LIFE IN A GLASSHOUSE: FROM CELL WALL MORPHOGENESIS TO NANOTECHNOLOGICAL APPLICATIONS

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The diatom cell wall structure is a species-specific characteristic demonstrating that its morphogenesis is genetically encoded. Understanding the molecular mechanisms by which a single cell executes the morphogenetic program for the formation of an inorganic material (biomineralization) is not only a fascinating biological problem, but also of great interest for nanomaterials science and technology. Recently, diatom genome sequencing projects have provided the opportunity to identify the entire set of proteins involved in silica formation. Although subsequent transcriptomics and proteomics analyses provided hundreds of potential candidate proteins they have failed to identify already known silica forming proteins. This has raised concerns regarding the specificity and suitability of such high-throughput methods for studying diatom silica formation. In this presentation I will describe the results that we have obtained using an entirely different approach. The genome database of the model diatom *Thalassiosira pseudonana* was screened *in silico* for proteins containing domains that mimic the amino acid compositions (rather than sequence) of silica forming proteins. The screen retrieved the known silica forming proteins in addition to 86 other proteins, of which most did not exhibit sequence homology to any proteins from other organisms. Among these diatom-specific proteins are six proteins, which we denoted cingulins, that exhibit unique and highly repetitive amino acid sequence motifs. Subsequent in vivo functional analysis of cingulins resulted in the identification of a previously unknown yet apparently general principle for diatom silica morphogenesis. In the final part of my talk I will demonstrate how the emerging insight into the molecular mechanism of diatom silica formation has enabled the development of an entirely biological method for the production of nanopatterned silica with desired catalytic activities.