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Using Metagenomics to Teach Biodiversity

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To data, there is still insufficient data on the diversity of bacteria that live in freshwater environments. In addition, the interaction between bacteria and the freshwater environment requires further evaluation. A gap in our knowledge of microbial diversity exists and the discovery and study of these organisms is greatly needed. Microorganisms play a key role on land and in water.

Insights gained from these organisms will:

1. Increase our knowledge about the strategies and limits of life,
2. Help with understanding the importance of sustainability of life on our planet,
3. Provide valuable new organisms and their genes for biotechnology through uncovering new species,
4. Microbial diversity can be used to monitor and predict environmental changes,
5. Microorganisms play a key role in the microbial food web for higher organisms, and
6. Microbes serve as excellent models for understanding biological interaction and evolutionary changes [1,2].

A recent article in the Microbe, entitle "Omic Approaches in Microbial Ecology: Charting the Unknown" makes the argument that metagenomics is a powerful tool for microbial ecologist. Data from complex environmental samples have revealed unique organisms and uncultured microbes that widen our knowledge of microbial diversity [3]. Traditional isolation of microbes using culture media has provided a great deal of information yet many organisms remain uncultured which is a major limitation of this technique. With the data derived from metagenomics, microbiologists are able to reconstruct genomes, transcriptomes, and proteomes of whole microbial communities [3]. Because microbes play such a key role in ecology and serve as models for evolutionary changes, it is critical that educators introduce this powerful tool to our next generation of scientist.

It is often difficult for students, who attend predominately undergraduate institutions, to comprehend the enormity of microbial diversity. This requires research, technology, and available faculty which are often not present at predominately undergraduate institutions, which historically have a primary focus on teaching. Therefore, a significant gap in our understanding of microbial diversity continues to exist. Using metagenomics is one way of teaching students the importance of environmental sampling along with the concepts and tools needed to analyze metagenomic data. Metagenomics is the sequencing of full or partial DNA extracts of all members of a microbial community from environmental samples [4]. By using metagenomics, data can be gathered to develop a profile of microbial diversity and taxonomy [5].

Allowing undergraduate students to sample aquatic or soil environments, gives them the hands on field experience that can be an invaluable tool later in their career. Those same students also get the benefit of laboratory experience by isolating DNA from the samples brought back into the laboratory. Although, samples are sent off for sequencing the data gathered is very useful in teaching microbial diversity, taxonomy, and evolutionary change.

References

1. American Society for Microbiology (2003) Microbial Diversity Research Priorities- A Working Document for Multi-Agency Consideration. American Society for Microbiology, USA.
2. Falkowski PG, Fenchel T, Delong EF (2008) The Microbial Engines That Drive Earth's Biogeochemical Cycles. Science 320: 1034-1039.
3. Baker BJ, Dick GJ (2013) Omic Approaches in Microbial Ecology: Charting the Unknown. Microbe 3: 353-360.
4. Nijkamp JF, Pop M, Reinders MJT, de Ridder D (2013) Exploring variation aware contig graphs for (comparative) metagenomics using Marygold. Bioinformatics.
5. Silva CC, Hayden H, Sawbridge T, Mele P, Kruger RH, et al (2012) Phylogenetic and functional diversity of metagenomic libraries of phenol degrading sludge from petroleum refinery wastewater treatment system. AMB Express 2: 18.

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