

FOUNDATIONS OF MICROBIAL ECOLOGY

Let's get to know the factors that shape microbial ecosystems!

WHAT ARE MICROBES?

Microscopic organisms that may be single-celled or grow in colonies.

* Major types of microbes:
Bacteria, archaea, viruses, fungi, and protists.

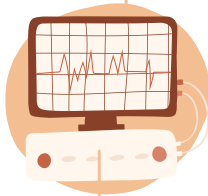


VOCABULARY

It can be difficult to define microbial taxonomy through definitions alone because of differences in vocabulary across biological disciplines.

TAXONOMY

Traditionally, studying species variation was only done in microbes that could be lab-grown in culture. Now, due to genetic sequencing, we are able to study variation between many more species than before.

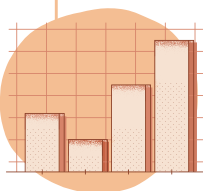


SEQUENCING

Sequencing techniques such as Sanger, Pyrosequencing, and Illumina were developed in order to determine the biological differences of microbes within the same community.

BETTER DATA

However, not all sequencing technologies are the same. Next-gen 16s rRNA Illumina sequencing can be trusted best to describe differences between DNA base pairs within microbial communities.



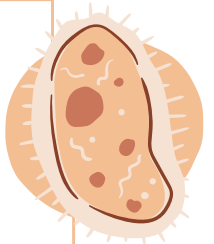
VELLEND'S PRINCIPLES

Beyond knowing the differences in DNA sequences of microbes, Vellend created a list of fundamentals that considered the factors that *shape* microbial ecosystems. These principles are selection, drift, mutation, and gene flow.



SELECTION

Selection is the process through which species adapt to changes in their environment. This may be phenotypic or genotypic changes that influence the increase of variation in the community.



DRIFT

Drift describes random fluctuations in the numbers of gene variants in a population. These random shifts in diversity can strongly influence small microbial populations.



MUTATION

The rate of mutation depends on population size and allele strength. The introduction of genetic variability in daughter cells influences the diversity of microbes in the community.



GENE FLOW

Gene flow is the transfer of genetic material from one population to another. Horizontal gene transfer is an important example of gene flow that frequently occurs within bacteria and influences their microbial communities.

IN SHORT,

In order to define microbial communities, a researcher should use strategic vocabulary to describe their taxonomic findings. Additionally, 16s rRNA Illumina sequencing can be done in order to determine differences in base pairs, mutations, genetic drift, etc.



SOURCES

- Van Rossum, T., Ferretti, P., Maistrenko, O.M. et al. Diversity within species: interpreting strains in microbiomes. *Nat Rev Microbiol* 18, 491–506 (2020). <https://doi.org/10.1038/s41579-020-0369-1>
- Ömeroglu, D. R., Schmidt, S. K., Fukami, T., O'Neill, S. P., Blinski, T. M., Stanish, L. F., Knelman, J. E., Darcy, J. L., Lynch, R. C., Wickey, P., & Ferrenberg, S. (2013). Patterns and processes of microbial community assembly. *Microbiology and molecular biology reviews*: MMBR, 77(3), 342–356. <https://doi.org/10.1128/MMBR.00051-12>