Comparative Genome Analysis Provides Insights into the Pathogenicity of Flavobacterium psychrophilum

Flavobacterium psychrophilum is a fish pathogen in salmonid aquaculture worldwide that causes cold water disease (CWD) and rainbow trout fry syndrome (RTFS). Comparative genome analyses of 11 F. psychrophilum isolates representing temporally and geographically distant populations were used to describe the F. psychrophilum pan-genome and to examine virulence factors, prophages, CRISPR arrays, and genomic islands present in the genomes. Analysis of the genomic DNA sequences were complemented with selected phenotypic characteristics of the strains. The pan-genome analysis showed that F. psychrophilum could hold at least 3373 genes, while the core genome contained 1743 genes. On average, 67 new genes were detected for every new genome added to the analysis, indicating that F. psychrophilum possesses an open pan genome. The putative virulence factors were equally distributed among isolates, independent of geographic location, year of isolation and source of isolates. Only one prophage-related sequence was found which corresponded to the previously described prophage 6H, and appeared in 5 out of 11 isolates. CRISPR array analysis revealed two different loci with dissimilar spacer content, which only matched one sequence in the database, the temperate bacteriophage 6H. Genomic Islands (GIs) were identified in F. psychrophilum isolates 950106-1/1 and CSF 259-93, associated with toxins and antibiotic resistance. Finally, phenotypic characterization revealed a high degree of similarity among the strains with respect to biofilm formation and secretion of extracellular enzymes. Global scale dispersion of virulence factors in the genomes and the abilities for biofilm formation, hemolytic activity and secretion of extracellular enzymes among the strains suggested that F. psychrophilum isolates have a similar mode of action on adhesion, colonization and destruction of fish tissues across large spatial and temporal scales of occurrence. Overall, the genomic characterization and phenotypic properties may provide new insights to the mechanisms of pathogenicity in F. psychrophilum.

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