In-Silico Study of the 16S Ribosomal RNA Gene of Campylobacters, Helicobacters and Arcobacters

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The explosion of gene sequences on public domain databases offers unique opportunities to study relationships between organisms. The taxonomy of campylobacters, helicobacters and arcobacters collectively referred to as campylobacteria is dynamic and there is need to obtain the current and comprehensive relationship among these increasingly important veterinary and human pathogens. A list of validly published campylobacteria was obtained from the website; www.sv.cict.fr/bacterio/. A total of 46 campylobacteria consisting of 23 Helicobacter, 16 Campylobacter, 4 Arcobacter and one each of Flexispira, Wolinella and Bacteroides were obtained. The 16S rRNA gene sequences of these taxa were retrieved from the GenBank. Phylogenetic analysis was done using ClustalX and the resulting tree viewed by TreeView with Escherichia coli 16S rRNA gene sequence as outgroup. A pairwise distance matrix and phylogenetic tree confirmed with statistically reliable bootstrap values the clustering of campylobacters, arcobacters and helicobacters into rRNA homology group I, II and III respectively. This is a contribution to bioinformatics approaches to study the campylobacteria.

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