

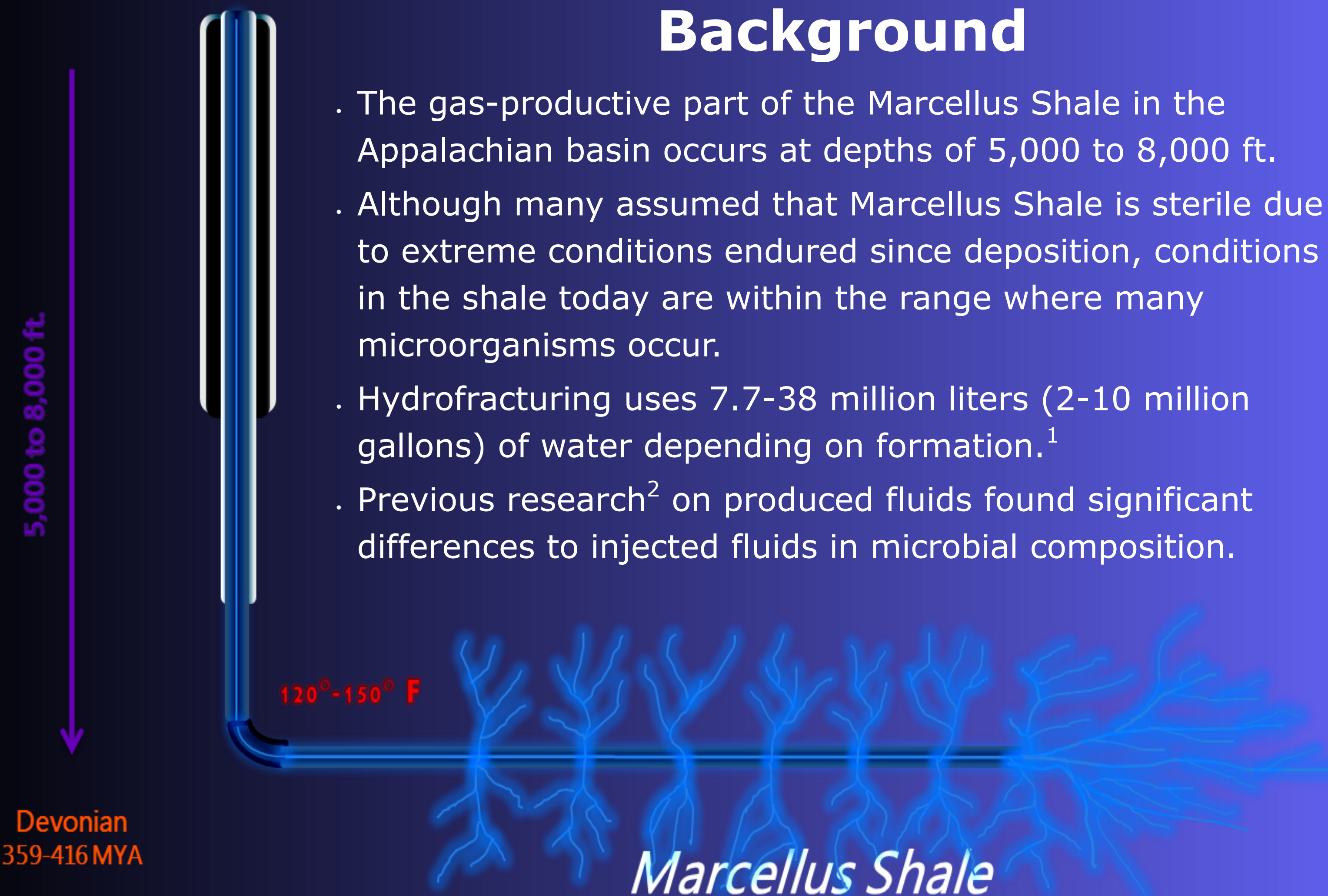
Microbiology of Marcellus Shale: *Life 5,000 Feet Underground*



by Yael Tarlovsky Tucker and Tom Mroz

Background

- The gas-productive part of the Marcellus Shale in the Appalachian basin occurs at depths of 5,000 to 8,000 ft.
- Although many assumed that Marcellus Shale is sterile due to extreme conditions endured since deposition, conditions in the shale today are within the range where many microorganisms occur.
- Hydrofracturing uses 7.7-38 million liters (2-10 million gallons) of water depending on formation.¹
- Previous research² on produced fluids found significant differences to injected fluids in microbial composition.



