

Quantification of deep sedimentary microorganisms and single-cell genomic analysis from IODP Leg 347 Baltic Sea Paleoenvironment

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The marine subsurface contains abundant, diverse, and uncultured microorganisms. Two outstanding questions are: 1) Can specific groups of these microorganisms be accurately quantified in situ? And 2) What are their ecophysiologicals? We conducted an interlaboratory comparison of tax-specific quantification methods (qPCR and CARD-FISH) on Baltic Sea Basin (IODP Exp. 347) sediment down to 85 m. Working with similar protocols, qPCR and CARD-FISH were reproducible across the laboratories, although 91% of CARD-FISH measurements were below the quantification limit. To examine potential microbial physiologies, we sequenced and assembled 27 single cell genomes from an organic poor site (Anholt Basin) and 16 from an organic rich site (Lille Belt); all from uncultivated clades within the Deltaproteobacteria, OPB41, Atribacterales (JS1), Aminicenantes (OP8), Chloroflexi, Bathyarchaeota (MCG), and MG-2. Although phylum-level identities were the same for both sites, local endemism was apparent because each SAG only recruited metagenomic reads from its own location. Predicted functions for SAGs were diverse within each phylum suggesting significant sub-phylum diversity of ecophysiological strategies.