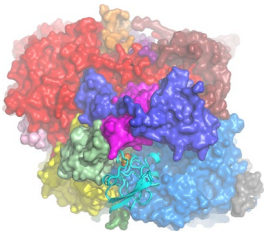
PHOTOSYNTHESIS

Electron handoff

Nat. Plants **4**, 218–224 (2018)



Credit: *Nat. Plants*

Photosynthesis involves three integral membrane complexes that mediate the transport of electrons initiated by light absorption. In the final steps of this electron transport chain, one of these complexes, photosystem I (PSI), transfers electrons to the carrier protein ferredoxin (Fd) via the PSI subunit PsaC. Although the electron transport complex formed between PSI and Fd has been previously investigated by electron microscopy, cross-linking, and EPR, Kubota-Kawai et al. now present a detailed X-ray crystal structure of the cyanobacterial complex, providing insights into the interaction surfaces between PSI and Fd. Additional mutagenesis, flash-absorption spectroscopy, and solution NMR further validate the importance of individual Fd residues for the interactions that mediate complex formation. Comparison of the PSI–Fd complex structure with that of PSI alone also reveals a relay of conformational changes in the peripheral subunits that occur upon Fd binding, resulting in translocation of PsaF from the stromal side of the membrane to the lumenal side. These results contribute to a more detailed understanding of PSI function and may also facilitate future engineering efforts. *CD*

https://doi.org/10.1038/s41589-018-0073-9

VIRUS ASSEMBLY

Functional phosphorylation

Nat. Microbiol. **3**, 588–599 (2018)

Vaccinia virus (VACV) is an enveloped virus containing ~80 different viral proteins. Several VACV enzymes, including F10 kinase, I7 protease, and H1 phosphatase, are required for proper viral assembly. To create a comprehensive network of functional viral phosphorylation events, Novy et al. used quantitative mass spectrometry-based proteotype analysis to define the role of F10 and H1 phosphorylation of viral proteins. In infected cells, the authors identified 43 phosphorylated proteins, 10 of which are shared F10/H1 substrates, and 9 of these are essential for VACV assembly. Comparing wild-type and H1-deficient virions led them to focus on two H1 substrates, F10 and I7, demonstrating that phosphorylation of F10 itself does not impact virus assembly, while dynamic phosphorylation of I7 S134 by F10 is required for I7 protease activity. F10 phosphorylation was required to regulate I7-mediated viral protein processing during both the initial viral membrane formation and the transition from immature to mature virions. Additionally, the authors showed that the transcription defect of H1-deficient mature virions is likely due to hyperphosphorylation of the transcription factor A7. These results uncover a key viral signaling network that controls assembly of infectious poxvirus particles and highlight the power of combining quantitative proteotype analysis with mutant viruses to unmask proteotype–phenotype–genotype relationships. *MB*

https://doi.org/10.1038/s41589-018-0075-7

GENE EXPRESSION REGULATION

SLAMing transcription

Science https://doi.org/10.1126/science.aao2793 (2018)

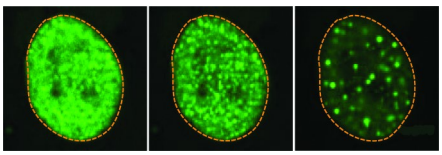
Deciphering direct transcriptional responses to cell perturbations is challenging because of vast differences in mRNA and protein turnover. One method that can potentially address this concern is SLAM-seq, which enables the direct quantification of newly synthesized mRNAs. In this approach, the nucleotide analog 4-thiouridine is incorporated during RNA synthesis and then alkylated by iodoacetamide, which can be detected by reverse-transcriptase-induced thymine-to-cytosine changes in mRNA 3′-end sequencing. Muhar et al. applied SLAM-seq in combination with the auxin-inducible degradation system or small-molecule inhibition to determine whether rapid loss of the transcriptional regulators MYC or BRD4 resulted in global or specific loss in downstream gene expression. Performing SLAM-seq following degradation or inhibition of BRD4 revealed global downregulation of transcription owing to alterations in Pol II–mediated promoter-proximal pause release. In contrast, loss of MYC led to a selective decrease in transcription of genes involved in protein and nucleotide synthesis. Taken together, the combination of SLAM-seq with small-molecule-mediated inhibition or degradation may provide an effective approach to measure global and specific transcriptional responses to cellular perturbations. *GM*

https://doi.org/10.1038/s41589-018-0074-8

PROTEIN AGGREGATION

Buffering transition

Science https://doi.org/10.1126/science.aar7366 (2018)



Credit: AAAS

Aberrant aggregation of normally soluble proteins into insoluble amyloid is involved in the onset and the progression of many neurodegenerative diseases, including amyotrophic lateral sclerosis (ALS). In the neurons of ALS patients, aggregation of prion-like RNA-binding proteins (RBPs) usually occurs in the cytoplasm rather than the nucleus. To investigate what prevents prion-like RBPs from forming solid-like aggregates in the nucleus, Maharana et al. used in vitro phase-separation assays and fluorescence correlation spectroscopy to show that RNA blocks the liquid–solid phase transition of prion-like RBPs, which is a prerequisite of aggregation. In living cells, assemblies of prion-like RBPs are observed by reducing the concentration of nuclear RNAs, by increasing intranuclear protein expression, or by impairing the RNA-binding ability of proteins. Photobleaching experiments showed that RNA kept condensates formed by prion-like RBPs in a dynamic state and prevented the formation of solid pathological assemblies. Overall, the findings sugges that nuclear RNA buffers the phase separation behavior of prion-like RBPs, provide insight into the chemical characteristics of this type of protein, and deepen the understanding of the pathological cause of prion-like RBP-related neurodegenerative diseases. *YS*

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