

Ubiquitous Episodic Selection on Protein Coding Genes in Vesicomylid Symbiont Genomes

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Vesicomylid clams inhabit vents and seeps around the world, and their intracellular chemosynthetic symbionts are maternally transmitted through eggs each generation. This tight association places evolutionary constraints on the symbionts that for the past 50-60 MY have been evolving into a plastid-like organelle. Population bottlenecks that symbiont populations experience due to maternal transmission are hypothesised to limit selection on intracellular symbiont genes by reducing effective population size and increasing the fixation of deleterious mutations. An intracellular lifestyle should limit opportunities for recombination resulting in the reduced efficacy of natural selection, but Stewart et al. (2008, 2009) detected lateral acquisition and instances of recombination challenging this expectation. This comparative genomics study, including 15 newly sequenced symbiont genomes and 9 host mitochondrial genomes, suggest that natural selection and symbiont replacement have been, and indeed still are, a strong force shaping this symbiotic association. About 17% of genes that we examined show evidence of episodic selection on at least one lineage. Much of the selection that we identify occurs within genes involved in genetic information processing including DNA metabolism, transcription, and translation. This selective landscape might be a response to the shift to AT rich genomes that these symbionts have experienced.