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

Ana Paula Trovatti Uetanabaro
Laboratório de Controle de Qualidade Microbiológico de Fármacos, Departamento de Saúde, Universidade Estadual de Feira de Santana (UEFS), Feira de Santana, BA, Brazil

Aristóteles Góes-Neto
Laboratório de Pesquisa em Microbiologia (LAPEM), Departamento de Ciências Biológicas, Universidade Estadual de Feira de Santana (UEFS), Feira de Santana, BA, Brazil

Luiz Henrique Rosa
Laboratório de Microbiologia, Departamento de Ciências Biológicas, ICEB, Universidade Federal de Ouro Preto, Ouro Preto, MG, Brazil

Alexandre Salino
Departamento de Botânica, ICB, C.P. 486, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil

Alfredo H. Wieloch
Departamento de Zoologia, ICB, C.P. 486, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil

Carlos A. Rosa
Departamento de Microbiologia, ICB, C.P. 486, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil

Keywords: diversity, prokaryotes, fungi, protozoa, Bryophytes, Pteridophytes, 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

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 microorganism 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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Bibliography

Alexopoulos, C.J.; Mims, C.E. (1996). *Introductory mycology*. (4. ed.) John Wiley & Sons, Inc. New York. [A comprehensive textbook on biology of fungi]

Costa, D.P.; Imbassahy, A; Silva, V.P.A.V. (2005). Checklist and distribution of mosses, liverworts and hornworts of Rio de Janeiro. *Journal of the Hattori Botanical Laboratory* No. 98, pp. 259-298. [This is a revised checklist of the bryophytes species for Rio de Janeiro state, Brazil].

Feuerer, T.; Hawksworth, D.L. (2007). Biodiversity of lichens, including a world-wide analysis of checklist data based on Takhtajan's floristic regions. *Biodiversity and Conservation* No 16, pp. 85-98. [A world-wide comprehensive study of lichen biogeography].

Foissner, W. (2006). Biogeography and dispersal of micro-organisms: a review emphasizing protists. *Acta protozoologica* No 45, pp. 111-136. [This review summarizes data on the biogeography and dispersal of bacteria, microfungi and selected protists, such as dinoflagellates, chrysophytes, testate amoebae, and ciliates. Furthermore, it introduces the restricted distribution and dispersal of mosses, ferns and macrofungi as arguments into the discussion on the postulated cosmopolitism and ubiquity of protists].

Fonseca, A.; Inacio, J. (2006). Phylloplane yeasts. In: The Yeast Handbook: Biodiversity and ecophysiology of yeasts. Edited by C. A. Rosa and G. Peter, Springer, pp. 263-302. [Ín this chapter, the authors discuss the extraordinary plasticity and diversity of phylloplane microbial populations, with emphasis on yeasts].

Goodal, R. (1947). *The Geography of Flowering Plants*. Longmans, Green and Co, New York. [A traditional biogeography textbook which places primary emphasis on plant distributions].

Gradstein, S. R.; Churchill, S.P.; Salazar-Allen, N. (2001). Guide to the bryophytes of Tropical America. *Memories of New York Botanical Garden* No 86, pp. 1-577. [The authors provide descriptions, illustrations, and keys to the 597 genera and 120 families of bryophytes recorded from tropical America. The generic descriptions include data on the diversity, distribution, and ecology of the group within the Neotropics, important morphological characters, salient features for identification, and relevant literature for species identification].

Hawksworth, D.L. (2001). The magnitude of fungal diversity: the 1.5 million species estimate revisited. *Mycological Research* No 105, pp. 1422-1432. [This paper evaluates the extent of fungal diversity in the world].

Hawksworth, D.L. (2004). Fungal diversity and its implications for genetic resource collections. *Studies in Mycology* No 50, pp. 9-18. [This article presents the importance of culture collections of fungi for supporting genomics and molecular biology studies, and for the documentation and conservation of the Earth's fungal genetic resources].

Horner-Devine M.C.; Carney, K.M. ; Bohannan BJM. (2004). An ecological perspective on bacterial biodiversity. *Proceedings of Royal Society of London Series* B No 271, pp.113–122. [This work shows that bacterial diversity may exhibit regular patterns, and in some cases these patterns may be qualitatively similar to those observed for plants and animals].

