IN VITRO GROWTH CHARACTERISTIC AND MICROBIAL COMMUNITY DYNAMIC OF ATLANTIC SALMON (*Salmo salar* L) GASTROINTESTINAL TRACT IN RELATION TO THE DIFFERENT DIET FORMULATIONS

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In order to better understand microbial changes within the salmon gastrointestinal tract as determined at the dietary level, the microbial community dynamics were assessed within a simple *in vitro* growth model system. In this system the growth and composition of bacteria were monitored within diet slurries held under anaerobic conditions inoculated with salmon faecal samples. This system was assessed using total viable bacteria counts (TVC), automated ribosomal intergenic spacer analysis (ARISA) and 16S rRNA pair-end Illumina-based sequence analysis. A total of 5 complete diets of low fish meal (LM), low protein (LP), high protein (HP), commercial standard (CS), and 2 plant meal diets (lupin kernel and pea extract, referred to as the LK and PE diets) were tested, and the *in vitro* model cultures were incubated at 20ºC to simulate warm summer temperatures. TVC data indicated that most bacteria that grew were bile salt tolerant. While, ARISA and sequencing data revealed there was very clear separation between the more traditional diets and the plant meal diets suggesting bacteria that grew were distinct. The sequencing analysis showed in the case of the complete diets members of the genera *Aliivibrio*, *Vibrio* and *Photobacterium* became greatly predominant. However, based on replicated experiments there was evident stochasticity of what exact species became dominant. *Vibrionaceae* may have become predominant due to their rapid growth capacity and relatively high abundance within the starting faecal material and salt tolerance though several other bacterial taxa were also present in great abundance initially. The plant meal-based diets only sustained the growth of the genus *Sphingomonas*, no other faecal-associated bacterial grew including *Vibrionaceae*, suggesting the *in vitro* model system could be used to test impact of feed ingredients on fish gastrointestinal tract communities.

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