In the famous work of Charles Darwin, “On the Origin of Species,” Darwin stated that species is a constructing unit that would not exist in the absence of human principle of classification^[[1](https://onlinelibrary-wiley-com.ezproxy.library.ubc.ca/doi/pdf/10.1002/9783527664283.ch)]^. However, biologist and conservationists need to establish a universally agreed system to circumscribe living beings for them to exchange idea. Since organisms are constantly evolving, the modern days biologist replaced Linnaean typological view of species by the concept of a reproductive community, where two organisms belong to the same species if they can produce fertile offspring through mutual lateral gene exchange by sexual contact. This definition clearly is not applicable to prokaryotes as they reproduce asexually through binary fission. Therefore, microbiologist adapts the theoretical value suggests by Wayne *et al.* that a species is where organisms share at least 70% or higher DNA similarity^[[2](https://www-jstor-org.ezproxy.library.ubc.ca/stable/pdf/25593154.pdf?refreqid=excelsior%3Afd274694fd1f935a990e810ac2b5457b)]^. This definition is pragmatic and universally applicable within the prokaryotes community, but it fails to establish a nested taxonomic level of eukaryotic species. Under this definition, all of the primates are essentially the same species^[[3](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC549018/?tool=pmcentrez#ref8)]^. Thus, the question remains: how can scientists come up with a stringent definition for microbial species? There are various issues and challenges that need to be resolved, including the technical difficulty of comparing the genomic information, but most importantly is to address confounding issue of horizontal gene transfer.

Wayne et al suggests that microbial species is a collection of strains that shared at least one diagnostic phenotypic traits and their purified DNA molecules need to be at least 70% or above similar to one another; however, there are many technological difficulties in recognizing diagnostic traits and in conducting the pairwise DNA-DNA similarity experiments. The 70% or higher becomes a “gold standard” for identifying a microbial species, which it allows a small subset of isolates to objectively represent a single species^[[4](https://ac-els-cdn-com.ezproxy.library.ubc.ca/S0168644500000401/1-s2.0-S0168644500000401-main.pdf?_tid=3cdc94ec-e901-4db0-a76a-f7d7bff1e7bb&acdnat=1524460688_9609d51339b5d41a2e39c792db19a585)]^. In addition, the traditional DNA-DNA hybridization (DDH) technique is too time-consuming and complex that it was impossible to build a large database based on DDH results. Therefore, in recent years, scientists use 16S rRNA phylogeny to circumscribe microbial species. However, since 16S rRNA gene is highly conservative, this approach is unable to show enough resolution as it neglects the strain diversity with a species^[[5](https://www-sciencedirect-com.ezproxy.library.ubc.ca/science/article/pii/S0723202015000223?_rdoc=1&_fmt=high&_origin=gateway&_docanchor=&md5=b8429449ccfc9c30159a5f9aeaa92ffb&ccp=y#bib0430)]^. Recent studies has suggests that species can have identical or nearly identical 16S rRNA marker sequence but traditional DDH method does not classify them to be the same species^[[6](http://www.microbiologyresearch.org/docserver/fulltext/ijsem/42/1/ijs-42-1-166.pdf?expires=1524462600&id=id&accname=guest&checksum=D09E6B32E2CB60E7DEF424907C8CE900)]^. In addition, 16S rRNA putative marker analysis is directed towards analyzing community composition of environmental samples against known database, which means that this approach is not capable of identify novel species that have unique phylogenetic marker^[4]^. Therefore, scientist is still struggling to identify method that can perform efficient pair-wise DDH and acknowledge the fast-changing genomic sequence of prokaryotes.

One of the prominent reason that makes circumscribing microbial species is the rapid change in genomic material of organisms, and this is primarily due to horizontal gene transfer in prokaryotes and archaea. In most cases, the source and the rate of horizontal gene transfer are highly related to the organism’s lifestyle. Horizontal gene transfer events can be acquisition of new genes or paralogs of existing gene or xenologous gene displacement of ortholog from another lineage^[7]^. These events make classification of organisms highly challenging because microbe’s genome can contain numerous other microbes’ genes, which makes strains of the same species highly variable. For example, Welch *et al.* ran a three-way genome comparison on three different strains of *E. coli*, and discovered that only 39.2% of their nonredundant set of proteins are common to all strains^[8]^. In another study performed by Bogdanova *et al.*, they discovered that mercury reductases gene are found among multiple phylogenetically distant gene, which suggests that horizontal gene transfer events occurred between these strains^[9]^. This suggests that acquisition of foreign gene through horizontal gene transfer can allow the recipient organism to become better adapted to its environment. For instance, CFT073 strain of *E. coli* acquired 12 distinct and putative fimbriae, which enables it to infect urinary tract; however, the two other strains of *E. coli* can only inhabit in gastrointestinal tract^[8]^. Therefore, the horizontal gene transfer among different lineages appear to be highly influenced by habitat and ecology as they are likely to increase fitness of the recipient organism. In conclusion, this suggests that rapid speciation due to high frequency of horizontal gene transfer is inevitable.

Recent studies suggest the massive amount of horizontal gene transfer is highly related to the positive selection pressure on the environmental niche, which allows many essential metabolic pathways to be retained throughout evolutionary time and allows rapid ongoing development of new pathways. It is estimated that between 1.6 to 32.6% of the genes in each microbial genome have been acquired through horizontal gene transfer, and the transfer can occur not only within the domain but also across the domains^[10]^. A recent study by Wagner and De la Chaux analyzed the evolution of 2091 insertion sequences in 428 completely sequenced prokaryotic genomes and discovered that there were only 30 cases of presumed transfer event, in which 23 events seemed to be ancient and only 7 were recent^[11]^. This suggests that organisms can have high frequency of horizontal gene transfer event, but it is observed that majority of the gene that are acquired through horizontal gene transfer may be lost over time as the novel ability may come with extra fitness cost or may disrupt the essential metabolism genes. Many have speculated that horizontal gene transfer was the first mechanism to preserve early metabolic pathway^[12]^. The communal evolution in the Archaeon era were based on the distribution of gene that are responsible catabolic and anabolic processes in the global gene pool. ∂-proteobacteria, Gram-positive bacteria and Archaea encode for dissimilatory sulfite reductases, which reflects the lateral propagation of sulfate respiration among various domains and niches^[12]^. In summary, horizontal gene transfer allows organism to acquiring new gene for better fitness, which also enables important metabolic pathways to be preserve across organisms in different domain.

As stated above, taxonomy is for scientist to differentiate and circumscribe living beings; however, it is not necessary for human to develop such classification of microbial species. With or without species definition, current technologies already enable scientists to extract useful information from microbes’ genomic information. For example, even if the researchers cannot establish CFT073 to a be novel species or a strain of E. coli, the researchers have identified its mean of infection, which allows the researcher to develop targeted treatment to remove it from human body. Therefore, the classification of a microbe can be highly irrelevant of its potential scientific use, which suggests that it may not worthwhile to develop a new taxonomic system to classify a microbial species.

Horizontal gene transfer and other technical challenges make the circumscription of microbial species highly infeasible. Horizontal gene transfer event not only preserve important metabolic pathway, but also allows the organism to be highly adaptable to changes in environment. Due to horizontal gene transfer event, many organisms are evolving at rapid speed, which makes classification of microbial species extremely challenging. Therefore, the student believes that it may not be necessary to develop new means to define microbial species.

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