Keeling, P.J.; Fast, N.M. (2002). Microsporidia: biology and evolution of highly reduced intracellular parasites. *Annual Review of Microbiology* No 53, pp. 96–115. [This article is a review of the biology of Microsporidia, a highly specialized fungal group].

Kemp, P.F.; Aller, J.Y (2004). Bacterial diversity in aquatic systems: what can we learn from 16S rDNA libraries? *FEMS Microbiology Ecology* No 47, pp.161-177. [This work suggests that, using 16S rDNA libraries described in published reports, aquatic bacterial diversity is much less than any predictions of their global diversity on local scales].

Kirk, P.M.; Cannon, P.F.; David, J.C.; Stalpers, J.A. (2001). *Ainsworth & Bisby's Dictionary of the Fungi*. 19 ed. CAB International, Wallingford, 655 p. [A traditional and very comprehensive dictionary of mycology which also includes a kingdom-wide classification down to the level of genus].

Lachance, M.A. (2006). Yeast biodiversity: How many and how much? In: The Yeast Handbook: Biodiversity and ecophysiology of yeasts. Edited by C. A. Rosa and G. Peter, Springer, pp. 1-10. [In this chapter, the author focuses on the yeast biodiversity, and discusses the measurement and significance of biodiversity, and predictions on the number of yeast species in nature]

Lamoreux, J.F.; Morrison, J.C.; Ricketts, T.H.; Olson, D.M.; Dinerstein, E.; McKnight, M. W.; Shugart H. H. (2006). Global tests of biodiversity concordance and the importance of endemism. *Nature* No 440, pp. 212-214. [This work provides evidence that endemism is also a useful surrogate for the conservation of all terrestrial vertebrates].

Lodge, D.J.; Cantrell, S. (1995). Fungal communities in wet tropical forests: variation in time and space. Canadian Journal of Botany No 73, pp. 733-738. [This article focuses on the variation in tropical forest fungal populations and communities as an important approach to assess fungal biodiversity and to understand the regulatory roles that fungi play in tropical forests].

Pace, N. R.; Stahl, D. A.; Lane, D. J.; Olsen, G. J. (1985). Analyzing natural microbial populations by rRNA sequences. *ASM News* No 51, pp. 4–12. [In this article, the authors describe technical strategies that are used to analyze the phylogenetic and quantitative aspects of mixed, naturally occurring microbial populations].

Piepenbring, M. (2007). Inventoring the fungi of Panama. *Biodiversity and Conservation* No 16, pp. 73-84. [This is a historical review about the studies of fungal diversity in Panama].

Roos, M. (1996). Mapping the world's pteridophyte diversity – systematics and floras. In: J.M. Camus, M. Gibby and R.J. Johns (editors). Pteridology in Perspective, pp. 29-42, Royal Botanic Gardens, Kew. [This is a critical analysis of the state of knowledge of pteridophyte diversity].

Ryvarden, L. (1993). Tropical polypores. In: Isaac, S.; Frankland, J.C.; Watling, R. and Whalley, A.J.S.

Aspects of Tropical Mycology. New York: Cambridge University Press. Pp. 149-170. [This is a comprehensive study of the diversity and biogeography of tropical polypores].

Shearer, C.A.; Descals, E.; Kohlmeyer, B.; Kohlmeyer, J.; Marvanová, L.; Padgett, D.; Porter, D.; Raja, H.A.; Schmit, J.P.; Thorton, H.A. and Voglymayr, H. (2007). Fungal biodiversity in aquatic habitats. *Biodiversity and Conservation* No 16, pp. 49-67. [This is a critical analysis of the current state of knowledge of fungal diversity and biogeography in freshwater, brackish, and marine habitats].

Schlegel, M.; Meisterfeld, R. (2003). The species problem in Protozoa revisited. *European Journal of Protistology* No 39, pp. 349-355. [The authors examine different morphological and molecular characters discovered and applied in taxonomy of Protozoa].

Schüssler, A.; Schwarzott, D.; Walker, C. (2001). A new fungal phylum, the Glomeromycota: phylogeny and evolution. *Mycological Research* No 105, pp. 1413–1421. [This is the original article that proposes the recognition of the monophyletic group, Glomeromycota, as a new fungal phylum].

See, N. (2004) More than meets the eye. *Nature* No 429, pp. 804-805. [This is a critical analysis showing that Earth's real biodiversity is invisible, whether we like it or not].

