Impacts of the Marine Hatchery Built Environment on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, Seriola Lalandi

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Research

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Abstract

Background

Microbial succession in vertebrates has primarily focused on vertical transmission and ontogenetic development in the mammalian gut. Teleosts comprise the majority of vertebrate diversity, yet little is known about how the microbiome develops in fish, particularly when vertical transmission is limited or absent for broadcast spawners. Biological factors such as diet, age, phylogeny, and trophic level along with environmental factors such as water salinity, temperature, and depth have been shown to influence the mucosal microbiomes of fish. Here we investigate how various microbial-rich surfaces from the built environment 'BE' influence the development of the mucosal microbiome (gill, skin, and digesta) of an economically important marine fish, yellowtail kingfish, Seriola lalandi, over time.

Results

For the first experiment, we sampled gill and skin microbiomes from 36 fish reared in three tank conditions, and demonstrate that the gill is more influenced by the surrounding environment than the skin. In a second experiment, fish microbiomes (gill, skin, and digesta) and the BE (tank side, water, inlet pipe, airstones, and air diffusers) were sampled from indoor reared fish at three ages (43 dph, 137 dph, 430 dph; n=12 per age). At 430 dph, 20 additional fish were sampled from an outdoor ocean net pen. A total of 304 samples were processed for 16S rRNA gene sequencing. Gill and skin alpha diversity increased while gut diversity decreased with age. Diversity was much lower in fish from the ocean net pen compared to indoor fish. We quantified the change in community dynamics driven by the BE and show that the gill and skin are most influenced by the BE early in development, with aeration equipment having more impact in later ages, while the gut microbiome becomes increasingly differentiated from the environment over time.

Conclusions

Our findings suggest that fish mucosal microbiomes are differentially influenced by the built environment with a high turnover and rapid succession occurring in the gill and skin while the gut microbiome is more stable. We demonstrate how individual components of a hatchery system, especially aeration equipment, may contribute directly to microbiome development in a marine fish. In addition, results demonstrate how early life (larval) exposure to stressors in the rearing environment may influence fish microbiome development which is important for animal health and aquaculture production.

Full Text

This preprint is available for download as a PDF.

