

shown that a group of bacteria, such as green sulphur bacteria, *δ-Proteobacteria* and *Chloroflexi*, cluster with *Methanosarcina* (*Euryarchaea*). Likewise, some *Firmicutes* (mainly *Clostridium* species) also cluster as a sister clade with the euryarchaeote *Methanoregula boonei* (14). This highlights the fact that different microbial lineages can acquire metabolic genes from one another (14).

Furthermore, even if a group of microbes containing genes of a certain metabolic pathway were eliminated by natural selection, supposing those genes were initially transferred to another microorganism, then the metabolic processes would be maintained through evolutionary time (14). Consequently, if microbial species are defined by metabolic repertoires encoded in their genome, the spread of metabolic functions via HGT could be a limitation to single out a microbe and call it a species. As an example, in a study by Welch *et al.*, three different *Escherichia coli* strains (CFT073, EDL933 and MG1655) which were categorized as one species, were found to only have 39% similarity with respect to its functional repertoire (16). In addition, sometimes metabolic pathways are not only within an organism; it could be within a population or even extend to a community level. Thus, the distribution of metabolic functions through evolutionary time and among different microbial groups make it more problematic to define species boundaries in prokaryotes.

Conclusion

While there are various species concepts available in microbiology, each of them has limitations. In addition, many microbiologists are challenged by the importance and influential role of horizontal gene transfer in microbial genome variability and divergence of metabolic functions, which all together complicates the issue of defining microbial species. For one thing, perhaps in order to fully capture genomic differences when defining species, whole genome analysis should be the basis for future microbial species classification. Nonetheless, having a clear definition of a microbial species is vital. It increases our understanding of microbial structures and communities, as well as surveying disease outbreaks (17). Most importantly, the convenience for communicating microbiology is undeniable and thus, defining microbes into species should continue.