Hypothesis

Differences in microbial composition of produced fluids could represent a native community of organisms in Marcellus Shale.

Materials and Methods

To determine if the microorganisms were indigenous to the shale itself, or introduced as contaminants during drilling and hydraulic fracturing:

- DNA was extracted from flowback fluids and shale cores from Marcellus wells.
- Once extracted, DNA was amplified using universal (515F) 16S rRNA primers
- Amplified DNA was sequenced using Illumina Sequencing
- Output was processed and blasted to find sequences similar to known organisms



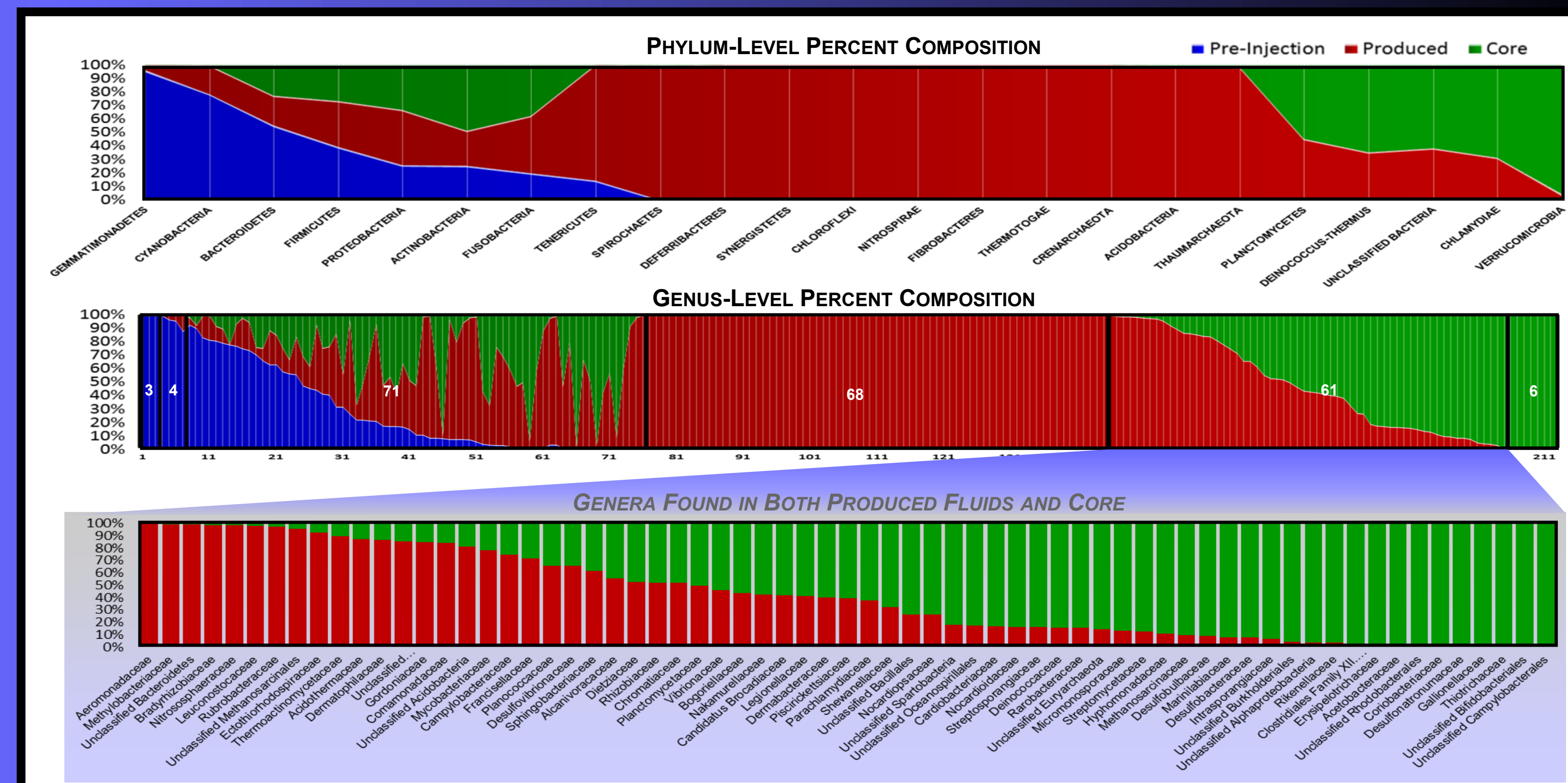
Acknowledgements and References

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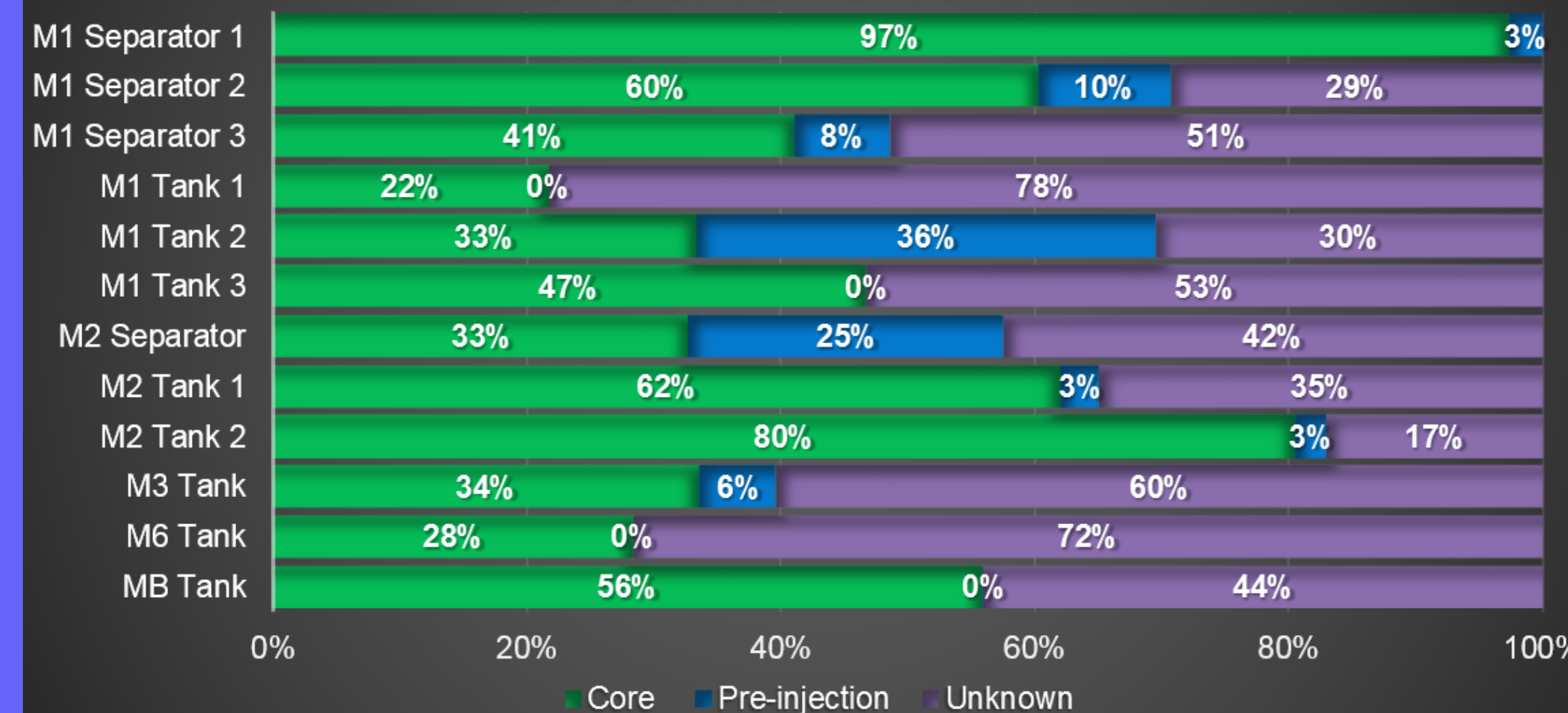
Results and Discussion

Taxonomic Analysis indicated several organisms found in shale core samples were also seen in produced fluids returning to the surface after contact with Marcellus Shale.



Of those identified, many are homologous to known extremophilic organisms that are anaerobic and halotolerant.