Figures

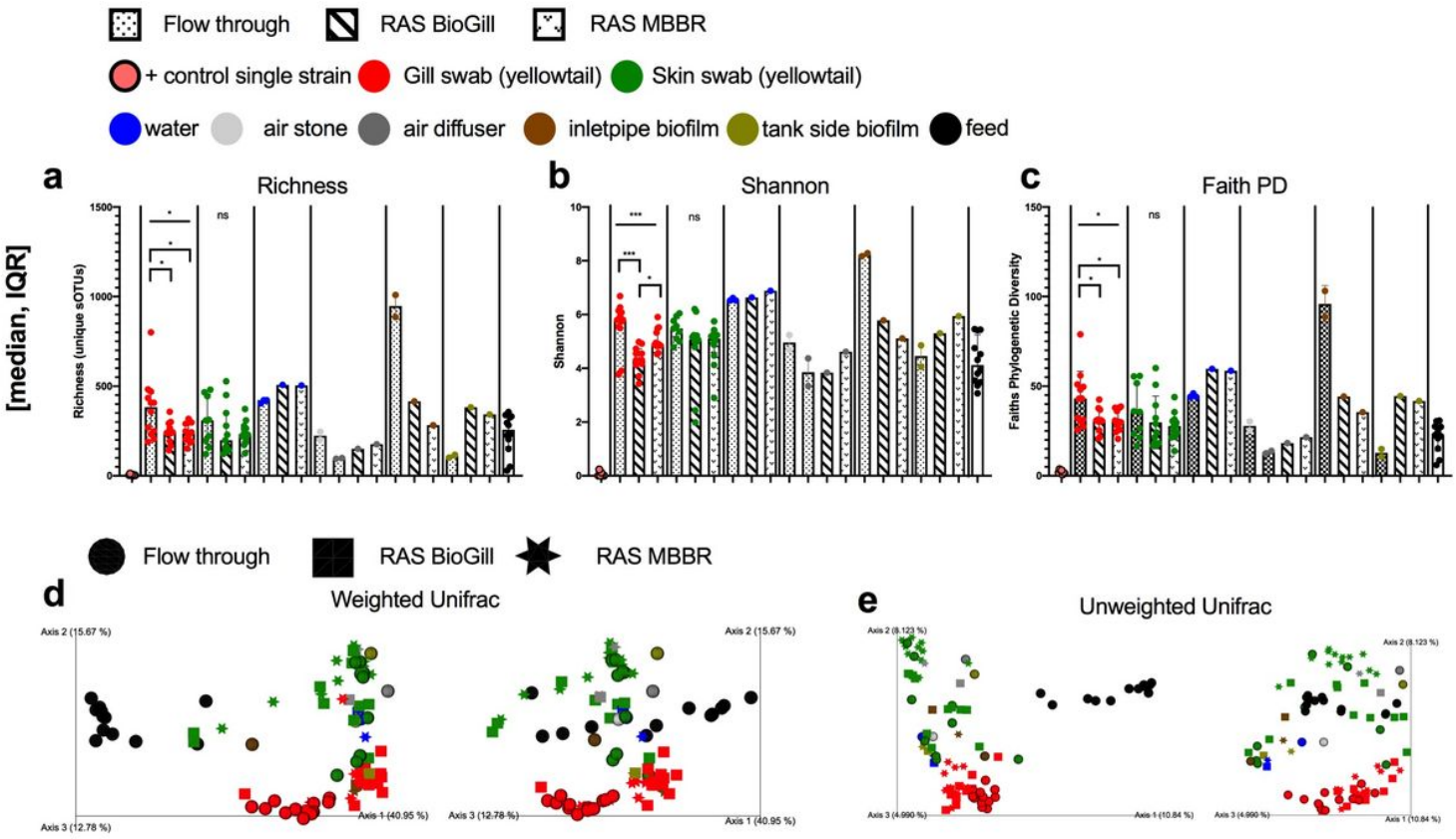

Figure 1

Microbial diversity of the hatchery built environment along with fish gill and skin mucus at 130 days post hatch across three rearing tanks (flow through, RAS BioGill, and RAS MBBR). Alpha diversity as measured by a) richness, b) Shannon, and c) Faith's phylogenetic diversity. Gill and skin (group comparison calculated with Kruskal-Wallis test, Benjamini Hochberg FDR 0.05). Beta diversity calculated using d) Weighted UniFrac and e) Unweighted UniFrac distance. (* P<0.05, ** P<0.01, *** P<0.001, **** P<0.0001)

