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Microbial Community and Metagenomics

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Introduction

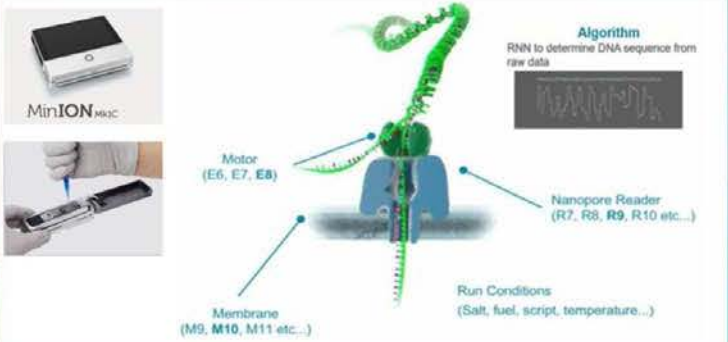
Public health is a priority when it comes to investigating the types of bacteria present in high traffic environments. There are a variety of harmful and beneficial bacteria that have been discovered through the use of metagenomics (citation). Metagenomics is a process used to identify mixed communities of microorganisms using molecular techniques, such as DNA purification, PCR, and Next Generation Sequencing. A metagenomics approach can be used to analyze bacterial communities from different environmental niches.

Metagenomics has been used to identify important environmental microbes and pathogens. Preliminary data, obtained from soil samples showed mixed microbial soil communities that were identified with the use of a metagenomics approach as part of 16S rDNA sequencing that lead to identification of a diverse community of bacteria including pathogens. The presence of pathogens in these areas indicate the public health importance for the use of metagenomic approaches. Through this research we aim to advance our understanding of the microbial communities that occupy high traffic areas in Pensacola, Florida.

Method

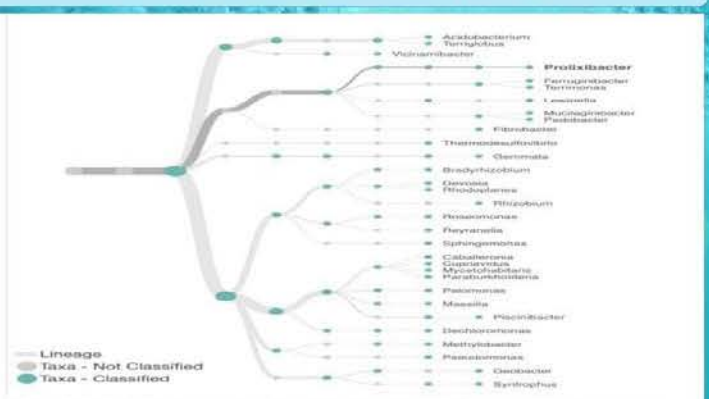
- Soil samples were initially collected from various high traffic areas around UWF and area beaches and bays.
- Various amounts of soil were used to extract and purify microbial DNA using an E.Z.N.A® Soil DNA Kit which uses reversible nucleic binding to eliminate Polymerase Chain Reaction (PCR) inhibiting compounds from soil samples.
- PCR is the process of amplifying DNA. The 16s region of the bacteria in the samples were PCR amplified using 16s rDNA primers from Oxford Nanopore.
- The PCR was cleaned up to facilitate separation of organic materials from the desired DNA. Sequencing occurred using the Oxford nanopore next generation sequencer. Data analysis using EPI2ME software.

Figure 2.
Oxford Nanopore flongle



Bacteria is identified down to the species level using the MK1C sequencer. This figure shows a picture of the flongle that contains the protein pores. The function is described in figure 4.

Preliminary Results & Conclusion



Within initial preliminary data, bacteria found with the use of metagenomics showed both pathogenic and beneficial genus. The use of preliminary data allows for a greater understanding of what bacteria can be found when studying samples from different areas. The process of metagenomics of analyzing sampled bacteria allows for the comparison of different regions in a local area, and research on the bacteria discovered in those samples.

Field Work

Figure 3. Pensacola Beach, Florida

Cited Works

- MJ;, S. (n.d.). Regional similarities and consistent patterns of local variation in beach sand bacterial communities throughout the Northern IIemisphere. Retrieved April 02, 2021, from https://pubmed.ncbi.nlm.nih.gov/26921429/
- Rodriguez-R LM;Overholt WA;Hagan C;Huettel M;Kostka JE;Konstantinidis KT;. (n.d.). Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. Retrieved April 02, 2021, from https://pubmed.ncbi.nlm.nih.gov/25689026/

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