

recombination occur on the same group of microbes, and thereby resulting in cross-classification of those microorganisms (1). Evidently, a study by Nesbø *et al.* shows that in the genus *Thermotoga*, some groups of microorganisms form single species based on the recombination approach but several species are classified using the ecological approach (11). Thus, this further complicates defining microbial species because this empirical evidence suggests that one group of prokaryotes can belong to two different species, though species of different types (1).

HGT transforms microbial genomes

As previously established, the acquisition of genomic material and/or extrachromosomal elements are possible via horizontal gene transfer. Consequently, it can lead to misclassification or misidentification of prokaryotes because of its role in re-shaping microbial genomes (6, 14). With HGT, prokaryotic genomes have been reported to possibly be subjected to homologous recombination with related species that are up to 25% different in the sequences of homologous genes (6). Microbes can also receive and express new genes on plasmids from extremely divergent sources (6). Thus, HGT can link genomes from distant lineages or even introduce new genes, making it difficult to dissect and analyze parts of the organisms' genomes, especially in terms of determining their evolutionary histories. Furthermore, it is important to note that not all genes transferred via HGT occur with equal probability (15). For example, it has been observed that, compared to operational genes (needed for housekeeping), informational genes (involved in transcription, translation, and other related processes) are rarely transferred (15). As this finding may question the stability of microbial genome, an important consideration on the extent of gene transfer among prokaryotes is thereby necessary to improve our current approaches for species assignment.

HGT spreads metabolic functions

While HGT can influence and expand microbial genomes, this process also contributes to the distribution of microbial metabolic functions. Through HGT, it is possible that operons encoding parts of, or the entire metabolic pathway, may be spread to closely or distantly related organisms (14). Taking the nitrogen fixation pathway as an example, there is evidence suggesting that HGT played a role in spreading nitrogen fixation genes within the microbial world (14). A phylogenetic analysis of different nitrogen fixation proteins (NifHDKEN) has