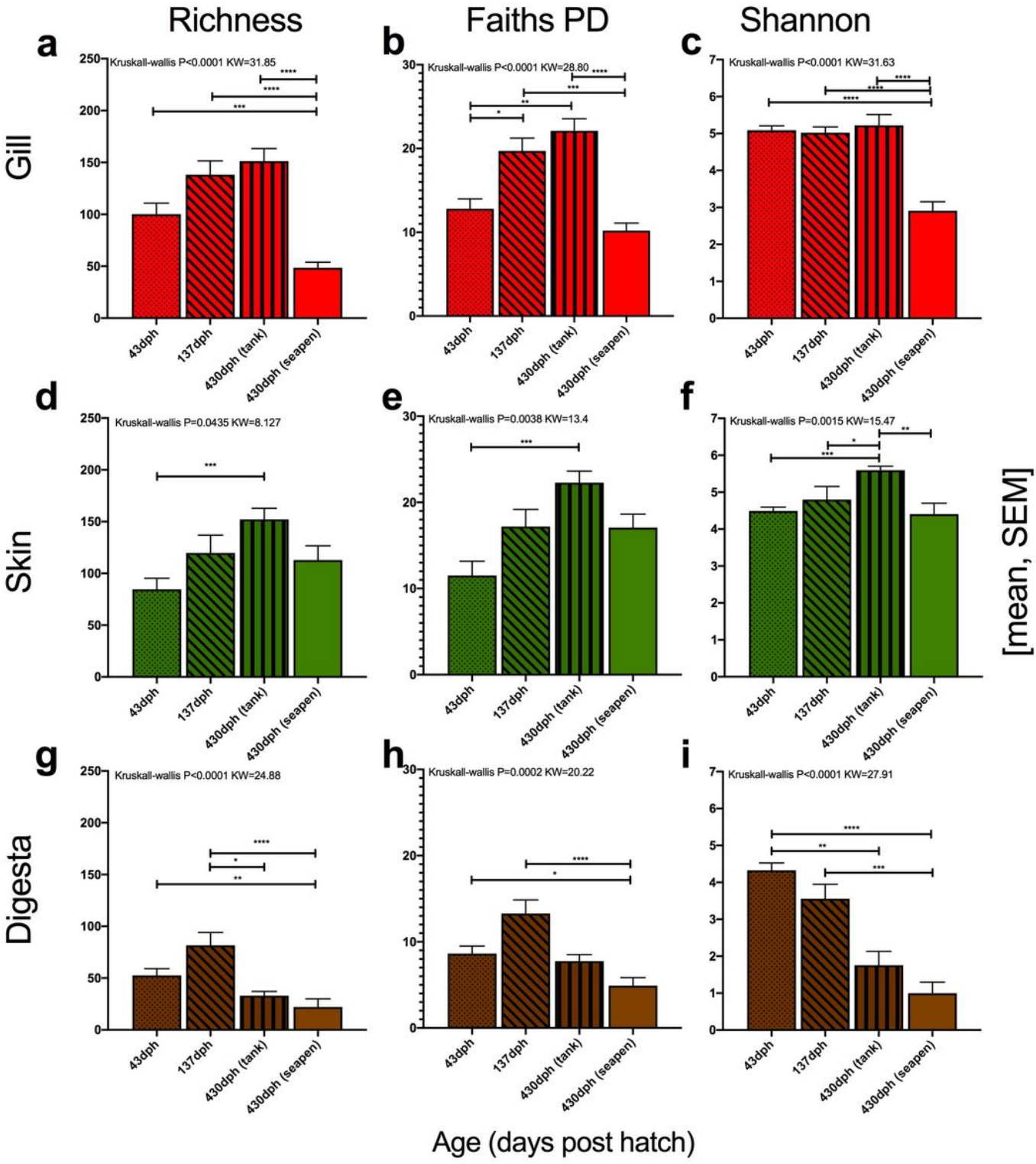

Figure 2

Alpha diversity measures: richness, Faith's Phylogenetic 934 diversity, and Shannon diversity grouped per body site (red = gill, green = skin, brown = digesta). Each body site assessed for diversity differences across age (Kruskal-Wallis, Benjamini-Hochberg FDR 0.05). Gill microbial diversity: a) richness, b) Faiths PD, c) Shannon; Skin microbial diversity: a) richness, b) Faiths PD, c) Shannon; Digesta microbial diversity: a) richness, b) Faiths PD, c) Shannon. (* P<0.05, ** P<0.01, *** P<0.001, **** P<0.0001)

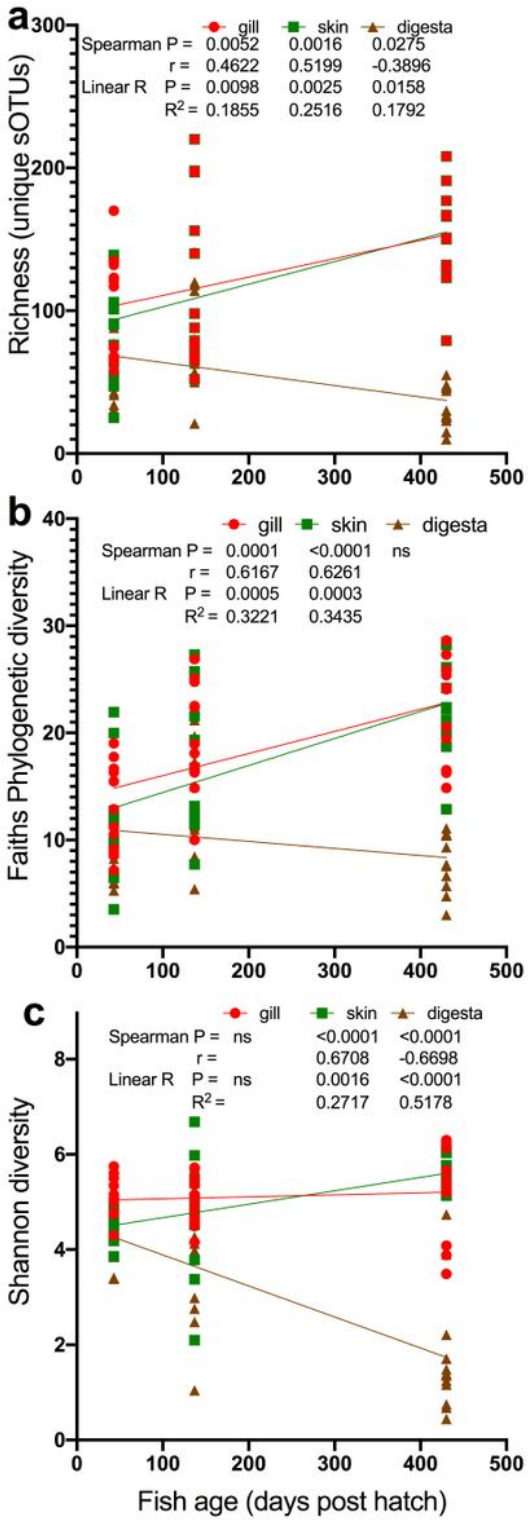

Figure 3

Modeling of changes in alpha diversity: a) richness, b) Faiths PD, and c) Shannon diversity over the age of the fish. Only fish reared in indoor systems included (430 dph seapen fish excluded). Statistical comparisons of both Spearman correlation and linear model (linear regression) calculated with results depicted on the legends.

