



Conference Abstract

# Global distribution and diversity of antimicrobial genes across subsurface bacterial and archaeal metagenome assembled genomes

Brandi Kiel Reese<sup>‡,§</sup>, Megan M. Mullis<sup>§</sup>, Jason Selwyn<sup>†</sup>

<sup>‡</sup> University of South Alabama, Mobile, United States of America

<sup>§</sup> Dauphin Island Sea Lab, Dauphin Island, United States of America

<sup>†</sup> Texas A&M University – Corpus Christi, Corpus Christi, United States of America

Corresponding author: Brandi Kiel Reese ([bkielreese@disl.org](mailto:bkielreese@disl.org))

Received: 17 Jun 2023 | Published: 17 Oct 2023

Citation: Kiel Reese B, Mullis MM, Selwyn J (2023) Global distribution and diversity of antimicrobial genes across subsurface bacterial and archaeal metagenome assembled genomes. ARPHA Conference Abstracts 6: e108167. <https://doi.org/10.3897/aca.6.e108167>

## Abstract

Microorganisms have the capability to produce antimicrobial compounds through secondary metabolism, which are not essential within their natural environments, but have been found to have many effects on the ecosystem. Antimicrobial production genes have been identified in a wide range of microorganisms; however, research into natural ecosystems has historically been limited to continental soil environments. Antimicrobial production research has been limited in the deep continental subsurface and marine environments, especially deeply buried marine sediments. We analyzed 466 high-quality metagenome assembled genomes (MAGs) collected from continental and marine subsurface environments through the Deep Carbon Observatory's Census of Deep Life. A total of 383 MAGs contained biosynthetic gene clusters, namely Type I and Type III polyketide synthase genes, non-ribosomal peptide synthetase genes, and other unspecified ribosomally synthesized and post-translationally modified peptide products. All of these genes were found across continental mines, subglacial lakes, hot springs, and serpentinizing environments. These environments have previously not been investigated via metagenomics for antimicrobial gene diversity, which may be produced for competition or communication purposes. All other biosynthetic genes identified in this study were less than 50% similar to reference biosynthesis genes indicating the novelty of secondary

metabolism in subsurface microorganisms. The majority of predicted antimicrobial products were found to be produced exergonically, which could indicate microbial populations use energy-conserving mechanisms to produce compounds that could offer a competitive advantage.

## **Keywords**

antimicrobial, secondary metabolite, microbe-microbe interactions, Census of Deep Life

## **Presenting author**

Brandi Kiel Reese

## **Presented at**

ISEB-ISSM 2023

Either oral or poster presentation is acceptable

Theme: Emerging Tools & Areas of Scientific Inquiry

## **Conflicts of interest**

The authors have declared that no competing interests exist.