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Finding patterns and differences on biomineralization-related proteins from Metazoans

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The protein sequences associated to calcium carbonate biomineralization in metazoans show particular characteristics since they seem to be organized in different modules and show tendency to adopt unfolded conformations. Some of these modules are of low complexity or seem to be specific for each organism suggesting that evolution is occurring independently multiple times. However, calcium carbonate proteins also show some remarkable sequence similarities and conserved domains in distantly related organisms, which suggest a Precambrian origin of the genes. For the first step of our work we compiled in a semi-automated manner a calcification-related proteins reference set. This collection could bring together all the domains, motifs and functions described until now in the biocalcification process. This data-set is currently in use to:

1) Develop an automated selection and analysis of the protein sequences associated to calcium carbonate mineralization in metazoans. Recently we were able to group these proteins by homologous regions and we are currently analyzing these results. The main goal is to characterize new motifs and domains, establish new functional relations and integrate these data into a specialized database.

2) Identify common biochemical and biophysical properties like high acidity, repeats sequences, little or no secondary structure, propensity for trans-membrane helices, and high percentages of highly acidic amino acids (Asp, Glu, and Ser) in protein composition, etc. In order to construct property profiles for known biomineralization proteins.

In a second part we expect to apply these profiles to predict biomineralization proteins from unknown gene sequences. For that purpose we expect to do a transcriptomic analysis of a coral species, *Acropora millepora*, recently subject to severe bleaching events. The transcriptomes obtained will be used together with the profiles in order to predict biomineralization genes.