Searching for principles of microbial physiology

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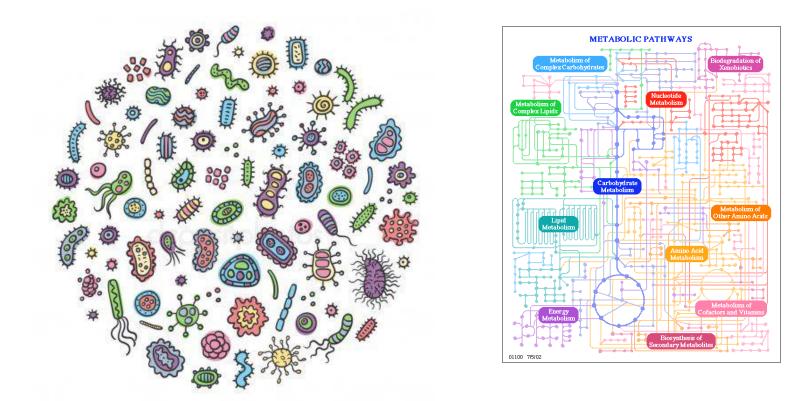
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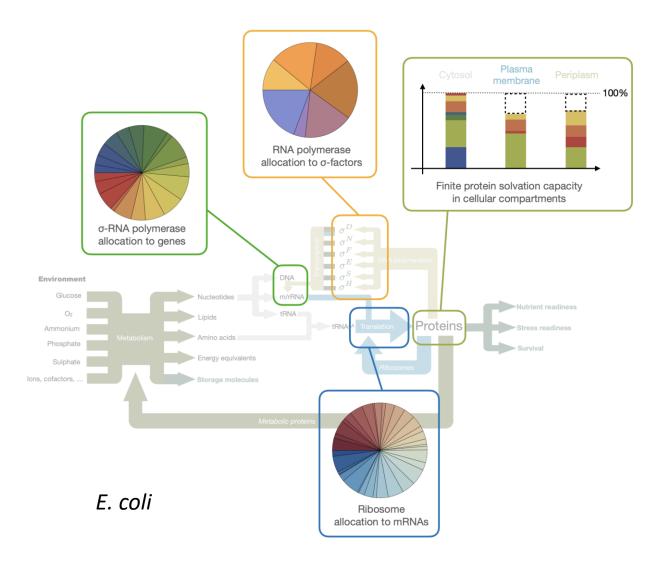
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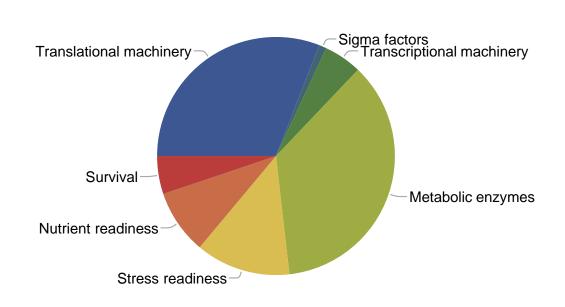
Molecular commonalities across microorganisms



- ✓ Conserved biochemistry and molecular biology
 - ✓ Biosynthesis machinery
 - ✓ Energy conservation and central metabolism
 - ✓ Conserved principles of enzyme kinetics

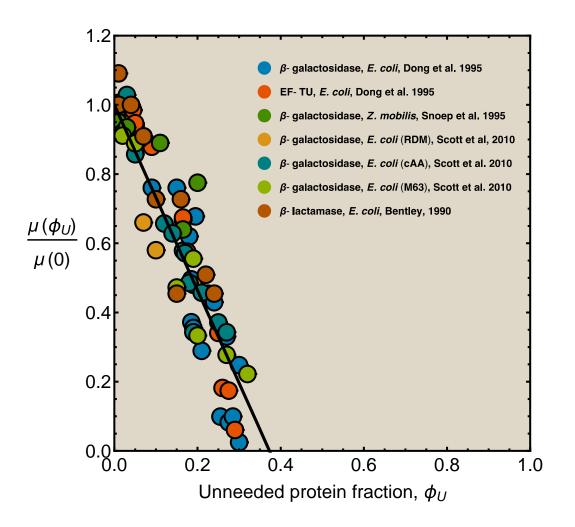
All microorganisms have a finite biosynthetic capacity such that the synthesis of one protein is that the expense of others



