Goldschmidt 2023 Abstract
https://doi.org/10.7185/gold2023.20391

Probing modern microbial genomes for resurrecting ancient metabolisms

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Extant genomic information can be used to resurrect ancestral protein networks to understand how past metabolisms may have functioned and evolved under early Earth conditions. To determine which proteins are required to resurrect ancient networks, we need to have a better understanding of the distribution and complexity of the proteins involved. Microbially-mediated nitrogen fixation (N_2-fixation), is an important example of an early-evolved and critical metabolic innovation, whose origin and evolution warrants further investigation. Nitrogenase, catalytically responsible for fixing N_2 to NH_3, interacts with a surrounding "N_2-fixation machinery"; enzymatic partners responsible for nitrogenase biosynthesis, regulation, and metabolic compatibility. The composition of this N_2-fixation machinery varies widely among different taxa, spanning from fewer than 10 genes to microorganisms that contain approximately 80 nitrogenase-associated genes. Thus, questions remain regarding how these genes are distributed across, and correlated with, the overall cellular functions and environmental surroundings of diverse organisms. It is also unclear whether certain environmental factors, such as oxygen concentration, temperature, or environmental niche, have impacted the diversification of N_2-fixation machinery. In this talk, I will present a comprehensive approach for determining the core N_2-fixation machinery across diverse microorganisms to be used for inferring ancestral networks. This approach can help guide early life biosignature and life detection studies by revealing how the molecular evolution of a metabolically critical protein, such as nitrogenase, is constrained by its overlying protein interaction network and surrounding environment.