

**Functional diversity within
monophyletic groups in the
uncultured archaea: Bathyarchaeota
and Altiarchaeales**

KAREN G. LLOYD¹, JORDAN T. BIRD¹, LAURA ZINKE²,
BRANDI REESE²

¹University of Tennessee, Knoxville, TN 37996 USA

(*correspondence: klloyd@utk.edu)

²Texas A&M Corpus Christi, Corpus Christi, TX 78412 USA

Most archaea in marine sediments are uncultured. Phylogenetic data for these groups are much richer than their functional information, the latter of which can be difficult to infer from genomic and transcriptomic data. We used genomic comparisons within the uncultivated group Altiarchaeales to show that, even though monophyly is clearly established by whole genome comparisons, there is significant functional diversity within the group. We also show that the uncultured phylum, Bathyarchaeota, has varied attributes depending on where it is found, and to which subgroup it belongs. These data support the hypothesis that functional variation within monophyletic uncultured groups of archaea rivals what is known from better-cultured clades of bacteria and archaea. Therefore, functions predicted from single genomes or metagenomic bins from uncultured archaea should not be extrapolated to the larger taxonomic group identified through 16S rRNA gene surveys. Rather, new genomic and transcriptomic interrogations are useful to perform in every study to investigate the particular properties of each clade in unique environments.