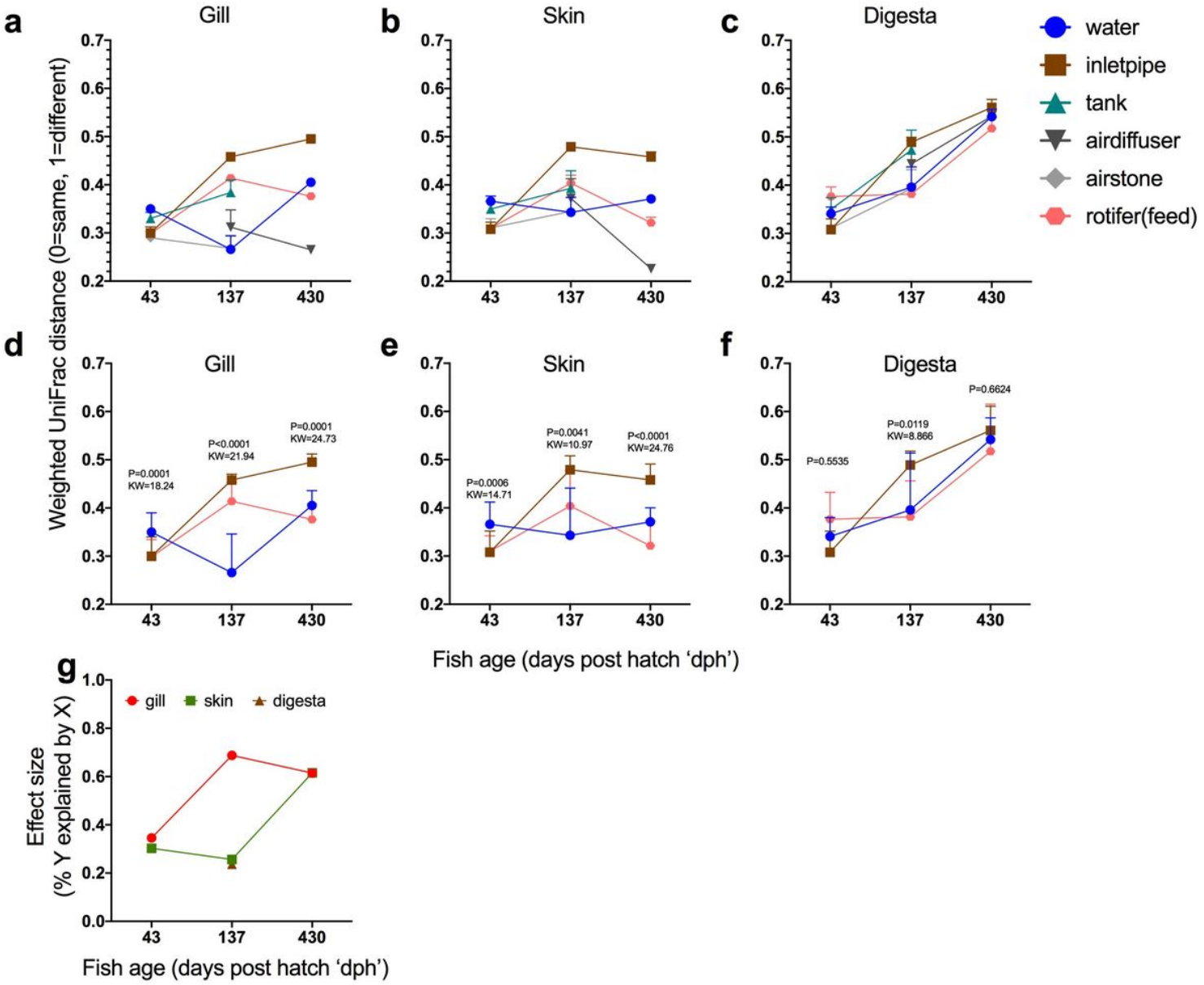

Figure 4

Niche differentiation within body sites over time. Beta diversity distances (weighted normalized UniFrac) of a) gill, b) skin, and c) digesta samples compared to six different hatchery built environment putative microbial sources (water, inlet pipe, tank side, air diffuser, airstone, and first feed (rotifers). Statistical comparison of microbiome differentiation across three BE comparisons (water, inlet pipe, first feed) over time and calculated independently across three body sites: d) gill, e) skin, and f) digesta (Statistical test: Kruskal-Wallis, P value and KW test statistic reported in figure panel. f) Results from the Kruskal-Wallis test for (d,e,f) depicted as effect size to demonstrate the rate of microbial community niche differentiation.

