Reshaping the mtDNA circle: new insights from four newly sequenced ascidian genomes

Iannelli F (1), Griggio F (1), Pesole G (2), Gissi C (1)

(1) Dipartimento di Scienze Biomolecolari e Biotecnologie, Università di Milano, Italy
(2) Dipartimento di Biochimica e Biologia Molecolare, Università di Bari, Italy

Motivation

The mitochondrial genome (mtDNA) of vertebrates evolves following few rules: compact structure, constant gene content, almost frozen gene order except for minor changes involving tRNA genes, one major non-coding region involved in genome replication and expression, and a strong compositional asymmetry (Saccone et al. 1999). Surprisingly, the mtDNA of basal chordates and vertebrate ancestors, Tunicata, seems to follow a completely different evolutionary trend, characterized by many gene rearrangements even in cogeneric species (Yokobori et al. 2003; Gissi et al. 2004) and accelerated evolutionary dynamics.

Methods

In order to further investigate the peculiarities of mtDNA evolution in tunicates, we amplified by long PCR and completely sequenced the mtDNA of four ascidians: two Stolidobranchia species, Microcosmus sulcatus (Pyuridae) and Styela plicata (Styelidae), and two cogeneric Phlebobranchia species, Phallusia mammillata and Phallusia fumigata (Ascidiidae). Gene rearrangements were carefully investigated.

Results

The analyses confirm previous observations of a high rate of gene rearrangement in these genomes. The two mtDNAs of the genus Phallusia have undergone even more gene rearrangements than the two Ciona species. Only three gene pairs retain a conserved order between the two Pyuridae, Microcosmus sulcatus and Halocynthia roretzi (Yokobori et al. 1999). Moreover the only gene block conserved in all previously available tunicate mtDNAs - the cox2/cob pair - is not conserved in the organism Styela plicata. This situation confirms the hypothesis that the only constrain to conserve this gene block is an overlap between the ORFs (Gissi and Pesole 2003). Furthermore, base compositional variability, shortness of rRNA genes, and absence of a main non-coding region were confirmed as common features of ascidian mitochondrial genomes and indicate that the evolutionary dynamics of ascidian mtDNA markedly diverge from those of vertebrates.

Contact email: fabio.iannelli@unimi.it
graziano.pesole@biologia.uniba.it
carmela.gissi@unimi.it

References

- Gissi C, Pesole G (2003) Transcript mapping and genome annotation of ascidian mtDNA using EST data. Genome Res. 13:2203-12.
- Gissi C, Iannelli F, Pesole G (2004) Complete mtDNA of Ciona intestinalis reveals extensive gene rearrangement and the presence of an atp8 and an extra trnM gene in ascidians. J. Mol. Evol. 58:376-389.
- Saccone C, De Giorgi C, Gissi C, Pesole G, Reyes A (1999) Evolutionary genomics in Metazoa: the mitochondrial DNA as model system. Gene 238:195-209.
- Yokobori S, Ueda T, Feldmaier-Fuchs G, Paabo S, Ueshima R, Kondow A, Nishikawa K, Watanabe K (1999) Complete DNA sequence of the mitochondrial genome of the ascidian Halocynthia roretzi (Chordata, Urochordata). Genetics 153:1851-62.
- Yokobori S, Watanabe Y, Oshima T (2003) Mitochondrial genome of Ciona savignyi (Urochordata, Ascidiacea, Enterogona): comparison of gene arrangement and tRNA genes with Halocynthia roretzi mitochondrial genome. J. Mol. Evol. 57:574-87.

Supplementary informations

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