Historically, it has been understood that for gene expression in eukaryotes, each molecule of mRNA encodes a single protein. With the recent development of technologies to sequence full-length transcripts en masse, we have discovered hundreds of examples in two species of eukaryotic green algae where two, three, or more proteins are translated from a single transcript. These “polycistronic” transcripts are conserved in diverse species throughout the green algal lineage, which highlights their biological importance. This discovery forces us to reevaluate our assumptions about eukaryotic gene expression. Lastly, we demonstrate how these findings can be leveraged to co-express pairs of heterologous proteins in plants and algae for research and industrial applications.

The SARS-CoV-2 Nucleoprotein (NCAP) functions in RNA packaging during viral replication and assembly. Computational analysis of its amino acid sequence reveals a central low-complexity domain (LCD) having sequence features akin to LCDs in other proteins known to function in liquid–liquid phase separation. We showed that in the presence of viral RNA, NCAP, and also its LCD segment alone, form amyloid-like fibrils when undergoing liquid–liquid phase separation. Within the LCD we identified three 6-residue segments that drive amyloid fibril formation. We determined atomic structures for fibrils formed by each of the three identified segments. These structures informed our design of peptide inhibitors of NCAP fibril formation and liquid–liquid phase separation, suggesting a therapeutic route for Covid-19.

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Friday, April 30, 2021
via Zoom
3:30 pm