

Background

The mitochondrial DNA (mtDNA) of most animals evolves more rapidly than nuclear DNA, and often shows higher levels of intraspecific polymorphism and population subdivision. The mtDNA of anthozoans (corals, sea fans, and their kin), by contrast, appears to evolve slowly. Slow mtDNA evolution has been reported for several anthozoans, however this slow pace has been difficult to put in phylogenetic context without parallel surveys of nuclear variation or calibrated rates of synonymous substitution that could permit quantitative rate comparisons across taxa. Here, I survey variation in the coding region of a mitochondrial gene from a coral species (*Balanophyllia elegans*) known to possess high levels of nuclear gene variation, and estimate synonymous rates of mtDNA substitution by comparison to another coral (*Tubastrea coccinea*).

Results

The mtDNA surveyed (630 bp of cytochrome oxidase subunit I) was invariant among individuals sampled from 18 populations spanning 3000 km of the range of *B. elegans*, despite high levels of variation and population subdivision for allozymes over these same populations. The synonymous substitution rate between *B. elegans* and *T. coccinea* (0.05%/site/106 years) is similar to that in most plants, but 50-100 times lower than rates typical for most animals. In addition, while substitutions to mtDNA in most animals exhibit a strong bias toward transitions, mtDNA from these corals does not.

Conclusions

Slow rates of mitochondrial nucleotide substitution result in low levels of intraspecific mtDNA variation in corals, even when nuclear loci vary. Slow mtDNA evolution appears to be the basal condition among eukaryotes. mtDNA substitution rates switch from slow to fast abruptly and unidirectionally. This switch may stem from the loss of just one or a few mitochondrion-specific DNA repair or replication genes.