

identifying phylo-phenetic microbial species is problematic as there are no theoretical evidences that prove these measures are correct (1). The 70% similarity in DNA:DNA hybridization and the 97% cut-off for 16S rRNA gene similarity are arbitrary numbers and were only adapted based on mounting previous work and experimental results (8). Hence, the phylo-phenetic species method may not be sufficient to guarantee microbial species identity.

Other current prokaryote species concepts listed in a review by Ereshefsky also highlight several points that make it even more challenging to choose a single method for species definition (1). For instance, the biological species concept states that “species are groups of interbreeding natural populations that are reproductively isolated from other such groups” (9). This traditional concept, however, does not appropriately apply to prokaryotes as they do not sexually reproduce. Instead, they use binary fission or vegetative means (1). As one may assume, a parent microbial species should then be genetically identical to its daughter cells, and yet this is not the case (10). Through horizontal gene transfer, prokaryotes can move genetic information between each other, creating chimeric genomes (11). Microbes can exchange homologous and non-homologous genes that recombine with its genome (4). HGT can occur via transformation (genetic material absorbed by a host), conjugation (cell to cell transfer), and/or transduction (viral transfer) (12). Thus, in the microbial world, evaluating what it means to be a species is more certainly not as absolute as the sexually reproducing (biological) species definition. It is instead much more fluid as it involves the movement and transfer of genetic material from one organism to another. Unfortunately, the current approach for defining species is relatively inadequate for detecting genetic rearrangement, gene amplification, mutation, and exchange of genetic material from different lineages (6, 8).

Another proposed prokaryote species concept by Cohan defines a species as follows: “a species in the bacterial world may be understood as an evolutionary lineage bound by ecotype-periodic selection” (13). This suggests that, in defining microbial species, one must consider where a prokaryote lives or is found, as well as the adaptations it has to specific environments. According to Ereshefsky, this ecological approach for delineating species assumes that natural selection is the main process responsible for maintaining species as “a cohesive group” and eliminating those that are niche-specific (1). However, it is possible that selection and