

# Gut microbial assembly among freshwater Atlantic salmon reared in a natural stream system during a simulated farm escape and introgression event

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## Abstract

Intestinal microbial communities are influenced by a confluence of ecological forces. Understanding the dynamics between environment, microbiota and host is essential to gain insights into microbial community assembly processes. However, few studies systematically assess the contribution of different environmental sources to gut microbial community composition. We used a common garden experiment to determine the roles of biotic, abiotic and stochastic processes shaping gut microbial communities in Atlantic salmon (*Salmo salar*) in a natural river during a simulated 10-month farm escape scenario. Most of the taxa found in the salmon intestine originated from macroinvertebrates (the potential food source) rather than the water column, indicating that diet is an important factor in community assembly. The contribution of food sources to the fish gut community was lowest in winter and increased over March and May, reflecting seasonality in fish appetite. Previous work in salmon has hinted at a role for maternal effects in driving inter-generational sharing of microbial taxa. Our results suggest a possible host and/or maternal genetic effect affecting inter-individual differences in gut microbial community composition, whereby distinct assemblages were noted between farmed, wild and hybrid fish. Neutral modelling estimated that the majority (86%) of taxa present in the gut are transient. Overall, our data highlight the significance of both deterministic and stochastic drivers influencing the seasonal fluctuations of gut microbial communities in young Atlantic Salmon and hint at potential genetic or maternal effects on fish microbiota. These findings greatly enhance our understanding of the complex interactions between hosts, their living environment and associated microbiota.

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