Geophysical Research Abstracts
Vol. 18, EGU2016-8835-1, 2016
EGU General Assembly 2016

# Biomineralization of Schlumbergerella floresiana, a significant carbonate-producing benthic foraminifer

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Most foraminifera that produce a shell are efficient biomineralizers. They contribute to the global carbon cycle, and thus influence ocean-climate regulation. Calcification in foraminifera is likely biologically controlled and is potentially similar to shell formation in metazoan taxa (e.g. mollusks, corals, sea urchins). However, foraminiferal biomineralization processes and the molecules involved are still poorly understood.

We analyzed the calcitic shell of the large tropical benthic foraminifer Schlumbergerella floresiana. We found a suite of macromolecules containing many charged and polar amino acids and glycine that are also abundant in biomineralization proteins of other phyla. As neither genomic nor transcriptomic data are available for foraminiferal biomineralization yet, de novo-generated sequences, obtained from organic matrices submitted to MS BLAST database search, led to the characterization of 156 peptides. Very few homologous proteins were matched in the proteomic database, implying that the peptides are derived from unknown proteins present in the foraminiferal organic matrices. The amino acid distribution of these peptides was queried against the UNIPROT database and the mollusk UNIPROT database for comparison. The mollusks compose a well-studied phylum that yield a large variety of biomineralization proteins. These results showed that proteins extracted from S. floresiana shells contained sequences enriched with glycine, alanine, and proline, making a set of residues that provided a signature unique to foraminifera. Three of the de novo peptides exhibited sequence similarities to peptides found in proteins such as pre-collagen-P and a group of P-type ATPases including a calcium-transporting ATPase. Surprisingly, the peptide that was most similar to the collagen-like protein was a glycine-rich peptide reported from the test and spine proteome of sea urchin. The molecules, identified by matrix-assisted laser desorption ionization-time of flight mass spectrometry analyses, included acid-soluble N-glycoproteins with its sugar moieties represented by high-mannose-type glycans and carbohydrates.

Describing the nature of the proteins, and associated molecules in the skeletal structure of living foraminifera, can elucidate the biomineralization mechanisms of these major carbonate producers in marine ecosystems. Foraminifera constitute an important tool used for paleo-environmental reconstructions because of their nearly continuous fossil record and abundance. Many studies focus on their biomineralization process using a geochemical perspective to record environmental and climate changes from shell isotopic and trace element compositions. Our results are a first step toward understanding the functioning mechanism behind biomineralization and the molecules involved. Coupling geochemical and biological perspectives will enhance interpretation of the proxies used for climatic reconstructions and improve future modeling efforts.