

- a. 57833-DNI
- b. Linking Methane Production to Methanogenic Gene Expression
- c. Principal Investigator: Brandi Kiel Reese, Texas A&M University-Corpus Christi
- d. Co-PI: None

### **Project Overview and Objectives**

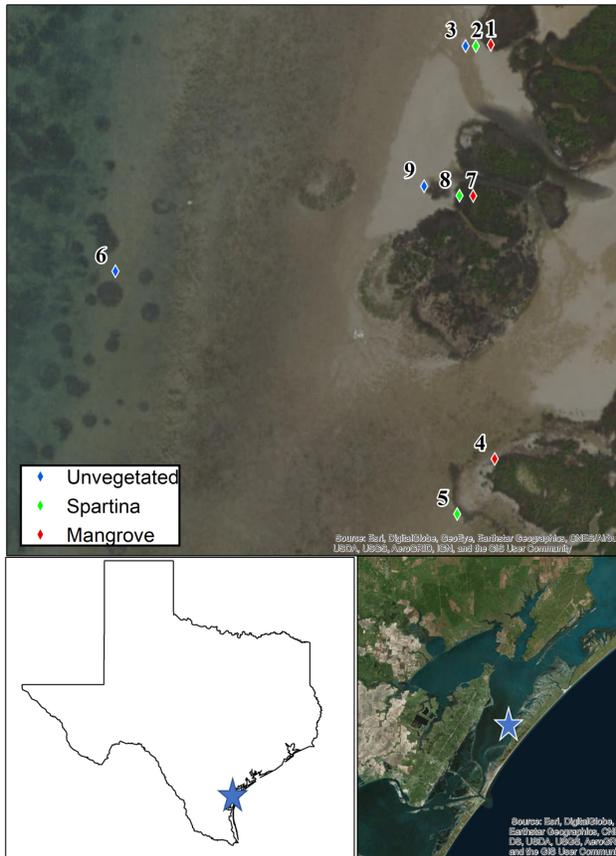
Methane is one of the most effective greenhouse gasses and potential energy source, yet the drivers of biological methane production and consumption are poorly understood. Global estimates of methane emissions and identification of potential sources of methane are impeded by this knowledge gap because we still do not understand what causes methane production to exceed consumption. Delineating the relationship between microbial activity and biogenic methane production is one approach to refining flux estimates. The degree of biological activity is reflected in the expression of methanogenic genes, or transcript abundance. Quantitatively connecting environmental methane flux to transcript abundance will open new doors for exploration and reevaluation of current environments. Warming temperatures will result in microbial population shifts; perhaps leading to increases in organic matter degradation. An environment particularly vulnerable to such climatic shifts is the wetland mangrove, one of the most productive ecosystems and a significant source of methane. Mangroves along the Texas coast are expanding due to the lack of winter freezes and die-offs. This gives us an unprecedented opportunity to study early sediment diagenesis and what drives methane production as mangroves overtake areas previously dominated by *Spartina*. This will be accomplished through the following objectives: 1) accurately determine amount of methane evolving from the sediment over extended periods of time; 2) evaluate shifts between methanogenesis and methanotrophy over spatial and temporal scales; 3) link rates of methane production to transcript abundance. Together, these objectives will culminate in a comprehensive understanding of how methane is sourced from the environment.

