

Genosets: Pangenomic view of *Vibrio vulnificus* Biotype 1 E-genotypes strains through use of next gen sequencing

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In the Genosets application we can manage, track and visualize multiple steps in microbial genome analysis, from sequence data processing steps, to annotation, comparison, and mapping of sequence reads from complementary experiments. Genosets provides a platform by which we can interrogate the data at different levels and compare the results of different methodological choices at different stages in the analysis.

Here, we show the application of Genosets to the sequencing and annotation of three strains of *Vibrio vulnificus*, and subsequent pangenomic analysis across data from several related genomes. *V. vulnificus*, a gram-negative bacterium, is the number one cause of seafood related deaths in the US. In order to better understand *V. vulnificus* as an agent of disease and to identify the molecular components of its virulence mechanisms, we have completed draft sequence assemblies of three isolates using a pyrosequencing approach. Genosets aided in the comparative analysis of these sequences using the previously published sequences of the two clinical isolates, as well as the other eleven characterized *Vibrio* sequences. Key differences between the core genomes of the clinical and environmental *vulnificus* isolates compromise 122 genes, including components of a Type IV secretion system that is associated with pathogenesis. At the genus level, 183 genes are in *vulnificus* that are not in other *Vibrios*.