

Retention of anaerobic physiology in phototrophic eukaryotes

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Abstract

There are many eukaryotes that thrive in anoxic environments. Well-known examples include parasites such as *Trichomonas*, *Entamoeba*, *Giardia*, and the nematode *Ascaris*, which represent examples of ecologically driven specializations to a specific habitat. The underlying biochemistry of anaerobic physiology has been characterized in detail, including its enzymes such as pyruvate:ferredoxin oxidoreductase (PFO) and the iron-only hydrogenase (FeHYD).

We screened available genome and transcriptome data of eukaryotes and confirm that the enzymes in question are encoded among representatives of all major eukaryotic groups. As some of the crucial enzymes are oxygen-sensitive due to their intrinsic iron-sulfur clusters, it is surprising to also find them encoded by genomes from representatives of all three major groups of phototrophic eukaryotes and not only individual algal species thought to encounter periods of hypoxia due to environmental changes. We found that the machinery associated with anaerobic physiology is expressed under the strict regime of the diurnal cycle in *Chlamydomonas reinhardtii* and independent of anaerobic culturing conditions. Some of the enzymes localize to the oxygen-producing organelle of algae, which suggests their retention for reasons associated with plastid physiology and maybe diurnal redox/metabolism balance. These results argue against the acquisition of anaerobic physiology by lateral gene transfer in eukaryotes for the purpose of *adapting to hypoxia* and speak in favor of their presence in the lineage that acquired the plastid through endosymbiosis.