

Anaerobic ATP generation enzymes in microbial opisthokonts

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Multiple distantly-related eukaryotic lineages have adapted to low-oxygen environments. Recent work has increasingly illuminated the biochemical pathways that allow these organisms to produce ATP under low-oxygen conditions; these pathways include alternate electron transport chain components, modified tricarboxylic acid cycles, and a suite of fermentation enzymes that, in bacteria, oxidize pyruvate and produce ATP with the concomitant production of molecular hydrogen. In the past few years, in-depth sequencing efforts have revealed that the enzymes involved are widely, yet patchily, distributed, and present in diverse combinations. Nevertheless, while anaerobic ATP generation is well understood in a small number of metazoans and fungi, microbial opisthokonts have remained understudied. These organisms represent several major, and basal, lineages of Holozoa and Holomycota, and are crucial to our understanding of the evolution of these enzymes in eukaryotes, and to the diversity of lifestyles in opisthokonts.

Using comparative genomics, we present a comparative study of anaerobic ATP generation enzymes across opisthokonts, integrating new genome data from ichthyosporeans, filastereans, choanoflagellates, and nucleariids. We show that enzymes associated with tolerance of anoxia are more widespread in opisthokonts than previously believed. We also show that a key enzyme, [FeFe]-hydrogenase, is frequently present without the pyruvate oxidation enzymes found together with it in bacteria. This apparent uncoupling between different parts of the fermentation pathway has been found in several eukaryote lineages in recent years, and suggests a possible novel function for [FeFe]-hydrogenase in some eukaryotes.