**“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?”**

It is human nature to classify things and put things into neatly organized bins that reflect the nature and characteristics of the object, and for science and research, proper naming enables communication regarding the object in question. With organisms at a macroscopic scale, species can be defined and distinguished mostly based on whether they can interbreed. However, when it comes to microbes, there are various challenges involved in defining what a microbial species is. This is further complicated by horizontal gene transfer (HGT). In this essay, the challenges surrounding the definition of microbial species will be discussed further, along with the role of HGT in the maintenance of global biogeochemical cycles through time. Additionally, I will also discuss why it is necessary to be able to have a clear definition of what a microbial species is, even with all the challenges that come with it.

Some of the challenges for defining a microbial species comes from the fact that many of the existing methods in use for organisms at a larger scale simply do not apply to microbes, and that existing methods are only operational. For example, the existence of asexual organisms makes it difficult to use interbreeding as a classification. Even with the use of genetic similarity to define species, including DNA hybridization and rRNA gene similarity, definitions for the cut off between what defines a species is only operational and arbitrary, and may not be reflective of actual evolutionary processes and species labelling [1]. Using this method of defining a species, there is shown to be tension between the taxonomic label, and actual similarity. For example, in the work by Thompson *et al*, extensive diversity was found within a group of coastal bacterioplankton, with greater than 99% 16S ribosomal RNA identity to *Vibrio splendidus* [2]. Specifically, they examined *Hsp60* and found that it varied greatly in genome size and even carbon substrates [2]. An even greater amount of diversity was found in the work by Welch et al, in *Escherichia coli*, where it was shown that strains were adapted to completely different ecological niches, and only 39.2% of their combined set of proteins were common to all three strains. Whether this sort of diversity should be allowed in a single species definition is also a challenge in defining a microbial species. However, with newer approaches, such as using amplicon sequence variants (ASVs), over operational taxonomic units (OTUs) may improve this labelling [1].

When defining a microbial species, horizontal gene transfer must also be considered, as HGT enables sharing of genes. This makes it difficult to examine evolution because evolution of microbial metabolic pathways, with HGT, may not occur linearly, as compared to other forms of events that could create genetic distance, such as mutations, insertions, and deletions. This increases the number of possible evolutionary pathways possible, and thus makes it more difficult to discern what the “true” evolutionary path is. While HGT may make phylogeny more difficult, it is an essential process in maintaining the global biogeochemical cycles. Entire metabolic pathways may be horizontally transferred, which protect the cycle, and through HGT, microbes are appropriately called the “guardians of metabolism” [3].

Even with all of the challenges in defining a microbial species, it is essential to have one. This is because definition of a species allows for communication surrounding the group of organisms, and ensures that there is a label that is consistent between different discussions. This allows integration and findings from other studies or work to be integrated into current and future work on the group of microbes, which is most important. It would be ideal that a labelled species indicates some sort of evolutionary origin, or biological function, but for now it is most important that the labels are consistent. Consistency is even more important when it comes to a clinical setting, so that doctors may communicate to each other in a standard vocabulary, and provide proper diagnosis and treatment.

In conclusion, while it is difficult to define a microbial species, and made even more complex with the existence of horizontal gene transfer, it is essential to have one so that discourse on the microbes can occur, and research may move forward with findings from the past. The current definition of microbial species is operational and arbitrary, and may not reflect accurately any evolutionary process or biological function, but most importantly it is consistent. Moving forward, if the definition of a microbial species does change, it would also be interesting to keep track of what organisms get moved to a different classification. As previously mentioned, consistency is most important, and if classifications do end up changing, it would also be important to consider “backwards compatibility” with the labels somehow, so that research from the past is still accessible. Hopefully, with improving methods of defining microbial species, it will be possible one day to have our definition encompass both consistency and biological meaning.

**References**:

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