

Genotypic characterization of *Vibrio parahaemolyticus* strains isolated in Brazil

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Vibrio parahaemolyticus is a Gram-negative bacterium that inhabits marine and estuarine environments. Many of its strains are pathogenic to man. In Brazil, *V. parahaemolyticus* has caused intestinal infection outbreaks following the consumption of raw or undercooked seafood, and has been isolated from clinical and environmental samples. Its main virulence factors are two hemolysins, TDH and TRH, and type III (T3SS) and type VI (T6SS) secretion systems. However, it is possible that other factors are involved in the pathogenicity of this species. We have been studying two environmental strains of *V. parahaemolyticus* (IOC 20128/10, 20138/10 IOC), isolated from an oyster farm in Santa Catarina state. PCR analysis indicated that both strains carry *tlh* gene that is a marker for the species, but do not have the TDH and TRH hemolysin genes. To be able to further characterize these isolates, compare them to reference strains from clinical and environmental origins, to identify novel and conserved features and to determine genotype-phenotype relationships, the whole genomes of IOC 20128/10 and 20138/10 IOC were sequenced using Illumina MiSeq. Following reads quality evaluation, with FastQC and Trimmomatic, the filtered reads were assembled in contigs using Velvet and Spades algorithms. Number and average size of contigs, as well as N50 values for the two assemblies were then compared.

The contigs of the draft genomes were mapped to the two chromosomes of the reference environmental strain, *V. parahaemolyticus* BB22OP, using Contiguator. The GView tool was then used to generate graphical representations of the bacterial chromosomes. We found that both strains contain two circular chromosomes of 3.1 and 1.7 Mb, with a mean G + C content of 45.6%. The assembled genomes were subjected to automated annotation using the RAST online tool, and searched for virulence-related genes. The absence of the virulence-related genes *tdh* and *trh* was confirmed. Furthermore, two clusters containing T3SS genes were identified in the genome of both strains. A conserved synteny of the T3SS cluster genes was observed by comparing the genomes of IOC 20128/10 and 20138/10 IOC with those of the reference strains, RIMD2210633 and BB22OP, and the clinical isolates, Cascavel and 17384. Genes of components of type VI secretion systems (T6SS) were also identified in the genome of IOC 20128/10 and 20138/10 IO. Further analysis of their complete genome sequences will help to evaluate their pathogenic potential, to analyze their similarity and/or differences and could provide insight into the diversity of this species.