

Molecular analysis of microbiota along the digestive tract of juvenile atlantic salmon (*Salmo salar* L.)

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Dominant bacterial microbiota of the gut of juvenile farmed Atlantic salmon was investigated using a combination of molecular approaches. Bacterial community composition from the stomach, the pyloric caeca, and the intestine was assessed by extracting DNA directly from each gut compartment. Temporal temperature gradient gel electrophoresis (TTGE) analysis of 16S ribosomal DNA (rDNA) amplicons showed very similar bacterial compositions throughout the digestive tract. Band sequencing revealed a narrow diversity of species with a dominance of *Pseudomonas* in the three compartments. However, cloning revealed more diversity among the *Pseudomonas* sequences. To confirm these results, we analyzed the bacterial community by amplifying the variable 16S-23S rDNA intergenic spacer region (ITS). Similar ITS profiles were observed among gastrointestinal compartments of salmon, confirming the TTGE results. Moreover, the dominant ITS band at 650 bp, identified as *Pseudomonas*, was observed in the ITS pr