

Fungal Survival in a Chemosynthetic Ecosystem. B. Kiel Reese¹, M. S. Sobol¹, T. Hoshino², F. Inagaki², E. Eder⁴, C. D. Nicora³, H. M. Heyman³, J. E. Kyle³, D. W. Hoyt⁴, M. M. Tfaily⁴, T. O. Metz³

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The characterization of metabolically active fungal isolates within the deep marine subsurface will alter current ecosystem models and living biomass estimates that are limited to bacterial and archaeal populations. Although marine fungi have been studied for over fifty years, a detailed description of fungal populations within the deep subsurface is lacking. Fungi possess metabolic pathways capable of utilizing previously considered non-bioavailable energy reserves. Therefore, metabolically active fungi would occupy a unique niche within subsurface ecosystems, with the potential to provide an organic carbon source for heterotrophic prokaryotic populations not currently being considered in subsurface energy budgets. Sediments from the South Pacific Gyre (SPG) subsurface, one of the most energy-limited environments on Earth, were collected during the Integrated Ocean Drilling Program (IODP) Expedition 329. Anaerobic and aerobic sediment slurry enrichments using fresh sediment began directly following the completion of the expedition in December 2010. From these enrichments, multiple fungal strains were isolated and cultured in several media types that varied in carbon concentrations. Metabolically active and dormant fungal populations were also determined from nucleic acids extracted from *in situ* cryopreserved SPG sediments. For further characterization of physical growth parameters, two isolates were chosen based on their representation of the whole SPG fungal community. Analyses such as whole genome sequencing, lipid characterization, global metabolomics, and growth experiments on the International Space Station have been performed in order to understand their adaptability to survive in extreme energy limited environments. Results from this study show that fungi have adapted to be metabolically active and key community members in SPG sediments and within global biogeochemical cycles.