MICROBIAL GENOMICS FOR THE DEVELOPMENT OF BIOCATALYSTS FOR LIGNOCELLULOSIC BIOREFINING

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Biorefineries are important for green processing and sustainable development because their objective is to convert lignocellulosic feedstocks into varied value-added products including biofuels (e.g. ethanol) and co-products (e.g. bio-plastics). The potential for biorefineries based on biomass derived from agricultural and/or agri-industrial by-products is enormous, but current biorefinery strategies are at an early phase of development and are focused on specific bioproduct generation based on sugars generated by hydrolysis of forestry derived lignocellulosic biomass. Development of industrially-robust bacteria for conversion of lignocellulosic biomass to fuels and/or value-added co-products requires a comprehensive understanding of the relationships between genome content, gene and gene product expression, enzyme activity levels, carbon and electron flow through metabolic pathways, and end-product synthesis patterns. This presentation will provide an overview of how genome sciences, including comparative genomics (1, 2, 3) proteomics and transcriptomics (4), can both provide an understanding of the metabolic pathways used (fig. 1), guide genetic engineering, and complement bioprocess engineering, to increase the efficiency of conversion of lignocellulosic biomass to biofuels (ethanol, hydrogen) using single organisms or "designer consortia" that will maximize substrate conversion to desired end. Specific examples of how these technologies help develop insights into thermophilic lignocellulolitic organims will be taken from the *Clostridium thermocellum, C. stercorarium,* and *Thermoanaerobacter thermohydrosulfuricum*.-

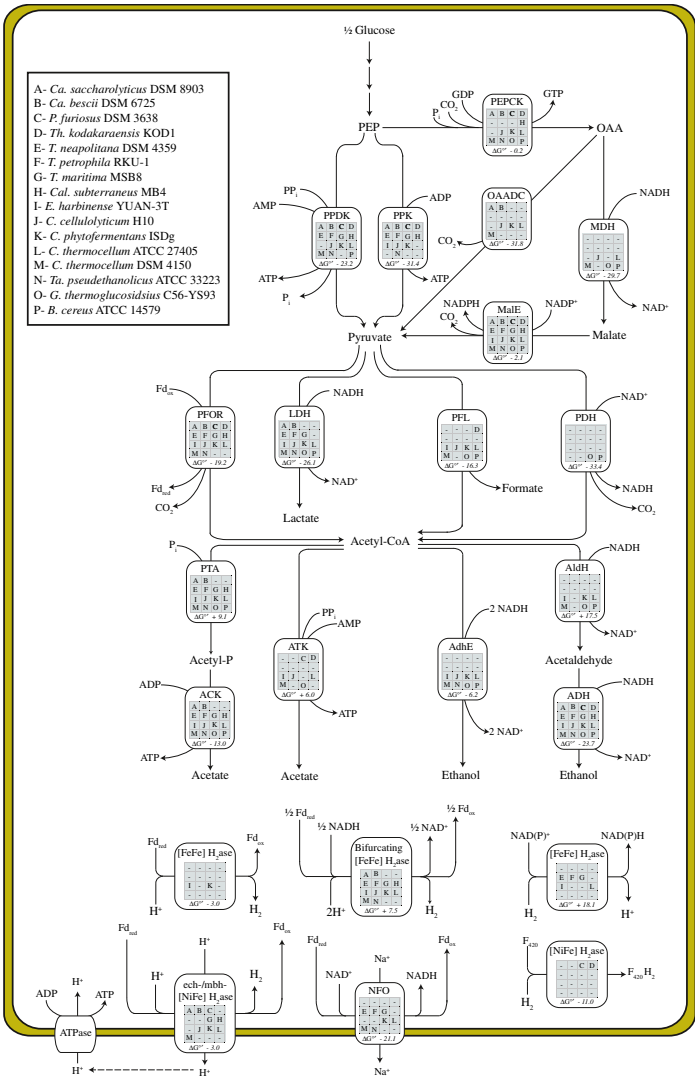

Fig. 1 Comparison of putative gene products involved in pyruvate metabolism among select hydrogen and ethanol-producing species. Presence of putative gene products are indicated in matrix with letters corresponding to selected organism (see legend).. Abbreviations: PEPCK, phosphoenolpyruvate carboxykinase; OAADC, oxaloacetate decarboxylase; MDH, malate dehydrogenase; MalE, malic enzyme; PPK, pyruvate kinase; PPDK, pyruvate phosphate dikinase; LDH, lactate dehydrogenase; PFL, pyruvate formate lyase; PFOR, pyruvate:ferredoxin oxidoreductase; PDH, pyruvate dehydrogenase; ADH, alcohol dehydrogenase; ALDH, acetaldehyde dehydrogenase; AdhE, bifinctional acetaldehyde/alcohol dehydrogenase; ACK, acetate kinase; PTA, phosphotransacetylase; NFO, NADH:Fd oxidoreductase. (2)

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