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Characterizing Microbial Communities of Chinook Salmon

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Microbiomes are microbial communities that develop in a variety of different environments including the skin and gut of various animals. Mammalian gut microbiomes have been extensively studied and they are known to play a key role in normal organism function. Although less is known about gut microbiomes of fish, they appear to contribute to critical processes such as digestion and immunity. Chinook Salmon (*Oncorhynchus tshawytscha*) are an important Canadian aquaculture product, so it is important to explore the role of the microbiome in their performance. This study characterizes the Chinook Salmon microbiome across multiple ages to test for age-related changes. Our hypothesis is that the gut and skin microbiomes will change as the fish age as a result of exposure to seasonal environmental variations, stressors relating to aging, and the development of the microbial community over time. We collected gut and skin microbiome samples from 43 farm raised Chinook Salmon ranging in age from one to five years old. We extracted microbiome DNA and amplified the 16S rDNA gene regions using PCR. The amplified microbiome DNA was sequenced using Next Generation Sequencing techniques to characterize the microbiome community composition and diversity. We will present preliminary results testing whether skin and gut microbiome change as the fish age. The knowledge of the composition of the microbiome is a crucial first step in understanding what role these communities play and how their function can then be optimized to increase the health, quality, and production of such an important aquaculture product.