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Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in *Escherichia coli* strains lacking the Phosphotransferase System

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Abstract

Aromatic metabolites provide the backbone for numerous industrial and pharmaceutical compounds of high value. The Phosphotransferase System (PTS) is common to many bacteria, and is the primary mechanism for glucose uptake by *Escherichia coli*. The PTS was removed to conserve phosphoenolpyruvate (pep), which is a precursor for aromatic metabolites and consumed by the PTS, for aromatic metabolite production. Replicate adaptive laboratory evolution (ALE) of PTS and detailed omics data sets collected revealed that the PTS bridged the gap between respiration and fermentation, leading to distinct high fermentative and high respiratory rate phenotypes. It was also found that while all strains retained high levels of aromatic amino acid (AAA) biosynthetic precursors, only one replicate from the high glycolytic clade retained high levels of intracellular AAAs. The fast growth and high AAA precursor

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