Comparative Genome Analyses of Vibrio anguillarum Strains Reveal a Link with Pathogenicity Traits - DTU Orbit (16/12/2018)

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Vibrio anguillarum is a marine bacterium that can cause vibriosis in many fish and shellfish species, leading to high mortalities and economic losses in aquaculture. Although putative virulence factors have been identified, the mechanism of pathogenesis of V. anguillarum is not fully understood. Here, we analyzed whole-genome sequences of a collection of V. anguillarum strains and compared them to virulence of the strains as determined in larval challenge assays. Previously identified virulence factors were globally distributed among the strains, with some genetic diversity. However, the pan-genome revealed that six out of nine high-virulence strains possessed a unique accessory genome that was attributed to pathogenic genomic islands, prophage-like elements, virulence factors, and a new set of gene clusters involved in biosynthesis, modification, and transport of polysaccharides. In contrast, V. anguillarum strains that were medium to nonvirulent had a high degree of genomic homogeneity. Finally, we found that a phylogeny based on the core genomes clustered the strains with moderate to no virulence, while six out of nine high-virulence strains represented phylogenetically separate clusters. Hence, we suggest a link between genotype and virulence characteristics of Vibrio anguillarum, which can be used to unravel the molecular evolution of V. anguillarum and can also be important from survey and diagnostic perspectives.

Importance: Comparative genome analysis of strains of a pathogenic bacterial species can be a powerful tool to discover acquisition of mobile genetic elements related to virulence. Here, we compared 28 V. anguillarum strains that differed in virulence in fish larval models. By pan-genome analyses, we found that six of nine highly virulent strains had a unique core and accessory genome. In contrast, V. anguillarum strains that were medium to nonvirulent had low genomic diversity. Integration of genomic and phenotypic features provides insights into the evolution of V. anguillarum and can also be important for survey and diagnostic purposes.

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