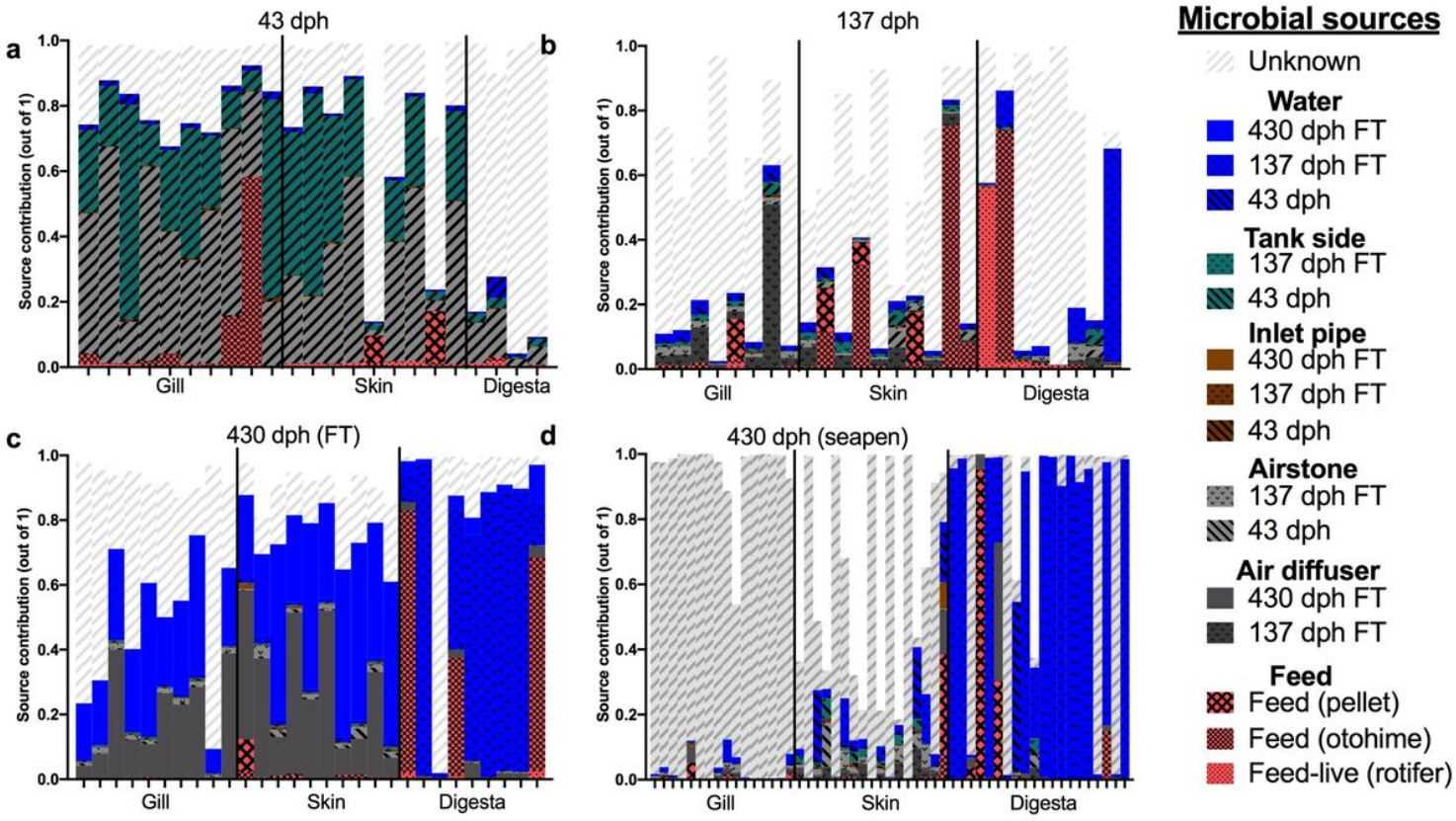

Figure 5

SourceTracker2 analysis of individual microbiome contributions from the built environment onto various mucosal body sites across time: a) 43 dph, b) 137 dph, c) 430 dph indoor, and d) 430 dph seapen. Features with less than 100 counts across all samples excluded. 'Unknown' indicates source population was not sampled or included thus would be the percentage of a given sample which has source microbes from an unknown location or undetermined source.

Supplementary Files

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