The free protein pool: quantitative insights into the 3 major photosynthetic complexes

Anna Williams[a], Philip J. Jackson[b], Steven M. Theg[c], Diana Kirilovsky[d], Terry M. Bricker[e], Niel C. Hunter[b], Michael Gross[f], Haijun Liu[a]

[a]*Department of Biology, Saint Louis University, St. Louis, MO, 63130, USA*
[b]*Plants, Photosynthesis and Soil, School of Biosciences, University of Sheffield, Sheffield, UK*
[c]*Department of Plant Biology, University of California, Davis, CA, 95616, USA*
[d]*Institute for Integrative Biology of the Cell (I2BC), CNRS, CEA, Université Paris-Sud, Université Paris-Saclay, 91198 Gif sur Yvette, France*
[e]*Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, 70803, USA*
[f]*Department of Chemistry, Washington University in St. Louis, St. Louis, MO, 63130, USA*

For decades, the thylakoid lumen of photosynthesizing organisms has been thought to harbor proteins associated with only a limited number of photosynthetic complexes. The question of what and how many proteins exist within the thylakoid lumen has remained largely unanswered. In this study, we utilized quantitative mass spectrometry to determine the abundance of photosystem II (PSII) lumenal proteins and the stromal subunits of photosystem I (PSI), that are presumably linked to two major pigment protein complexes. Phycobilisome (PBS) components were also quantified, including the physiologically relevant orange carotenoid protein (OCP) and ApcG. A substantial free pool of PSII components on the thylakoid lumenal side exists while an additional free pool of PSI components is present on the stromal side. This model challenges the current structural stoichiometry of these two reaction centers previously revealed by X-ray crystallography and cryo-EM through propositions of natively unfolded PsbO. The stoichiometry of OCP and PBS offers a better understanding of the photoprotective mechanisms in cyanobacteria.

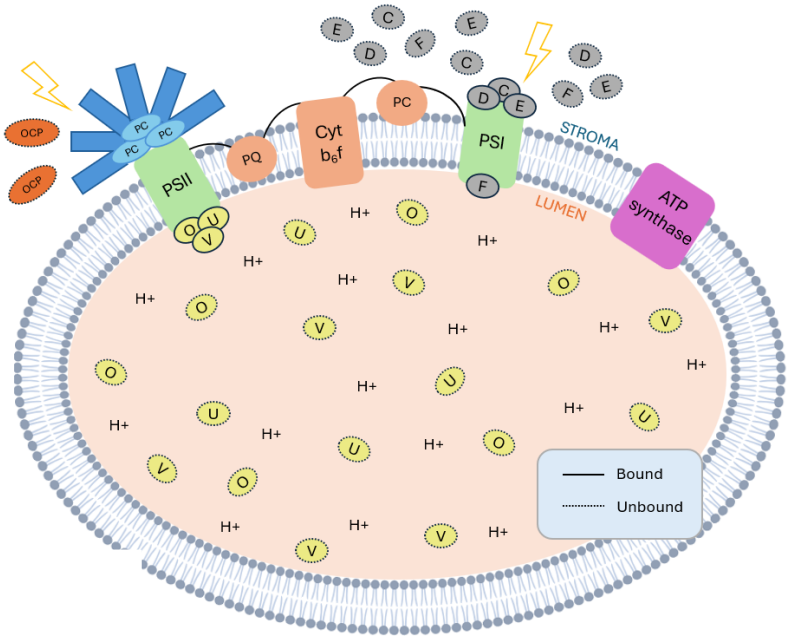

Figure 1. A schematic representation of the free-floating pool of proteins for PSII (lumen), PSI (stroma), and OCP. Dashed perimeters show unbound proteins while solid perimeters demonstrate protein binding to a complex.
Proteins are annotated by their last letter (i.e. PsaF is "F").