Prompt: Discuss the challenges involved in defining a microbial species and how HGT complicates matters, especially in the context of the evolution and phylogenetic distribution of microbial metabolic pathways. Can you comment on how HGT influences the maintenance of global biogeochemical cycles through time? Finally, do you think it is necessary to have a clear definition of a microbial species? Why or why not?"

If one was to sequence the genome of every cell derived from a millilitre of seawater or a gram of soil, they might be surprised by the number of different microbes they would find in the sample. However, classification of these microorganisms into separate species remains a controversial issue. Although there are various concepts that have been suggested for this process, microbiologists do not have a consensus on which species definition should be accepted (1, 2). This lack of a robust microbial species definition is in part due the advancements in DNA sequencing techniques and genetics analyses, which have unveiled the complexity and processes involved in prokaryotic variation (3-5). In particular, horizontal gene transfer (HGT) and homologous recombination make it difficult to properly demarcate species (5). In this paper, I will discuss the different ways microbial species are defined and their limitations. I will also consider the roles of horizontal gene transfer in shaping microbial genomes and distributing metabolic pathways, while highlighting the fact that this process further complicates classification of different microbial lineages.

Limitations of current approaches to microbial species definition

Today's gold standard for species delineation is inadequate as it uses arbitrary measurements. The current method for defining prokaryotic species is based on the phylo-phenetic species concept by Rossello´-Mora and Amann (6). It defines microbial species as, "monophyletic and genomically coherent cluster of individual organisms that show a high degree of overall similarity with respect to many independent characteristics, and is diagnosable by a discriminative phenotypic property" (6). Firstly, it uses a genetic marker such as the 16S rRNA gene to initially classify organisms into a taxa (i.e. family or genus level) (1, 7). Followed by DNA:DNA hybridization, organisms belonging to the same species are identified based on 70% genomic similarity set as the threshold (6). Then, phenetic measures are used to differentiate the microbial species in question from existing identified species (8). Although both genomic information and phenotype are examined, the use of empirical parameters (genetic markers for phylogeny, percentage of DNA:DNA hybridization, and phenotypic properties) at each step of