

Evolution of exonic nucleotide variation at the exon-intron boundary in coral symbiotic dinoflagellates

S. Maruyama, Yuu Ishii, T. Makino, and M. Kawata

Department of Environmental Life Sciences, Graduate School of Life Sciences, Tohoku University, Sendai, Miyagi, Japan

Dinoflagellates are known for their unique genome architectures and gene expression systems. Despite the enormously huge genomes which hamper molecular studies of this lineage, recent genome and transcriptome studies using *Symbiodinium*, an ecologically important coral symbiont dinoflagellate, have provided a wealth of data for understanding the regulatory mechanisms of genes and genomes. Although genotype-phenotype correlation analyses using the *Symbiodinium* mutant strains showed that the exonic guanine adjacent to the exon-intron boundary was important for proper splicing, evolutionary trajectories of this unique exon-intron recognition remains unknown. In this study we showed that, using multiple *Symbiodinium* genomes, amino acid compositions in the codons surrounding the exon-intron boundaries were non-homogenous in all the genomes analyzed. Interspecies comparison also showed that base compositions of the exon-intron boundaries were biased in a group of conserved introns, of which the positions were conserved among the orthologous genes, relative to all the introns in the genomes. These data suggest that coral symbiont algae possess unique exon-intron boundary recognition mechanisms and be a useful model for studying how introns could affect the evolution of coding sequences in eukaryotic genomes.