Flavobacterium psychrophilum, the etiological agent of rainbow trout fry syndrome and bacterial cold-water disease in salmonid fish, is currently one of the main bacterial pathogens hampering the productivity of salmonid farming worldwide. In this study, the genomic diversity of the F. psychrophilum species is analyzed using a set of 41 genomes, including 30 newly sequenced isolates. These were selected on the basis of available MLST data with the two-fold objective of maximizing the coverage of the species diversity and of allowing a focus on the main clonal complex (CC-ST10) infecting farmed rainbow trout (Oncorhynchus mykiss) worldwide. The results reveal a bacterial species harboring a limited genomic diversity both in terms of nucleotide diversity, with similar to 0.3% nucleotide divergence inside CDSs in pairwise genome comparisons, and in terms of gene repertoire, with the core genome accounting for similar to 80% of the genes in each genome. The pan-genome seems nevertheless "open" according to the scaling exponent of a power-law fitted on the rate of new gene discovery when genomes are added one-by-one. Recombination is a key component of the evolutionary process of the species as seen in the high level of apparent homoplasy in the core genome. Using a Hidden Markov Model to delineate recombination tracts in pairs of closely related genomes, the average recombination tract length was estimated to similar to 4.0 Kbp and the typical ratio of the contributions of recombination and mutations to nucleotide-level differentiation (r/m) was estimated to similar to 13. Within CC-ST10, evolutionary distances computed on non-recombined regions and comparisons between 22 isolates sampled up to 27 years apart suggest a most recent common ancestor in the second half of the nineteenth century in North America with subsequent diversification and transmission of this clonal complex coinciding with the worldwide expansion of rainbow trout farming. With the goal to promote the development of tools for the genetic manipulation of F. psychrophilum, a particular attention was also paid to plasmids. Their extraction and sequencing to completion revealed plasmid diversity that remained hidden to classical plasmid profiling due to size similarities.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Fish Diseases, Universite Paris-Saclay, Norwegian Veterinary Institute, Åbo Akademi University, University of Applied Sciences and Arts of Southern Switzerland, University of Bern, Instituto Zooprofilattico Sperimentale delle Venezie, United States Department of Agriculture, Kindai University, Universidad Andres Bello
Number of pages: 20
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Frontiers in Microbiology
Volume: 9
Article number: 138
ISSN (Print): 1664-302X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Web of Science (2017): Impact factor 4.019
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
Web of Science (2016): Impact factor 4.076
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.15 SJR 1.869 SNIP 1.193
Web of Science (2015): Impact factor 4.165
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.76 SJR 1.879 SNIP 1.148
Web of Science (2014): Impact factor 3.989
Web of Science (2014): Indexed yes