Rationale:

• This study investigated the genetic similarity and microbial communities associated with red and green morphs of the colonial ascidian *P. constellatum* in actively filtering and resting (non-filtering) states.

Methods:

• Sample collection in Puerto Rico (2019 and 2020).

• DNA extraction and sequencing of host COI mtDNA (*n* = 56) and 18S rRNA (*n* = 37) gene fragments.

• Sequences aligned with Geneious® and consensus used to create NJ & ML phylogenetic trees with MEGA®.

• 16S rRNA gene fragments were used to characterize microbial communities (*n* = 17) from the ascidian tunic.

• Quality filtering of microbial sequences, OTU clustering, and taxonomic assignment using Mothur®.

• Alpha diversity metrics were conducted on microbial communities to estimate richness (S, d, 1/D, E1/D) and beta diversity analyses based on Bray-Curtis to identify differences in the overall communities.

Results:

• COI & 18S rRNA phylogenetic analyses placed all color morphs within the same genetic clade (Fig. 1).

• Similar microbial communities in each color morph.

• No richness change in microbial communities from different colors or physiological states, but there was a significant shift in microbial community structure between actively filtering and resting colonies (Fig. 2).

• Two bacterial symbiont taxa (genus *Kiloniella* & *Ruegeria*) were the main drivers of microbial community dissimilarity.

Discussion & Implications:

• COI variability in *P. constellatum* is due to phenotypic plasticity (intra-species variation) and results in similar microbial communities, whereas distinct genetic lineages (inter-species variation) correspond to different microbial communities.

• The physiological state of the host significantly alters microbiome structure, but not richness.

• Resting states are associated with variable oxygen concentrations and the presence of anaerobic and facultatively anaerobic (f.i. *Kiloniella*) bacteria.

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