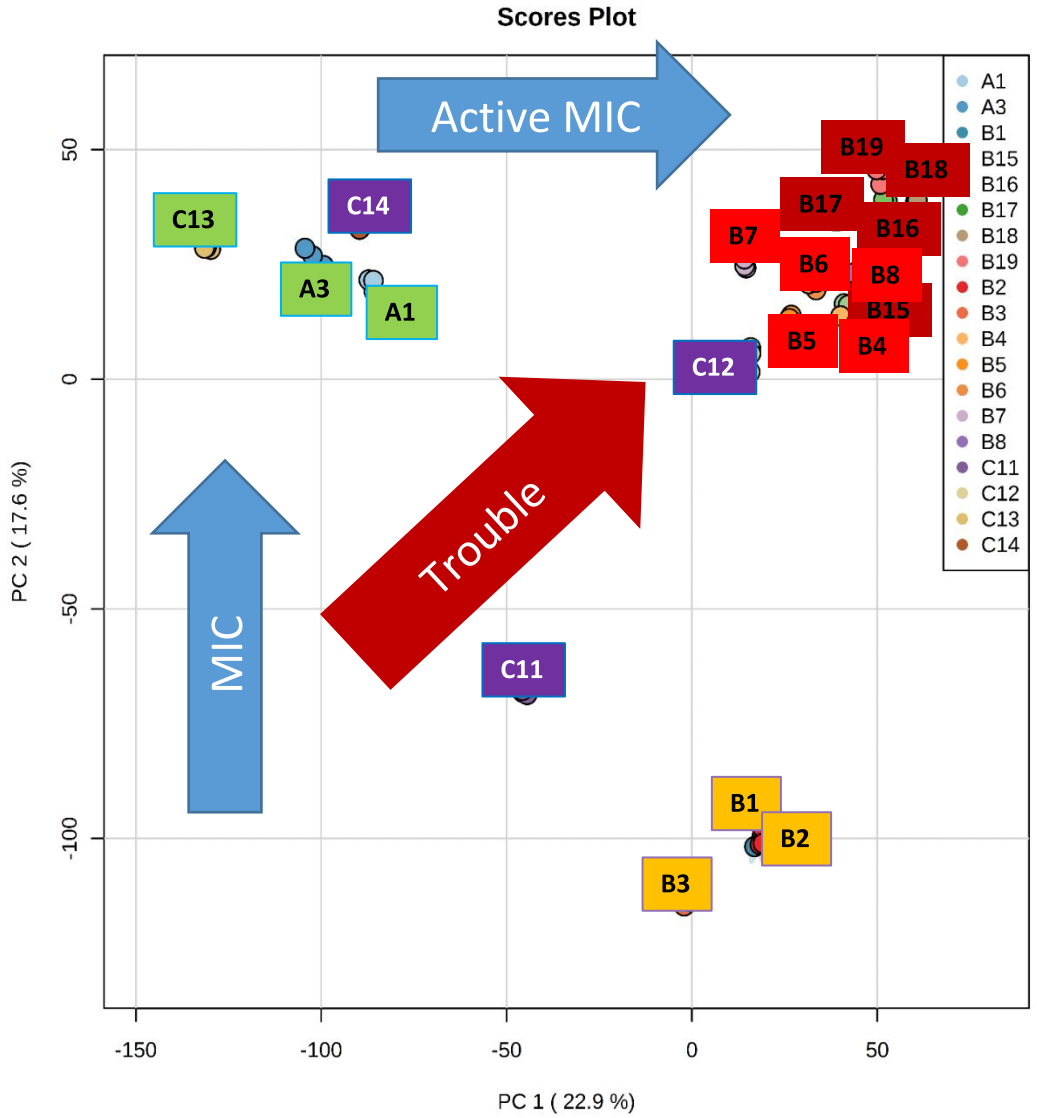
B CO_2 corrosion

C Low MIC

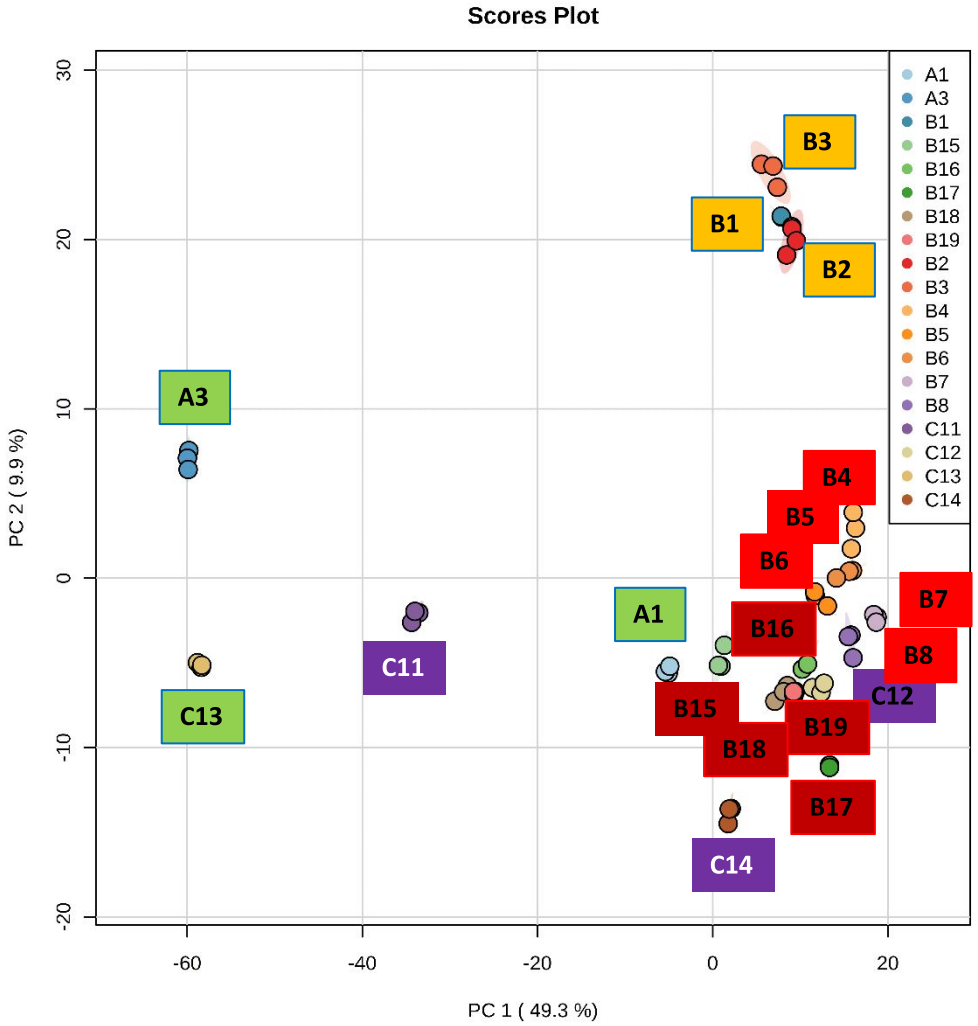
B High MIC – sampling 2015

B High MIC – sampling 2016

