

**THE SOLAR SUPERCHARGE: BIOLOGICAL FLUXES AND ENERGY CYCLING BEFORE AND AFTER THE INVENTION OF PHOTOSYNTHESIS.** Jason Raymond<sup>1</sup>, <sup>1</sup>School of Earth and Space Exploration, Arizona State University, PO Box 871404, Tempe, AZ 85287, jason.raymond@asu.edu

**Introduction:** The global scale repercussions of the invention of photosynthesis are oft-cited and are widely agreed to be tightly linked, if not imperative, to the evolution of complex life. At face value, this photosynthesis imperative is a logical result of the injection of solar free energy into biological--particularly redox--processes and, following the evolution of oxygenic photosynthesis, the availability of O<sub>2</sub> as a potent electron acceptor. While perfectly plausible, these hypotheses offer few details that might constrain attempts to define planetary habitability or--other than the detection of oxygen proxies in extrasolar atmospheres--identifying habitable worlds. Recent advances have begun to elucidate the 'devil in the details' associated, in particular, with the advent of oxygenic photosynthesis and how it changed not only the energy balance of the biosphere, but its very composition [1, 2]. Indeed, early aerobic organisms developed a repository of new compounds that became critical to form and function in the progressively more complex lifeforms that arose in an oxygenated atmosphere [1].

In this presentation, I detail attempts to push forward on these recent advances by exploring how the dynamics of biochemical network function were altered as a result of the invention of photosynthesis. By integrating and comparing genomic reconstructions of ancestral photosynthetic and non-photosynthetic organisms (see e.g. [3, 4]), our present work is able to infer the core conserved biochemical networks that arose as a result of the invention of both anoxygenic (AP) and oxygenic (OP) photosynthesis from non-photosynthetic (NP) ancestors.

By carrying out flux balance analysis of these reconstructed networks, solution spaces of feasible fluxes can be calculated and contrasted across reconstructed genomes, identifying pathways whose fluxes changed substantially following the addition of photosynthesis as a metabolic capability. Interestingly, a number of the pathways whose fluxes changed most dramatically in both anoxygenic and oxygenic photosynthetic genomes are conserved across all known phototrophic phyla, suggesting energetic chokepoints that might be difficult for life on 'dark worlds' to overcome. Fluxes through anabolic pathways show the most variation across all three groups (NP, AP, OP) of reconstructions, while catabolic pathways in general show higher fluxes in OP versus the NP and AP sets, arguably linked to the role of oxygen utilizing mono- and di-oxygenases in difficult-to-catalyze decompositions of a myriad of organic

compounds. Understanding if and how photosynthesis was required to establish the molecular framework and meet the energetic demands of a progressively more complex and diverse biosphere on a young (but still comparatively habitable) Earth is absolutely essential to informing and constraining our hunt for life elsewhere.

#### References:

- [1] Raymond J. and Segre D. (2006) *Science*, 311, 1764-1767. [2] Dupont et al. (2006) *Proc Natl Acad Sci*, 103, 17822-17827. [3] Knoop H. et al. (2013) *Plos Comput Biol*, 9, e1003081. [4] Braakman R. and Smith E. (2014) *PLoS ONE*, 9, e93345.