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INVESTIGATION ON GENETIC DIVERSITY OF *YERSINIA RUCKERI* ISOLATES FROM TROUT HATCHERIES IN NORTH-WESTERN GERMANY

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Purpose

Yersinia ruckeri is the causative agent of Enteritic Red-mouth Disease, one of the most important infectious diseases in rainbow trout hatcheries in Europe. The aim of this study was to investigate the biochemical and genetic diversity of *Y. ruckeri* isolates collected in north-western Germany.

Methods

83 isolates collected from clinical cases in Lower Saxony, North Rhine-Westphalia and Hesse, Germany, were investigated and confirmed to be *Y. ruckeri* by the API 20E system. The isolates were characterized by biochemical tests, fatty acid composition analysed by gas chromatography, cytotoxicity assays to Common carp brain (CCB), epithelioma papulosum cyprini (EPC), fathead minnow epithelial cell (FHM) and rainbow trout gonad-2 (RTG-2), 16S rRNA sequencing, pulsed-field gel electrophoresis (PFGE) and repetitive sequence-based PCR assays, including (GTG)₅-PCR, BOX-PCR, ERIC-PCR and REP-PCR.

Results and Conclusions

Eight different API 20E profiles, different from that of the *Y. ruckeri* reference strain DSMZ18506, were obtained. Five isolates were confirmed as *Y. ruckeri* by 16S rRNA sequencing. Sixteen isolates hydrolyzed Tween 80/20. Fatty acid composition of *Y. ruckeri* isolates was homogenous. In addition to 17 PFGE patterns, two different REP-PCR patterns, five ERIC-PCR patterns, four (GTG)₅-PCR patterns and three BOX-PCR patterns were obtained. Five isolates which were positive in sorbitol fermentation lacked the 430-bp band in ERIC-PCR. According to the results of API 20E, PFGE and the various PCR assays, the isolates could be divided into 27 different groups. More than two different isolates were present in the same fish farm. Non-motile strains were more active to cause cytotoxicity than motile ones at the lower temperature. Our results suggest the presence of a wide variety of *Y. ruckeri* isolates in German aquaculture.

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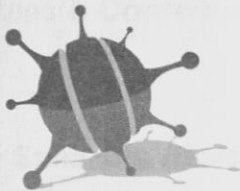
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