

Characterizing insertion sequence abundance and diversity in genomes of the marine invertebrate-associated symbiont *Candidatus* Thiosymbion

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Bacterial symbionts and pathogens of animals that become host-restricted undergo several major genome changes, one of which is the massive proliferation of mobile genetic elements (MGE). Proliferation of the most abundant MGEs, insertion sequences (ISs), can lead to gene regulatory shifts, pseudogenization, and deleterious homologous recombination. Despite the significant effect of IS proliferation on the evolutionary trajectory of host-restricted bacteria, there is limited work investigating the role of IS diversity and distribution in genome evolution, and how this is influenced by environmental factors. We aimed to explore the factors that interact with IS abundance and diversity using an ecologically diverse marine symbiont. We characterized ISs in over 160 *Candidatus* Thiosymbion genomes and identified patterns associated with genomic characteristics. We found that the number of ISs decreases with increased GC content, while IS diversity increases. However, these patterns seem to be partially influenced by the host organism group, suggesting that the relationship between IS proliferation and evolution of symbiont genomes could be influenced by host-specific factors (e.g., symbiont localization/sexual isolation, habitat). Our results reveal how the fundamental evolutionary mechanisms driving genome structure and composition in a single bacterial symbiont clade can vary according to host population.

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Rank	Presentation type
1	Oral
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