### **Progress 1 October 2018 – 31 August 2019**

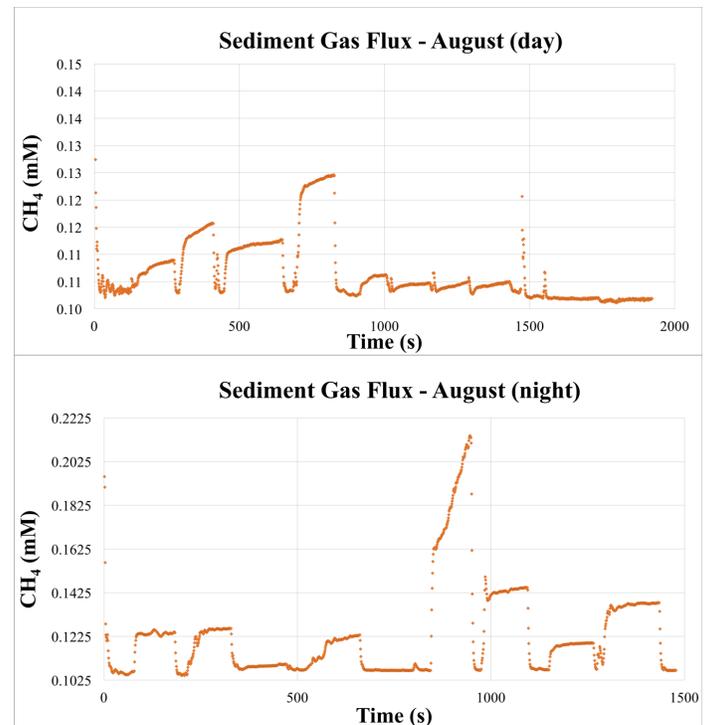
The receipt of this award enabled me to recruit a top graduate student and begin a successful career within a burgeoning field of microbial biogeochemical cycling. A Master's graduate student was recruited and joined this project in July 2018. His first academic year commenced in August 2018 and this award will allow him to have tuition and stipend fully covered during his graduate studies. Due to the timing of the funding of this award, progress on this project has been limited. We collected preliminary field data on the methane concentrations within several regions of the Mission-Aransas National Estuarine Research Reserve (NERR; Figure 1). Soil gas accumulation chambers were deployed in August 2018 at nine locations within the NERR during the day and again at night to determine the diurnal variability of methane flux (Figure 2). The methane concentrations appear to be greater during the night than during the day. Additional data on seasonal variability will be collected during the upcoming year.

Concurrently, samples were also collected for culturing methanogens and methanotrophs. The enrichments began in mid-August 2018 and thus far have shown promising results that we have successfully enriched for methanogens. Active methanogenic processes will be indicated by the presence of methyl coenzyme M reductase (*mcrA/B*) and methyltransferase (*mtrA/B*) genes. The presence of particulate methane monooxygenase (*pmoA/B*) and soluble methane monooxygenase (*mmoX/Y*) will indicate active aerobic oxidation of methane. Thus far, *mcrA* from the

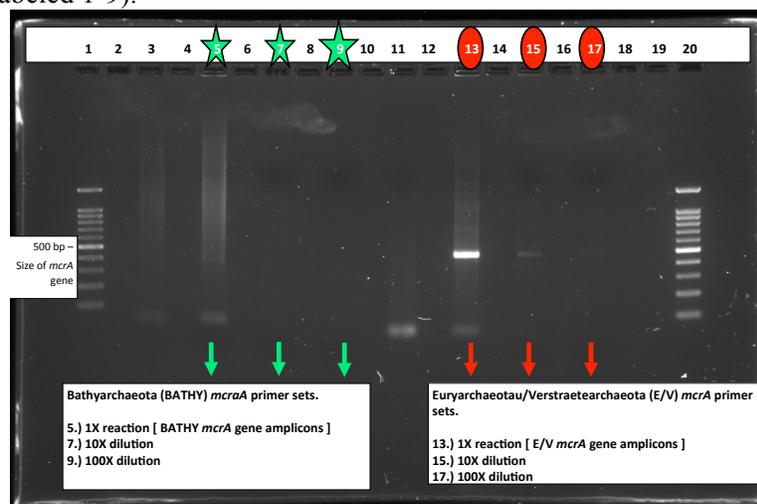
Euryarchaeota has been amplified indicating the presence of this Archaea as a methanogen. I predict that a co-location of enzyme transcripts for methanogenesis and methanotrophy will exist within the sediment, which will provide evidence for a “cryptic” methane cycle.



**Figure 1:** Location of National Estuarine Research Reserve on the Texas coast and the preliminary sample locations (labeled 1-9).



**Figure 2.** Concentrations of methane from accumulation chambers deployed during the day of August 17<sup>th</sup> and night of August 19<sup>th</sup>, 2018 at Mission-Aransas NERR.



**Figure 3:** Initial culturing efforts of methanogenic Archaea show positive amplification of *mcrA* gene.