

Utility of mitochondrial gene orders for the inference of broad and deep animal phylogeny

Kazuyoshi Endo[1]; Isao Sarashina[2]

[1] Earth Evolution Sci., Tsukuba Univ.; [2] Life and Environmental Sciences, Tsukuba Univ.

Gene orders, or relative positions of particular genes on a genome, provide unique characters for phylogeny reconstructions independent of nucleotide or amino acid sequences. In particular, those in mitochondrial genomes are usually comparable among different animal phyla, and therefore have been used for the estimation of deep metazoan phylogeny. Application of this approach to a wide range of phyla, however, often failed in recognizing widely accepted bilaterian clades such as lophotrochozoa and ecdysozoa, raising skepticism about its utility as a phylogenetic tool. Inspection of the studies that yielded such bizarre results indicated that they mixed up and included both well conserved and randomized gene maps in their analysis, with the latter contributing only to make unwanted noises. Here, I introduce a simple statistic method to discriminate between well conserved and randomized gene maps, and argue that mitochondrial gene orders are useful in unveiling broad animal phylogeny if and when the randomized gene maps are excluded from the data set.