

Figure 1. ATP requirements for maintenance and growth. Panel A shows the model estimated maximum ATP hydrolysis rates needed to match experimentally measured lactate consumption rates and cellular growth rates at four different dilution rates (D = 0.025, 0.04, 0.055,  $0.085 \, h^{-1}$ ). The slope and intercept represent the growth- and nongrowth rate dependent ATP requirements, GAR and NGAR, respectively. Panel B shows ATP requirements for various microbes that have been reported in the literature [26-32]. The reported GAR values for other microbes were adjusted to remove ATP used for protein polymerization (4 ATP/peptide bond) since ATP used for protein synthesis is accounted for separately in the S. oneidensis MR-1 model and is not part of the MR-1 GAR value. Panel C compares model estimates of maximum growth rates (solid line) at different lactate consumption rates (using ATP requirements as reported in panel A) with experimental data. Additional data points were included that were not used in the estimation of the ATP requirements.

doi:10.1371/journal.pcbi.1000822.g001

- 26. Teusink B, Wiersma A, Molenaar D, Francke C, de Vos WM, et al. (2006) Analysis of growth of Lactobacillus plantarum WCFS1 on a complex medium using a genome-scale metabolic model. J Biol Chem 281: 40041–40048.
- 27. Oh YK, Palsson BO, Park SM, Schilling CH, Mahadevan R (2007) Genome-scale reconstruction of metabolic network in Bacillus subtilis based on high-throughput phenotyping and gene essentiality data. J Biol Chem 282: 28791–28799.
- 28. Oliveira AP, Nielsen J, Forster J (2005) Modeling Lactococcus lactis using a genome-scale flux model. BMC Microbiol 5: 39.
- 29. Reed JL, Vo TD, Schilling CH, Palsson BO (2003) An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR). Genome Biol 4: R54.
- 30. Mahadevan R, Bond DR, Butler JE, Esteve-Nunez A, Coppi MV, et al. (2006) Characterization of metabolism in the Fe(III)-reducing organism Geobacter sulfurreducens by constraint-based modeling. Appl Environ Microbiol 72: 1558–1568.
- 31. Borodina I, Krabben P, Nielsen J (2005) Genome-scale analysis of Streptomyces coelicolor A3(2) metabolism. Genome Res 15: 820–829.
- 32. Jamshidi N, Palsson BO (2007) Investigating the metabolic capabilities of Mycobacterium tuberculosis H37Rv using the in silico strain iNJ661 and proposing alternative drug targets. BMC Syst Biol 1: 26.