Phylogenetic comparisons of innate immune gene repertoires, microbiome structure, and disease susceptibility across coral diversity

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Abstract

Coral innate immunity plays a key role in regulating coral microbiomes. These microbiomes may contribute to corals' resistance or susceptibility to environmental stress, predation or disease. Changes in immunity over coral evolution may therefore have driven changes in microbiome structure, which may in turn contribute to modern cross-species differences in disease susceptibility. We used phylogenetic comparative methods to test for correlations between coral innate immune gene repertoire, microbiome structure, and disease susceptibility across genera representing >240 million years of coral evolution. This analysis drew on 1440 microbiome 16S rRNA samples from coral mucus, tissue and endolithic skeleton from our Global Coral Microbiome Project (GCMP); three long-term regional disease datasets; and innate immune gene repertoires annotated from all publicly available coral genomes. Across sequenced coral genomes, we find that gene family expansions of TIR-domain containing innate immune genes strongly predict reduced microbiome richness (PGLS R^2 = 0.40, p = 0.021), especially within coral's endolithic skeleton (PGLS R^2 =0.791 p = 0.0003). Indeed, gene copy number expansions of IL-1R genes alone explain an astounding ~83.5% of overall variance in microbiome richness across coral genera in our data (PGLS R^2 = 0.84, p = 5.13 x 10^{-15}). We further find that across 40 coral genera with both microbiome and disease data available, disease susceptibility doesn't significantly correlate with microbiome richness. Instead, ecological dominance of the most abundant microbial taxon increased overall disease susceptibility (PGLS R^2 = 0.27, p = 0.0006), especially in corals with more γ- than α- proteobacteria (PGLS R^2 = 0.40, p = 0.0003). We are investigating whether a growth/defense tradeoff in symbiotic association with *Endozoicomonas* explains this correlation between ecological dominance in the microbiome and disease susceptibility. Overall, these results demonstrate the utility of consistently collected cross-species datasets for exploring the interactions between coral immunity, microbiome structure, and disease susceptibility.

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