
Convention on Microbial Diversity and its Genetic Nature

'Microbial diversity' considers the vast array of microorganisms—the smallest forms of life—which exist everywhere. The three primary groups of microorganisms are bacteria, archaea, and eukaryotes. Bacteria and archaea are prokaryotes with their genetic material held in a single chromosome. In eukaryotes, most of the genome is held in multiple chromosomes. Over 11,000 species of bacteria have been identified using microscopic identification of cell shape and metabolic activity, Gram-staining techniques, and genetic identification of RNA and DNA sequences. There are 500 named species of archaea, divided into two phyla the euryarchaeota and the crenarchaeota. There are eight super groupings of eukaryotes, all of them include single-celled organisms, and five are entirely microbial.

According to the biological species concept, the existence of species in many animals and some plants is ensured by the cohesive evolutionary forces that result from pre- and post-zygotic barriers between eukaryotic species. The earth contains a huge number of largely uncharacterized Bacteria and Archaea. Microbiologists are struggling to summarize their genetic diversity and classify them, which has resulted in heated debates on methods for defining species, mechanisms that lead to speciation and whether microbial species even exist. This Review proposes that decisions on the existence of species and methods to define them should be guided by a method-free species concept that is based on cohesive evolutionary forces. It summarizes current approaches to defining species and the problems of these approaches, and presents selected examples of the population genetic patterns at and below the species level.

Various concepts have been suggested for microbial species, but none have been generally accepted possibly because all of these concepts include methodological considerations. In contrast to concepts based on particular methods, the method-free unitary species concept that is, "species are meta population lineages". Meta populations are "sets of connected subpopulations" that are "maximally inclusive" and the limits of which are set by evolutionary cohesive forces. A lineage can be thought of as a meta

population that extends through time, "occupies an adaptive zone minimally different from that of any other lineage in its range" and "evolves separately from all lineages outside its range". Unlike other species concepts, "meta population lineages do not have to be phenotypically distinguishable, or diagnosable, or monophyletic, or reproductively isolated, or ecologically divergent, to be species. They only have to be evolving separately from other such lineages." Microbes that form distinct groups owing to a cohesive force are meta population lineages and thus form species, whereas microbes without limits imposed by a cohesive force do not.

The sustenance of life on earth depends on maintaining the diversity of microorganisms. Human intervention is resulting in depletion of biodiversity and many hotspots are also fast losing their endemic biodiversity. While specific data is hard to come by, it is likely that loss of macro life forms also results in loss of the associated microbial species: symbionts as well as the rhizosphere-colonizing microbes. The significant contribution made by microorganisms in ecosystem sustainability as well as the industrially important biomolecules obtained from them antibiotics, anti-cancer drugs, enzymes, biofuel and various other compounds, implies that cataloguing them is imperative. However, a simple and effective microbial identification system is still far off. The available tools for classification and identification of microorganisms rely on a number of different technologies. This chapter provides an overview of taxonomy tools for understanding prokaryotic and eukaryotic microbial diversity. Taxonomy (or biosystematics) consists of three main parts: classification (arrangement of organisms based on similarity), nomenclature (naming of the organisms) and identification (determining whether an organism belongs to the group under which it is classified and named). Modern biosystematics also includes phylogeny as an integral part of the classification process