Genome Composition Plasticity in Marine Organisms

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Abstract

The molar ratio of the nucleotides (GC%, i.e. the Guanine+Cytosine content) is well known to evolve through the genomes of all the organisms. Several hypotheses have been drawn out to explain the causes of the nucleotide composition variability among orgnisms.

In the Thesis project major attention has been directed to the Metabolic Rate hypothesis (MRh). The main goal was to test if the MRh, first proposed to explain the nucleotide variability within mammalian genomes, could also explain the base composition variability among lower vertebrates and invertebrates. To this aim an extensive analysis of more than two hundred teleostean species has been carried out, followed by a pioneering study of annelid polychaete and tunicate genomes.

Regarding teleosts, the results clearly highlighted that environment (i.e. salinity) and lifestyle (i.e. migration) both affect simultaneously the physiology (the metabolic rate), the morphology (the gill area) and the genome composition (GC%). Thus supporting a link between the metabolic rate (MR) and the genome base composition, as expected in the light of the MRh. Moreover, a comparative analysis of completely sequenced teleostean genomes showed that the metabolic rate was correlated not only with the GC content of the genome, but also with the intron structures. Indeed, at increasing metabolic rates introns were shorter and GC-richer.

A preliminary analysis of annelids polychaetes showed that motile and sessile species were characterized by different MR and GC%, being both higher in the former than in the latter.

The investigation was extended to the well known solitary tunicates, *C. robusta* and the congeneric *C. savignyi*. Our data revealed slight but significant morpho-physiological differences between the two species, consistent not only with an ecological niche differentiation, but also with their genomic GC content.

All the above results converge towards the same conclusion, thus giving consistency to the MRh as major factor driving the genome base composition evolution of all living organisms.