Molecular epidemiology of Photobacterium damselae subsp. damselae outbreaks in marine rainbow trout farms reveals extensive horizontal gene transfer and high genetic diversity

The marine bacterium Photobacterium damselae subsp. damselae is a pathogen for a variety of marine animals, as well as for humans, and is nowadays considered an emerging pathogen for fish of importance in marine aquaculture. Recent studies have suggested that outbreaks in fish farms are caused by multiclonal populations of this subspecies that exist in the environment. Here, we report the study of a collection of 31 strains isolated during the course of disease outbreaks in marine rainbow trout farms in Denmark in 1994, 1995, and 2006, respectively. A phylogenetic analysis based on the toxR gene sequence, and the screening of virulence-related genes uncovered a high genetic heterogeneity, even among strains isolated from the same fish farm at the same time. Moreover, comparative analysis of the whole genome sequences of four selected strains revealed a large number of differentially occurring genes, which included virulence genes, pHDD1 plasmid, polysaccharide synthesis gene clusters, CRISPR-Cas systems and putative new mobile genetic elements. This study provides sound evidence that P. damselae subsp. damselae outbreaks in Danish rainbow trout farms were caused by multiclonal populations and that horizontal gene transfer constitutes a strong driving force in the generation of intraspecific diversity in this pathogen.

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