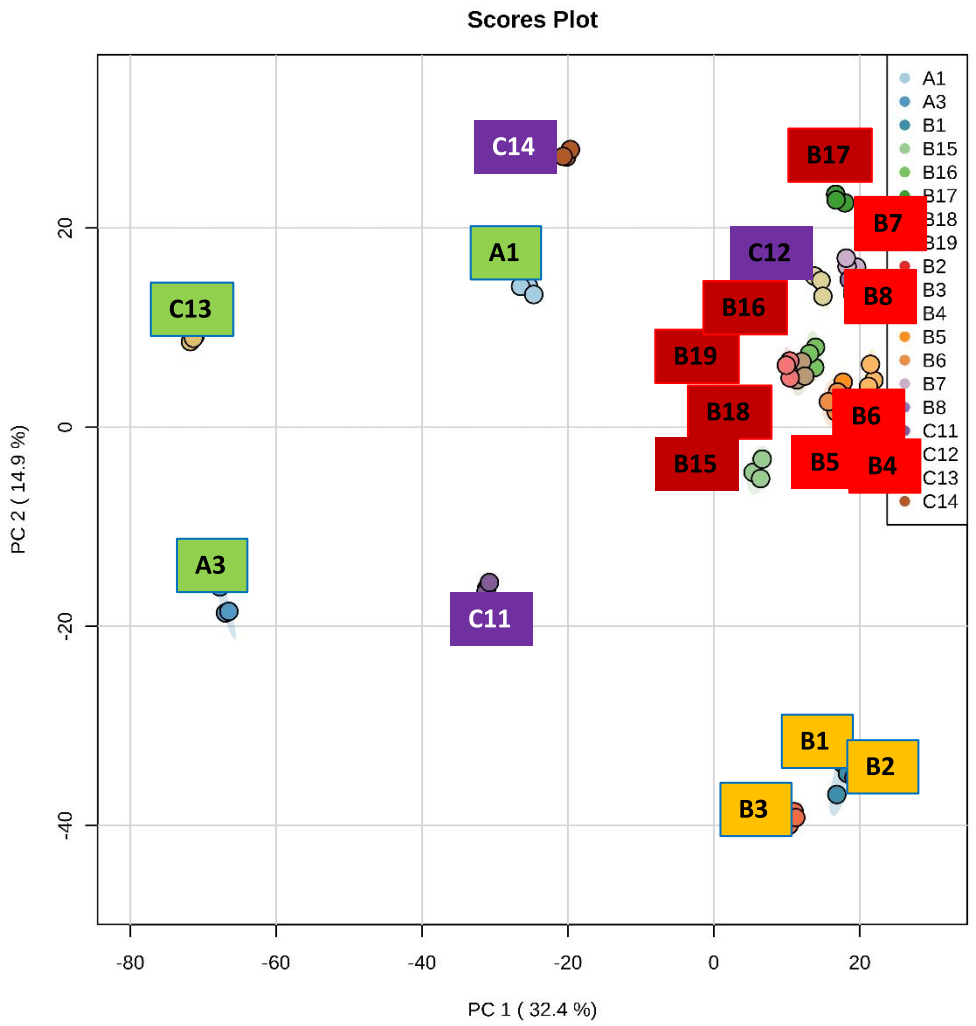
- PC1 is separating biocide treated vs others
- PC2 is separating CO_2 corrosion from MIC and no MIC



