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The path to preservation: Using proteomics to decipher the fate of diatom proteins during microbial degradation

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ABSTRACT: We drew upon recent advances in tandem mass spectrometry-based proteomic analyses in order to examine the proteins that remain after a diatom bloom enters the stationary phase, precipitates out of the photic zone, and is subjected to microbial degradation over a 23-period within a controlled laboratory environment. Proteins were identified from tandem mass spectra searched against three different protein databases in order to track proteins from *Thalassiosira pseudonana* and any potential bacterial contributions. A rapid loss of diatom protein was observed over the incubation period; 75% of the proteins initially identified were not detected after 72 h of exposure to a microbial population. By the 23rd day, peptides identified with high confidence correlated with only four *T. pseudonana* proteins. Five factors may have influenced the preservation of diatom proteins: (1) protection within organelles or structures with multiple membranes, (2) the relative cellular abundance in the photosynthetic apparatus, (3) the number of transmembrane domains in the protein sequence, (4) the presence of glycan modification motifs, and (5) the capability of proteins or peptides to aggregate into supramolecules.

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