DIVERSITY OF PROKARYOTES, FUNGI, PROTOZOA, BRYOPHYTES, AND PTERIDOPHYTES IN TROPICAL ECOSYSTEMS

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Summary

For centuries, biologists have studied patterns of plant and animal diversity at continental scales. Until recently, similar studies were impossible for microorganisms due that the subjects of the census are not visible to the naked eye or easily differentiated by morphology. Microorganisms are the most diverse and abundant group of organisms on Earth. A major part of the unknown microbial taxa is supposed to be found in the tropics than in temperate regions because of the presence of more favorable environmental conditions all throughout the year, high diversity of vascular plants, and numerous niches and microhabitats, at least in tropical forests. Microbial researches have applied DNA-based methods to better understand the composition of complex microbial communities of prokaryotes, fungi and protozoa. In addition, tropical regions are far richer in bryophytes and pteridophytes than temperate ones. Eighty percent of the pteridophyte species occur in tropical areas and 20% in temperate areas. In this chapter, we will discuss the diversity and distribution of prokaryotes, fungi, protozoa, bryophytes and pteridophytes in tropical ecosystems.

1. Introduction

Global species diversity and community structure of bacteria, fungi, and protozoa around the world are unknown. Additionally, a vast majority of the species have yet to be named. Global patterns of species richness for microorganisms and the correlation with endemism patterns are lacking. Understanding patterns of biodiversity distribution is essential to conservation strategies (Lamoreaux et al. 2006). Scientific study of biodiversity has become increasingly urgent due to the realization that only approximately 8% of the total diversity of life is known and that species extinction is occurring at a measurable and increasing rate (Lachance 2006). Several authors have estimated the species richness of different organisms. Hawksworth (2001) has estimated that the global diversity of fungi to be well above one million species. Global ciliate diversity is not known, but it is estimated to be more than 30,000 (Foissner 2006). Molecular techniques have revealed a surprisingly high prokaryotic diversity and some studies have reported an unsuspected abundance of, or even dominance of, groups that were previously unknown or thought to be relative rare (Kemp and Aller 2004). Molecular studies based on sequence analysis resulted in an enormous increase in the ease and speed at which microbial species identifications occurred, making intense biodiversity surveys more manageable (Lachance, 2006). See (2004) suggested that we are still at the very beginning of a golden age of biodiversity discovery, driven largely by the advances in molecular biology and a new open-mindedness about where life might be found.

In this chapter, we will discuss the tropical diversity of prokaryotes, fungi, protozoa, bryophytes, and pteridophytes. Distribution and ecological relations of these organisms in tropical ecosystems will be discussed in the following sections.

2. Microbial Diversity

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2.1. Methods to Study Microbial Diversity

Microorganisms have a wide range of metabolic diversity and are considered the central catalytic agents in the global carbon cycle. They also have a key role in the cycles of nitrogen, sulfur, oxygen, phosphorus, and different metals. However, the real role of microbial communities in ecosystems and sustaining life on earth is underestimated. Moreover, only a small portion of microorganisms is able to grow on conventional culture media used in ecological studies. Microbe cultivation requires the preparation of complex culture media, which leads to microbe growth and subsequent isolation of a high number of individuals and species from the microbial community. In addition to the nutritional requirements, parameters such as pH, oxygen levels, temperature, redox (oxidation-reduction) potentials, luminosity, water activity, and humidity, can influence the growth of microbial species. Thus, studies on species composition and their frequencies in microbial communities using culture media only shed light on a small portion of these biologically diverse organisms. Counting and isolation of single colonies for subsequent identification have limitations, since unrelated species may present similar colony morphology and fast growing microorganisms are generally isolated at high frequencies. Many times, fastidious species or minor populations in a community are not detected using cultivation-based methods. It is often difficult to compare results from different studies owing to different sampling strategies, culture media, and incubation conditions (Fonseca and Inacio 2006).

Nowadays, rRNA sequences, that are found in all living organisms, obtained in cultivation-independent studies, have revealed a previously unappreciated amount of diversity in the microbial world that is not represented in cultures. Molecular, DNA-based methods for community profiling have been used for detection and enumeration of microorganisms in recent years. Microbial researches have applied these methods to better understand the composition of complex microbial communities. Methods based on the polymerase chain reaction (PCR) are rapid, as there is no need to culture organisms prior to their identification. They are specific, since identification of species is made on the basis of genotypic differences, and are highly sensitive, detecting target DNA molecules in complex mixtures. However, most of these studies were not conducted under ideal conditions, such as soils contaminated with polycyclic aromatic hydrocarbons, wastewater treatment plants, extreme environments, rhizospheres of agricultural crops, etc. Studies in tropical ecosystems using DNA-based methods are scarce and crucial in understanding the microbial biodiversity of these environments. These studies could be helpful in characterizing functional diversity of microbial communities.

It is now generally accepted that rRNA is the best target for studying microbial diversity and phylogenetic relationships because it is present in all Bacteria, Archaea, and Eukarya, and it is functionally constant, composed of highly conserved, as well as more variable domains. The components of the ribosome (rRNA and ribosomal proteins) have been the subject of different phylogenetic studies for several decades. The gradual development of new molecular techniques enabled microbiologists to focus on the comparative study of rRNA molecules. Sequencing of 16S rRNA with conserved primers and reverse transcriptase was a very important advancement in microbial phylogeny and resulted in a spectacular increase in 16S rRNA sequences. Nowadays,
these techniques have mostly been replaced by direct sequencing of parts or the entire 16S or 23S rDNA molecules by PCR and a selection of appropriate primers. This provides a phylogenetic framework, which serves as the backbone for modern microbial taxonomy. Taking into account the specific resolution of each method, the results and dendrograms constructed with data obtained from the above methods are similar.

Molecular methods for characterization of microorganism genotypes that do not require any cultivation steps include temperature and denaturing gradient gel electrophoresis (TGGE and DGGE), clone libraries of rRNA sequences, fluorescence in situ hybridization (FISH), among others. These methods allow an accurate identification of microbial communities, although primer selection can influence the species identification and chimeras (artifact sequences formed during the PCR process) are a serious concern in direct PCR applications targeting microorganisms in environmental samples. For studies of microbial diversity, it is very important to have the information about rDNA sequences deposited in reliable databases. Type strains of microorganisms should be deposited in public culture collections around the world and information about valid species also should be published periodically with open access for the scientific community.

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Biographical Sketches

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