Lipids and glycophospholipids are often used to identify organisms, their abundance, activities and environment

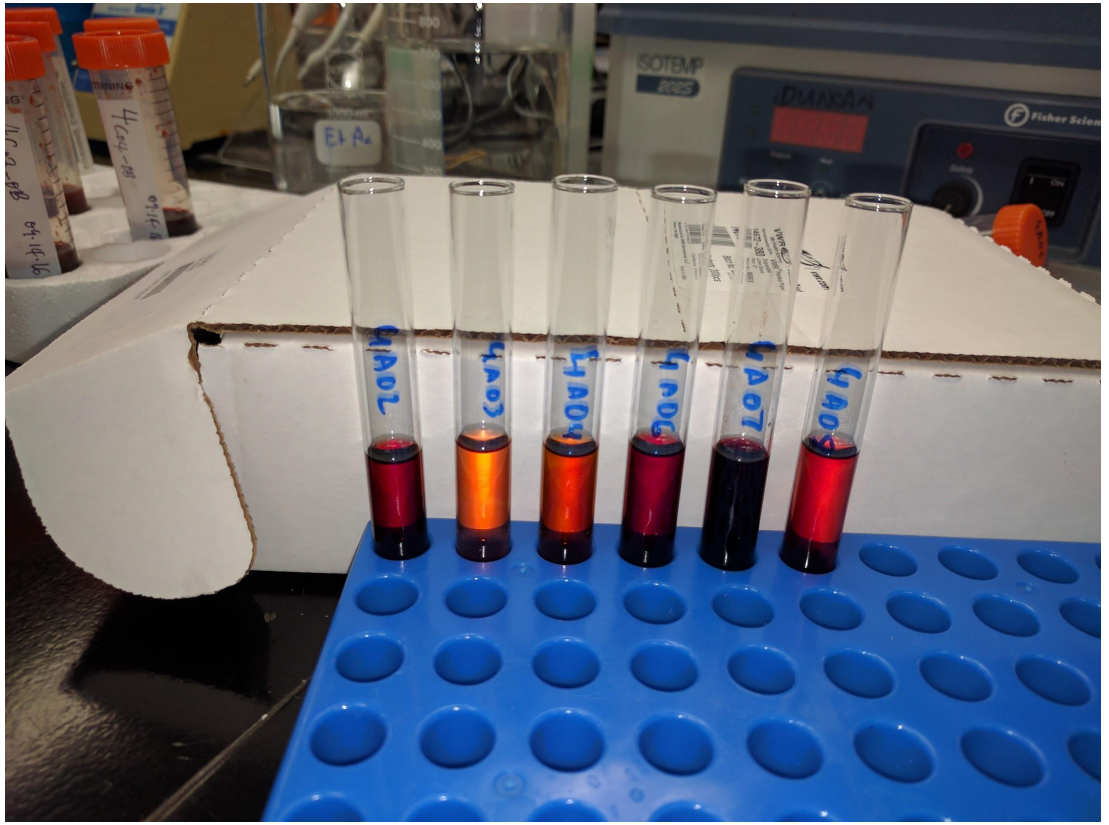


Glycophospholipids



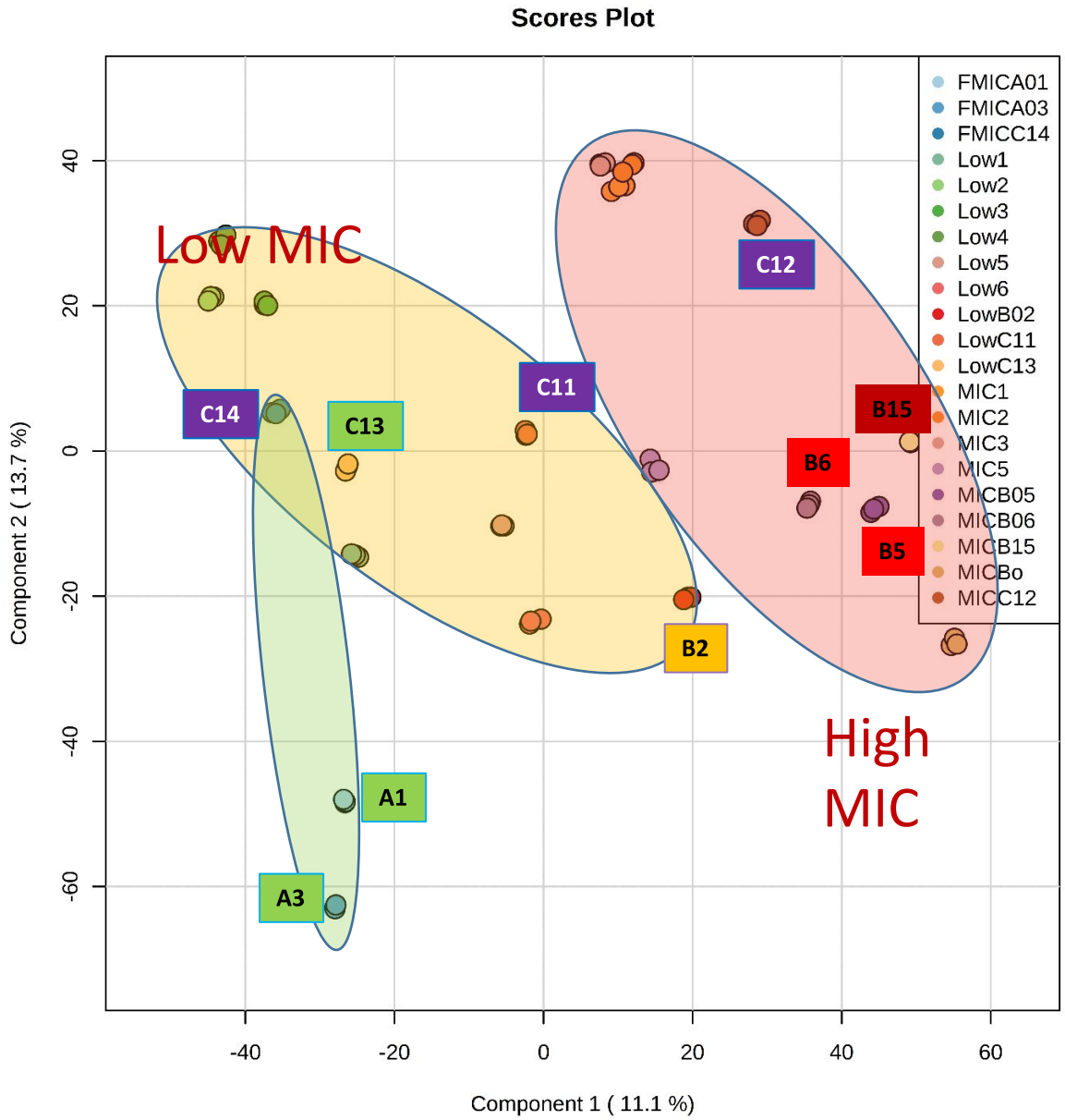
All lipids

How does the samples compare to others?



The severity of the MIC in these fields is in agreement with previous studied samples

- Standards are produced water from different fields/operators
- Similar observations are seen for this case study and standards



Summary and take-home message

- Metabolomic analysis of water produced samples from pipeline experiencing different rates of corrosion were analysed
- Metabolome showed differences that were supportive to the field and metagenome data
- Lipidomic can be used for characterization of severity of MIC in oil and gas industries
- Mitigation of an oilfield corrosion status has been identified using metabolomic
- Metabolomic and/or lipidomic can be used to diagnose and subsequent monitor the oilfield structure (Bulk Liquid surface, Bulk fouling layers, Surfaces or Innermost parts of fouling layers)

Acknowledgements

University of Oklahoma

Metabolomic and Biofilm Group

Pr. Jan Sunner

Pr. Iwona Beech

Metagenomic data

Dr. Kathleen Duncan

Collaboration, sampling and support from TOTAL

Pierre Souquet

Jean Malinge

Mioara Stroe

Thiago Mesquito