Methionine synthase interreplacement in diatom cultures and communities: Implications for the persistence of B_{12} use by eukaryotic phytoplankton

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ABSTRACT: Three proteins related to vitamin B_{12} metabolism in diatoms were quantified via selected reaction monitoring mass spectrometry: B_{12}-dependent and B_{12}-independent methionine synthase (MetH, MetE) and a B_{12} acquisition protein (CBA1). B_{12}-mediated interreplacement of MetE and MetH metalloenzymes was observed in *Phaeodactylum tricornutum* where MetH abundance was highest (0.06 fmol μg^{-1} protein) under high B_{12} and MetE abundance increased to 3.25 fmol μg^{-1} protein under low B_{12} availability. Maximal MetE abundance was 60-fold greater than MetH, consistent with the expected ~ 50 – 100-fold larger turnover number for MetH. MetE expression resulted in 30-fold increase in nitrogen and 40-fold increase in zinc allocated to methionine synthase activity under low B_{12}. CBA1 abundance was 6-fold higher under low-B_{12} conditions and increased upon B_{12} resupply to starved cultures. While biochemical pathways that supplant B_{12} requirements exist and are utilized by organisms such as land plants, B_{12} use persists in eukaryotic phytoplankton. This study suggests that retention of B_{12} utilization by phytoplankton results in resource conservation under conditions of high B_{12} availability. MetE and MetH abundances were also measured in diatom communities from McMurdo Sound, verifying that both these proteins are expressed in natural communities. These protein measurements are consistent with previous studies suggesting that B_{12} availability influences Antarctic primary productivity. This study illuminates controls on expression of B_{12}-related proteins, quantitatively assesses the metabolic consequences of B_{12} deprivation, and demonstrates that mass spectrometry – based protein measurements yield insight into the functioning of marine microbial communities.

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