Computational and Experimental Approaches to Controlling Bacterial Microcompartment Assembly

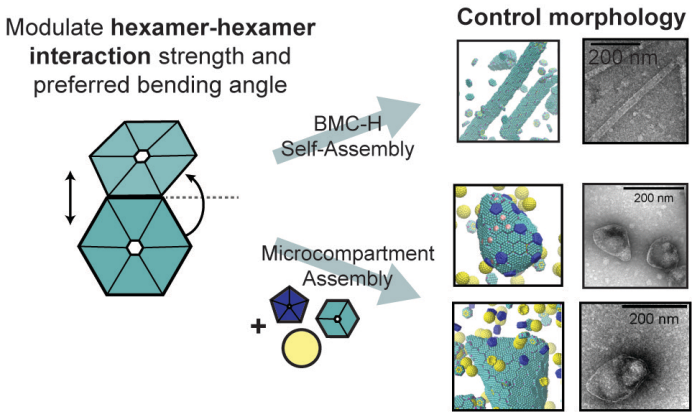

Figure 1: Illustration of various assembly morphologies obtained by modulating hexamer interactions and component content. Extended cylinders are obtained when only hexamers are present, which is consistent with the shapes observed in experiments. When other protein components and cargos are added, closed or samosa shaped shells are formed by varying the stoichiometric ratio.

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Work was performed at Northwestern University.

Scientific Achievement

Combining computational, theoretical and experimental approaches, this study shows how modulating hexamer-hexamer interactions and component stoichiometric ratio can result in different microcompartment morphologies.

Significance and Impact

This work develops a multi-scale computational approach to study how amino acid mutations alter hexamer-hexamer interactions and control the assembly morphology. The findings will help guide future studies to assemble specific BMC structures with desired functionality.

Research Details

- We first use all-atom molecular dynamics (AAMD) simulation to determine the interaction strength and bending angles between hexamers. Then from AAMD simulation, we construct a coarse-grained model to study the assembly morphology.
- We compare the assembly morphology with experimental data and determine how mutations of amino acids can alter the assembly shapes.
- Using CG simulation and thermodynamic models, we also determine the role of stoichiometric ratio of the three major component proteins in microcompartments and explore how modulating protein interactions can regulate the assembled morphology.