

# Multiple Ribosomal RNA operons in bacteria; Their concerted evolution and potential consequences on the rate of evolution of their 16S rRNA

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Bacterial species differ greatly in the number and location of the rRNA operons which may be present in the bacterial chromosomes and plasmids. Most bacterial species contain more than one ribosomal RNA operon copy in their genomes, with some species containing up to 15 such copies. We review the number and location of the rRNA operons and discuss evolution of 16S rRNA (*rrs*) genes -which are considered as ultimate chronometers for phylogenetic classification- in bacteria with multiple copies of these genes. In these bacterial species, the *rrs* genes must evolve in concert and sequence changes generated by mutation or horizontal gene transfer must be either erased or spread to every gene copy to avoid divergence, as it occurs when they are present in different species. Analysis of polymorphic sites in intra-genomic *rrs* copies identifies putative conversion events and demonstrates that sequence conversion is patchy and occurs in small conversion tracts. Sequence conversion probably arises by a non-reciprocal transfer between two or more copies where one copy contributes only a small contiguous segment of DNA, whereas the other copy contributes the rest of the genome in a fairly well understood molecular process. Because concerted evolution implies that a mutation in any of the *rrs* copies is either eliminated or transferred to every *rrs* gene in the genome, this process should slow their evolution rate relative to that of single copy genes. However, available data on the *rrs* genes in bacterial genomes do not show a clear relationship between their evolution rates and the number of their copies in the genome. © 2018

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16S rRNA

Concerted

Evolution

Multiple-copies

Polymorphism

Rrs

ribosome RNA

RNA 16S

bacterial gene

bacterium

gene mutation

horizontal gene transfer

molecular evolution

nonhuman

operon

phylogeny

Short Survey