

Control of Flavobacteriaceae infections in European fish farms (EMIDA-project “Pathofish”)

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Key words

Salmonid fish, *Flavobacterium psychrophilum*, Phylogeny, qPCR

Aim of the study

The aim of this multipartner project was to establish a European *Flavobacterium psychrophilum* and *Tenacibaculum maritimum* collection, to characterize the collected isolates, to analyze the genetic relationship between isolates by Multilocus Sequence Typing (MLST), to fully sequence the genome of selected isolates and to develop new diagnostic tools and vaccines.

Material and methods

The Swiss partner was involved in collecting *F. psychrophilum* isolates in Switzerland, to characterize the collected isolates and to test new diagnostic tools on field material. A total of 112 isolates originating from 1993 through 2012 was sampled. MLST analyses was performed in collaboration with a French partner. A qPCR developed by another French project partner was evaluated on material from the routine diagnostic work of the Centre for Fish and Wildlife Health in comparison to two own methods.

Results and significance

MLST analyses revealed that the Swiss isolates belonged to 27 different sequence types (STs). Most of the Swiss outbreaks were associated with strains belonging to clonal complexes CC-ST2 and CC-ST90, found in both rainbow trout and brown trout and represented by several STs. Eight ST singletons could not be connected to any known clonal complex. The occurrence of sporadic STs suggests high *F. psychrophilum* diversity and may reflect the presence of different sequence types in the environment.

The evaluation of the newly developed qPCR proved it's suitability for the detection of *F. psychrophilum* in organ material of fish. This qPCR reacted slightly less sensitive than a qPCR developed at the FIWI, which however, was based on a different method (SYBR instead of Taqman qPCR).

Publications, posters and presentations

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