SourceTracker % Composition of Produced Fluids

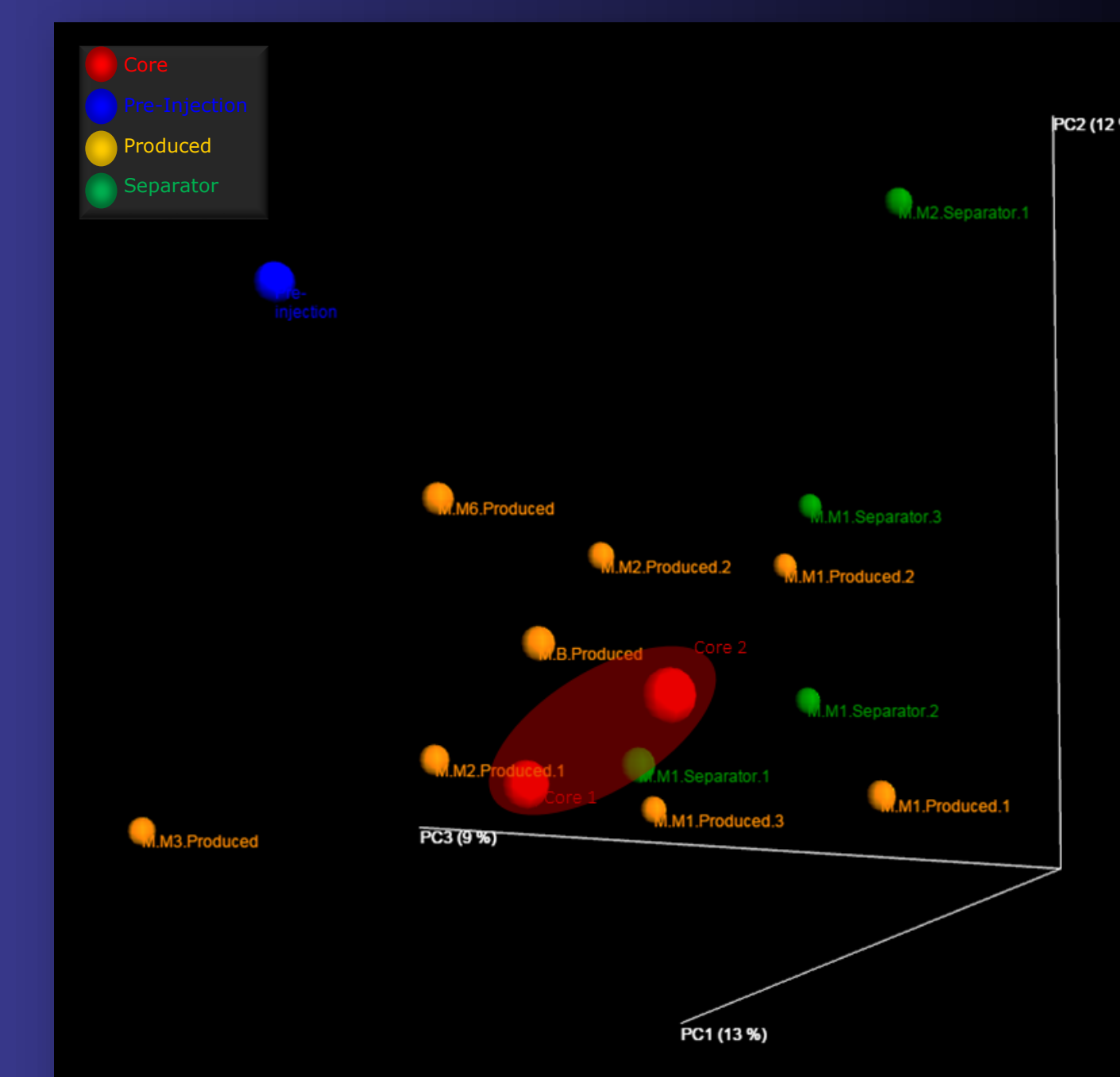


SourceTracker³ indicated that the majority (28-97%) of microbes found in the produced fluids likely sourced (derived) from core samples and the minority from injected fluids.

Principal Components Analysis

grouped samples consistently with SourceTracker results, produced waters grouped closest to core and away from injected fluids.

Unifrac⁴ was used to weigh percent similarity values at several different percentage levels independent of taxonomic classification to provide an unbiased three dimensional graph of groupings.



Conclusion

Some microbial disparity between injected and produced fluids can be explained by core samples so it is possible a native microbial community exists in Marcellus Shale.