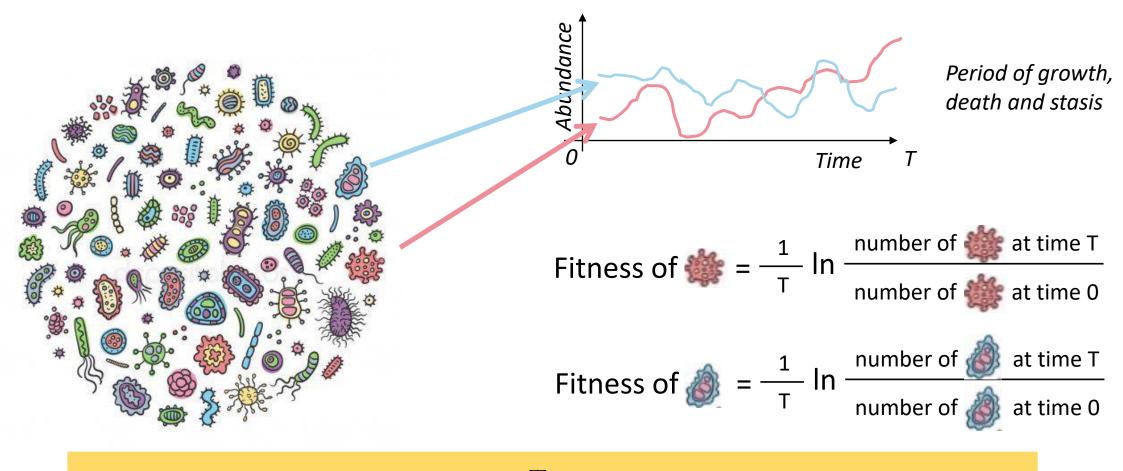


Phenotypic adaptation --Environment dependent "protein pools"

Unneeded proteins are at the expense of growth proteins in E. coli

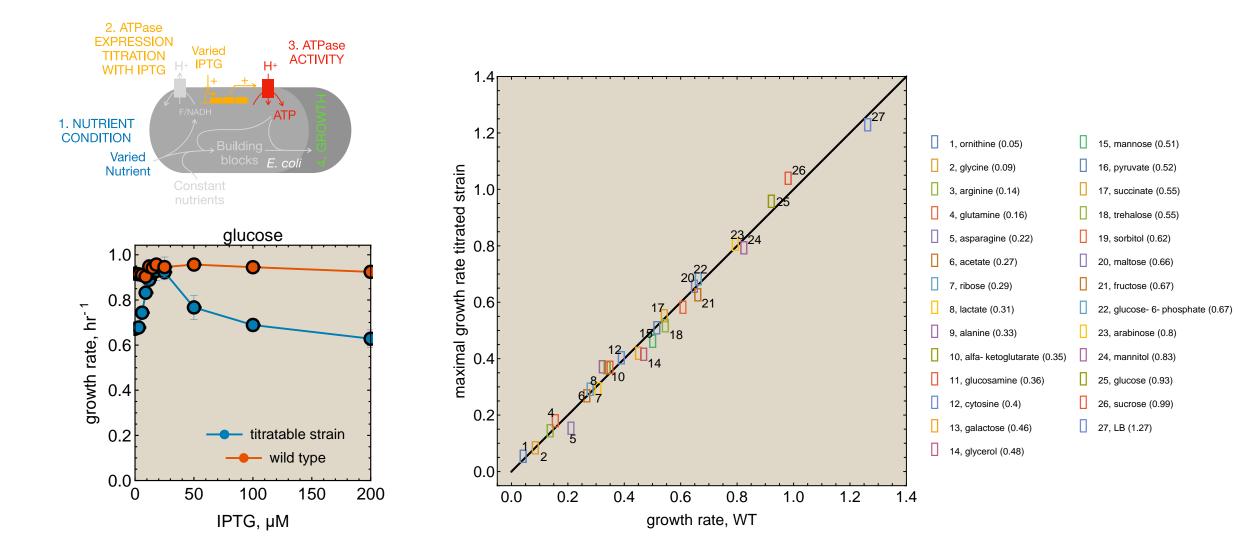


Identical fitness measure for all microorganisms

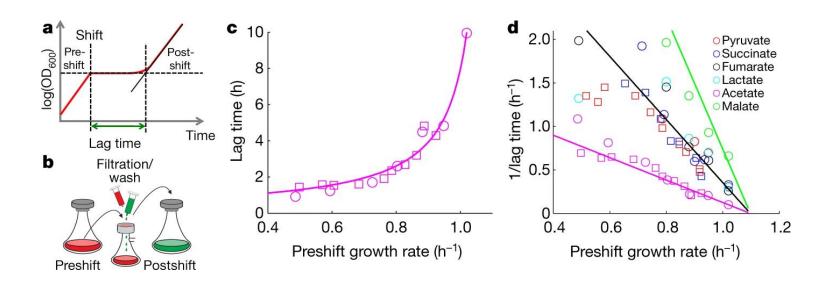


Fitness =
$$\frac{1}{T} \ln \frac{N(T)}{N(0)} = \frac{1}{T} \int_0^T \mu(t) dt$$
 = Average growth rate

Protein expression of H-ATPase maximizes growth rate in E. coli for S. cerevisiae evidence see Keren, et al. Cell, 2016 and for L. lactis evidence see Peter Jensen's papers



The trade off between growth, stress readiness and adaptation capacity implied by the finite biosynthetic resources



E. coli study: Basan et al. Nature, 2020.

Slower growth of *Escherichia coli* leads to longer survival in carbon starvation due to a decrease in the maintenance rate