Smith, A.R.; Pryer, K.M.; Schuettpelz, E.; Korall, P.; Schneider, H.; Wolf, P. (2006). A classification for extant ferns. *Taxon* No 55, pp. 705-731. [This paper presents a revised classification for extant ferns, with emphasis on ordinal and familial ranks, and a synopsis of included genera].

Stuart, S.A.; Choat, B.; Martin, K.C.; Holbrook, N.M.; Ball, M.C. (2007). The role of freezing in setting the latitudinal limits of mangrove forests. New Phytologist No 173, pp. 576-583. [In this paper there is a precise circumscription of the range of mangroves, which is one of the concepts used to define the range of tropical fungi].

Woese, C. R.; Fox, G. E. (19770. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. *Proceedings of the National Academy of Sciences of USA* No 74, pp. 5088–5090. [A phylogenetic analysis based upon ribosomal RNA sequence characterization reveals that living systems represent one of three aboriginal lines of descent: the eubacteria, the archaebacteria, and the eukaryotes].

Biographical Sketches

Ana Paula Trovatti Uetanabaro received the Biology degree from Federal University of Minas Gerais in 1996, the Master degree in Agricultural Microbiology from Federal University of Viçosa in 1999, and Ph.D. in Food Science from State University of Campinas (UNICAMP) in 2004. Currently, she is assistant professor of the Department of Health, State University of Feira de Santana (UEFS), Brazil. She is the curator of the Culture Collection of Microorganisms from Bahia and coordinator of Laboratory of Microbiological Quality Control of Medicines at the same University. Her research lines include bacterial diversity and biotechnology of microorganisms.

Aristóteles Góes-Neto received the Biology degree from Federal University of Bahia in 1994 and Ph.D. in Botany from Federal University of Rio Grande do Sul in 2001. Currently, he is titular professor of the Department of Biology, State University of Feira de Santana (UEFS), Brazil. He is the coordinator of Research Laboratory in Microbiology (LAPEM), and coordinator of the Graduate Program in Biotechnology (M.Sc. and Ph.D. levels) at the same University. He is also member of the Scientific and Technical Chamber of Biological Sciences and Environment of the Science Foundation of the State of Bahia, Brazil (FAPESB). His research lines include diversity and evolution, genomics/proteomics and biotechnology of fungi with emphasis on Basidiomycota.

Luiz Henrique Rosa received the Biology degree from Catholic University of Minas Gerais in 1998, the Master degree in Microbiology from Federal University of Minas Gerais in 2002, and Ph.D. in Microbiology from Federal University of Minas Gerais in 2004. Currently, he is professor of the Department of Biological Sciences at the Federal University of Ouro Preto. His research lines include studies on tropical Agaricales (Basidiomycota) and endophytic fungi with focus on taxonomy, phylogeny, biogeography, and biotechnological applications.

Alexandre Salino received the Biology degree from State University of São Paulo in 1989, the Master degree in Botany from State University of Campinas (UNICAMP) in 1993, and Ph.D. in Botany from

State University of Campinas (UNICAMP) in 2000. Currently, he is professor of Botany of the Department of Biological Sciences at the Federal University of Minas Gerais. He is also the curator of BHCB Herbarium at the Federal University of Minas Gerais. His research lines focus on systematic and biogeography of pteridophytes.

Alfredo Hannemann Wieloch received the Biology degree from Catholic University of Minas Gerais in 1983, the Master degree in Zoology from Federal University of Paraiba in 1990, and Ph.D. in Zoology from Federal University of Rio de Janeiro in 2006. He is professor of zoology of the Department of Zoology at the Federal University of Minas Gerais. His research lines focus on protista and invertebrate biology, mainly taxonomy and ecology of ciliates and *Onychophora*.

Carlos Augusto Rosa received the Biology degree from Federal University of Minas Gerais in 1984, the Master degree in Microbiology from Federal University of Minas Gerais in 1989, and Ph.D. in Microbiology from Federal University of Rio de Janeiro in 1993. Since 1994 he has been professor of Microbiology at the Institute of Biological Sciences of the Federal University of Minas Gerais. He was a Postdoctoral researcher at the Department of Biology of the University of Western Ontario, Canada, in 1997. His main fields of research are systematic and biodiversity of yeasts from tropical ecosystems. He has described several novel yeast species from tropical substrates.