

A complex ecological role for submarine groundwater discharge in the formation of toxic *Pseudo-nitzschia* spp. blooms

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Abstract

The potentially-toxic diatom *Pseudo-nitzschia* is common in the northern Gulf of Mexico (NGOM), including the coastal waters of Alabama. The NGOM shoreline near Little Lagoon, AL, is a hot spot for blooms of *Pseudo-nitzschia* spp. and their population density is correlated with proximity for groundwater discharge [1]. Little Lagoon, AL (USA) is a shallow coastal lagoon that lacks riverine inputs but has persistent salinity gradients between the ends and the narrow pass connecting it to the Gulf of Mexico. Covariances between salinity and the groundwater tracer ²²²Rn in Little Lagoon indicate that submarine groundwater discharge (SGD) is responsible for the salinity gradients and is likely the primary source of freshwater to the lagoon. Cluster analysis based on temperature, salinity and two proxies of SGD revealed two regimes with different drivers for nutrient concentrations and chlorophyll: samples characterized by high discharge, total nitrogen (TN) was negatively correlated with salinity and total phosphorus (TP) was correlated with temperature. In samples characterized by low discharge and higher temperatures, both TN and TP were highly correlated with temperature and inferred to originate from benthic efflux.

Monitoring within Little Lagoon from 2007 to 2010 showed that the phytoplankton community structure during periods of high aquifer discharge was distinct from other periods and tended to be dominated by diatoms and chlorophytes. *Pseudo-nitzschia* spp. abundances were also greatest during these periods and were correlated with increases in groundwater elevation. *Pseudo-nitzschia* spp. abundance had a negative relationship with measures of nutrient availability and nutrients were relatively low during periods of high *Pseudo-nitzschia* spp. and high aquifer discharge. Other blooms of *Pseudo-nitzschia* spp. in coastal Alabama were also associated with periods of high aquifer discharge and low nutrient availability. Dilution grazing experiments also indicated that the effects of SGD are likely to favor *Pseudo-nitzschia* spp. due to their high growth rates and susceptibility to grazing. We hypothesize that the link between SGD and *Pseudo-nitzschia* spp. blooms is not due simply to nutrient inputs, but rather that SGD is part of a disturbance regime that favors fast-growing, heavily grazed diatoms like *Pseudo-nitzschia* spp.

[1] Liefer et al. (2009) *Harmful Algae* 8: 706-714.

Relating microbial community structure and geochemistry in the Bisley watershed, Puerto Rico

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Abstract

Using next generation sequencing and metagenomics analysis tools, bacterial community composition and structure were assessed in the context of chemical and mineralogical characteristics of a 9.2 m depth regolith profile developed on volcaniclastic material of the Fajardo formation in the Bisley watershed in Puerto Rico. We have hypothesized that Fe oxidation is important in weathering of intact bedrock to disaggregate regolith, and that chemolithoautotrophic microorganisms play a role in Fe cycling at depth.

The regolith forms along a gradient between conditions of low oxygen and higher pH at depth, to higher oxygen and lower pH at the surface. Secondary clay minerals and Fe oxides are present from the surface down to 8.3 m, while the weathered primary minerals chlorite and feldspar were detected from 8.3 m to the bedrock at 9.2 m. Both total cell counts and heterotrophic cell counts generally decreased from the surface to ~9 m, with variations in bacterial numbers correlating with variations in clay content. Cell numbers in iron-oxidizing media decreased with depth, but increased near the weathering front at 8.3 m depth. Increased concentrations of organic-bound iron at 8.3 m were observed as well.

Rarefaction curves generated at a 97% similarity value indicated that the regolith was representatively sampled for determining community richness. At all depths analyzed, 4 phyla were dominant – Proteobacteria, Acidobacteria, Planctomycetes, and Actinobacteria. Sub-phylum groups containing known iron-oxidizing microorganisms (e.g. subclass Acidimicrobiales) were found in the deepest samples, near the regolith-bedrock interface, consistent with the hypothesis that chemolithoautotrophic bacteria play an important role in weathering and element cycling in the deep regolith. Iron-reducing groups (e.g. *Geobacter* and *Anaeromyxobacter*) were detected as well. The data obtained from this study are consistent with the hypothesis of an iron-cycling community that in turn supports heterotrophs at depth. It is furthermore possible that this Fe-related ecosystem at depth contributes to disaggregation of bedrock to form noncohesive regolith.