

## Study guide 1: Prokaryotic diversity and natural populations

1. Where are most of the earth's prokaryotes found?
2. How does the abundance of prokaryotes compare to that of plants and/or animals?
  1. Describe the principles of mass spectroscopy.
2. What is isotope fractionation. Given the ratio of  $^{13}\text{C}/^{12}\text{C}$  in a sample and the PDB standard, calculate the  $\delta^{13}\text{C}$ . If the  $\delta^{13}\text{C}$  is very low, the material is enriched in  $^{13}\text{C}$  or  $^{12}\text{C}$ ?
5. Describe a consensus model for the early evolution of prokaryotic life. If this model is correct, what are the implications for the evolution of eukaryotes?
5. Describe the different types of diversity?
6. What practical problems can be solved by studying prokaryotic diversity?
7. Describe how numerical taxonomy is performed. Describe how DNA hybridization is performed.
8. Describe the advantages and limitations of numerical taxonomy.
9. Compare different types of diversity between prokaryotic and eukaryotic taxa.
10. Given a phylogenetic tree, determine the % similarity (or % difference) between any two taxa.
11. What taxonomic ranks are widely used in bacteriology?
12. Describe how multilocus enzyme electrophoresis is performed. In your description, be sure to include how one might lyse the cells and the role of PMS and MTT.
13. Given a list of electrophoretic types for a number of strains (like Table 9 in your handout), be able to construct a dendrogram (like Figure 2 on the same page of your handout).
14. What is the clonal model for the population structure of prokaryotic species? Is this model applicable to all prokaryotic species?
15. What is the Index of Association and why is it used?
16. Be able to discuss the question of whether or not prokaryotic species exist in nature.
17. Be able to describe how PCR amplification of genes from the environment is used to learn the nature of prokaryotic communities.
18. Describe some potential errors or artifacts that can occur when studying the distribution of 16S rRNA or other genes in environmental DNA. Include in your answer descriptions of chimeras, affect of gene composition (such as high mol % G+C), heteroduplexes in PCR of closely related templates, and heterogeneity within a single organism.
19. Describe how FISH might be used to identify organisms in natural samples.
20. For soil, compare the differences in the number of prokaryotes observed by microscopic and culture techniques. Why are these values different? What about the gastrointestinal tract of humans? Why are the cell number observed and the CFUs different?
21. Compare the microbial diversity in soil, the gastrointestinal tract, and subgingival plaque.

Define, distinguish, and/or describe the following terms:

|                         |                                      |
|-------------------------|--------------------------------------|
| isotope fractionation   | taxon                                |
| stromatolites           | phylogeny                            |
| microfossils            | numerical taxonomy                   |
| RNA world               | unit character                       |
| banded iron formations  | hypothetical median organism         |
| endosymbiosis           | species (prokaryotes and eukaryotes) |
| systematics             | phase variation                      |
| taxonomy                | genospecies                          |
| classification          | DNA hybridization                    |
| natural classification  | $T_m$                                |
| identification          | $\Delta T_m$                         |
| GC ratio (or mol % G+C) | MLST                                 |

FAME analysis  
Indel  
polyphasic taxonomy  
specific epithet  
type strain  
neotype strain  
Approved List  
Validation List  
Bacteriological Code  
Bergey's Manual  
ICSP  
IUMS  
IJSEM  
homology  
orthology  
paralogy  
multilocus enzyme electrophoresis  
allozyme  
activity stain  
population  
clone

recombination  
Index of Association  
gene tree  
organismal tree  
PCR  
Cot curve  
molecular chronometer  
chimera  
DAPI  
FISH  
MAR  
DGGE  
TGGE  
enrichment culture  
DAPI  
Microelectrode  
Viability staining  
Winogradsky column  
MPN  
Metagenome

Some general questions:

1. Why is the abundance of prokaryotes (or any other group of living organisms) important?
2. Eukaryotes appeared to have arisen 1.5-2.0 Gy ago, at a time when prokaryotes were already a major component of the biosphere. What are the implications of this observation on the nature of the eukaryotes?
3. Given some objects, be able to determine their similarity using a numerical scheme.
4. If prokaryotes are clonal with little exchange of genetic information within the population, why do we observe large groups of phenotypically similar and genetically related strains?
5. Compare what can be learned by conventional and molecular techniques for studying natural communities of prokaryotes.
6. In soil and many other environments, only a small fraction (typically 1-5 %) of the cells observed microscopically can be cultivated in laboratory medium. Why?
7. How might one characterize the organisms in some of these unclassified groups that have only been detected by rRNA gene sequencing?

## **Additional Resources:**

Readings from Madigan and Martinko, 2006, *Biology of Microorganisms*  
Chapters 1, 2, 11, and 18.

Readings from Staley et al. 2007, *Microbial Life*  
Chapters 1, 17, and 24.1-24.4.

*The Prokaryotes*, vol. 1; chapter 2 (Stackebrandt)

Bergeys, vol. 1; chapters entitled:

- Classification of Prokaryotic Organisms..

- Numerical Taxonomy

- Polyphasic Taxonomy

- Overview: a phylogenetic backbone...

- Nucleic acid probes ...

- Bacterial nomenclature

- Microbial ecology...