

INVITED PRESENTATION: Evolutionary Features of Genomes as Disclosed by Comparative Analysis of Complete Genome Sequences

Takashi Gojobori, T. Daniel Andrews, Takeshi Itoh Center for Information Biology National Institute of Genetics Mishima, Japan

Abstract

Our comparisons of complete genome sequences revealed that the genome structures have been extensively shuffled among eubacteria, particularly when the orders of orthologous genes were examined. Moreover, archaebacterial and eukaryotic genome structures were found to be unstable, too, as were the cases of eubacteria. We then turned our attention to operon structures, which were expected to be well conserved during evolution because of their regulatory importance. Surprisingly enough, however, we found that even within operons, gene orders have not been conserved, with exception to only a few cases such as ribosomal operons. When we reconstructed the ancestral genome structure of eubacteria and archaebacteria, and examined the relative instability of the genome structures among eubacteria, we found that there were differences in the degree of the genome instability among the examined species. The genome instability appears to be correlated with the number of insertion sequences. Interestingly enough, the intensity of the intrastrand bias of nucleotide composition (G-C skew) was found to be affected by the genome instability, implying that accumulation of strand-specific mutations depends heavily upon the stability of a genome. These findings imply that the gene orders have not been essential for survival of microbes in long-term evolution, and that the evolutionary instability of the genome structures is an intrinsic nature common to eubacteria, archaebacteria and eukaryotes. For eukaryotic genomes, we found that a lot of gene fusion events might have happened in the early evolution of eukaryotes so as to compensate for the loss of bacterial operon structures. The evolutionary instability of the genome structures can be one of the most important factors in understanding the evolutionary processes of the genome evolution.

Permission to make digital or hard copies of all or part of this work for personal or classroom use is granted without fee provided that copies are not made or distributed for profit or commercial advantage and that copies bear this notice and the full citation on the first page. To copy otherwise, to republish, to post on servers or to redistribute to lists, requires prior specific permission and/or a fee RECOMB 2000 Tokyo Japan USA Copyright ACM 2000 1-58113-186-0/00/04 \$5.00