**Introduction**

Microbial ecology is reshaping our understanding of the natural world by revealing the large phylogenetic and functional diversity of microorganisms. However, the vast majority of these microorganisms remain poorly understood, as most cultivated representatives belong to just four phylogenetic groups and more than half of all identified phyla remain uncultivated. Characterization of this microbial dark matter will thus greatly benefit from new metagenomic methods for its isolation and identification. Read this text with other colored data sets to make a more complete list of known representatives. A comprehensive microbial community from a lake known to predominantly contain phylogenetically pure strains of culturable bacteria is thus greatly beneficial to using metagenomic methods for characterizing community diversity.

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**Improved Accuracy from Full-Length 16S**

- Figure 1 (Right): Histogram of post-filter reads-of-insert consensus
- Figure 2 (Top-Left): Forward and reverse reads-of-insert consensus
- Figure 2 (Top-Left): Orange: Forward 1
- Figure 2 (Top-Left): Blue: Reverse 1
- Figure 2 (Top-Left): Green: Forward 3
- Figure 2 (Top-Left): Yellow: Reverse 5
- Figure 2 (Top-Left): Pink: Forward 7
- Figure 2 (Top-Left): Brown: Reverse 7

**Reads-of-Insert Consensus**

- Community analysis of environmental 
- Environmental Sample
- Table 1 (Below): Grouping
- Table 1 (Below): Taxa
- Table 1 (Below): E. coli
- Table 1 (Below): M. Bacteroides

**Environmental Sample**

- Table 1 (Below): Grouping
- Table 1 (Below): Taxa
- Table 1 (Below): E. coli
- Table 1 (Below): M. Bacteroides

**Mock Community Classification**

- Table 2 (Left): Analysis of the OTU consensus sequences generated by iTagger (Di). Classification of the OTU consensus sequences generated by rDnaTools (Di)
- Table 2 (Left): Analysis of the OTU consensus sequences generated by iTagger (Di). Classification of the OTU consensus sequences generated by rDnaTools (Di)

**Conclusion**

- • The PacBio RSII enables high-throughput sequencing of full-length 16S amplicons
- • Full-length 16S amplicons show both greater sensitivity and specificity to the clustering of OTUs than 16S tag sequencing
- • Comparisons of short-read and full-length 16S sequences from environmental samples show high concordance with SMRTLink Sequencing being a robust, cost-effective method for multiplexed strain identification

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**References**


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**Acknowledgments**

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