Elena Biselli^{1,†}, Severin Josef Schink^{1,2,†} & Ulrich Gerland^{1,*}

Environmental Microbiology (2005) 7(10), 1568-1581

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doi:10.1111/j.1462-2920.2005.00846.x

Global physiological analysis of carbon- and energylimited growing *Escherichia coli* confirms a high degree of catabolic flexibility and preparedness for mixed substrate utilization

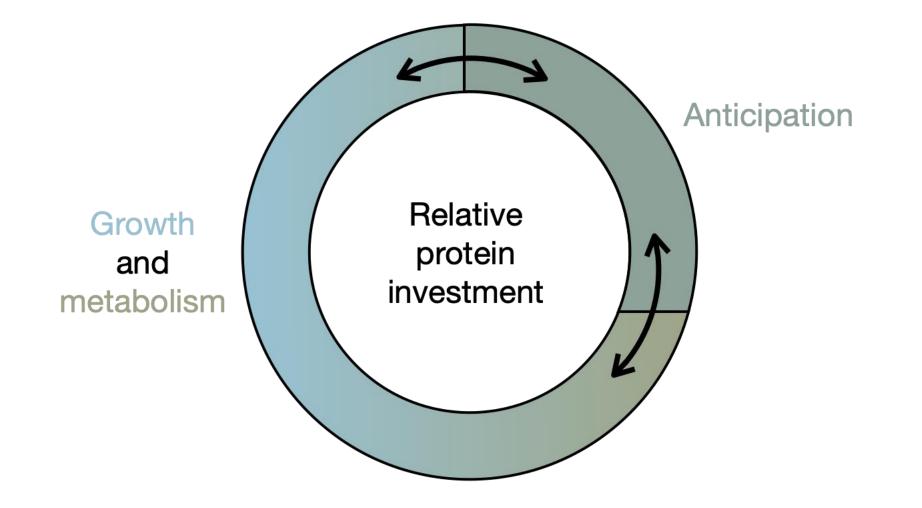
crobiology (2004), 150, 1637–1648 DOI 10,1099/mic.0.26	
	Specific growth rate and not cell density controls the general stress response in <i>Escherichia coli</i>
	Julian Ihssen and Thomas Egli
Correspondence Thomas Egli egli@eawag.ch	Swiss Federal Institute for Environmental Science and Technology, PO Box 611, Überlandstrasse 133, CH-8600 Dübendorf, Switzerland

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Apr. 2006, p. 2586–2593 0099-2240/06/\$08.00+0 doi:10.1128/AEM.72.4.2586–2593.2006 Copyright © 2006, American Society for Microbiology. All Rights Reserved. Vol. 72, No. 4

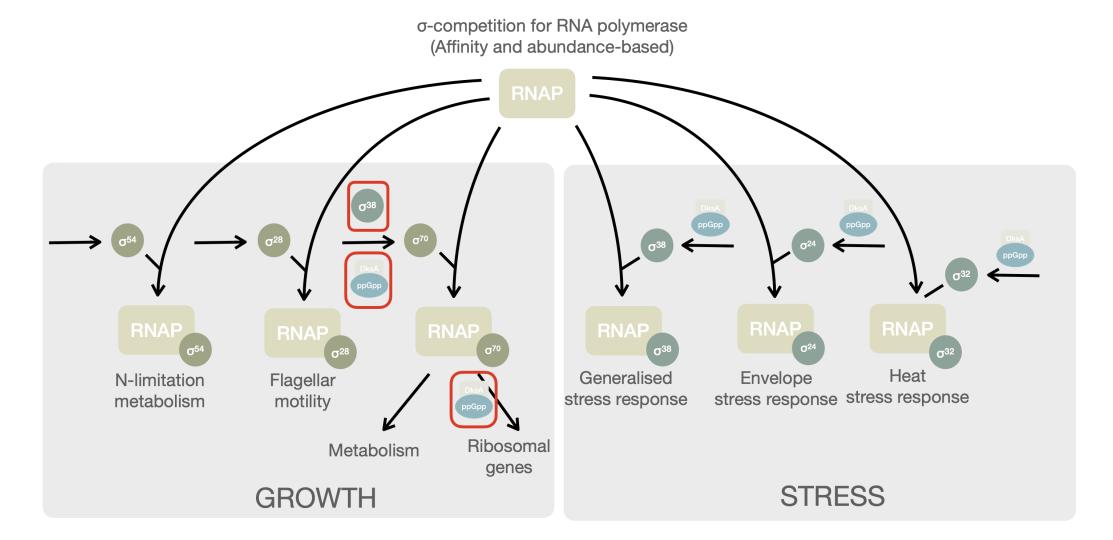
Specific Growth Rate Determines the Sensitivity of *Escherichia coli* to Thermal, UVA, and Solar Disinfection

Michael Berney, Hans-Ulrich Weilenmann, Julian Ihssen, Claudio Bassin, and Thomas Egli* Swiss Federal Institute of Aquatic Science and Technology (Eawag), Überlandstrasse 133, P.O. Box 611, CH-8600 Dibendorf, Switzerland

The trade off between growth, stress readiness and adaptation capacity implied by finite biosynthetic resources



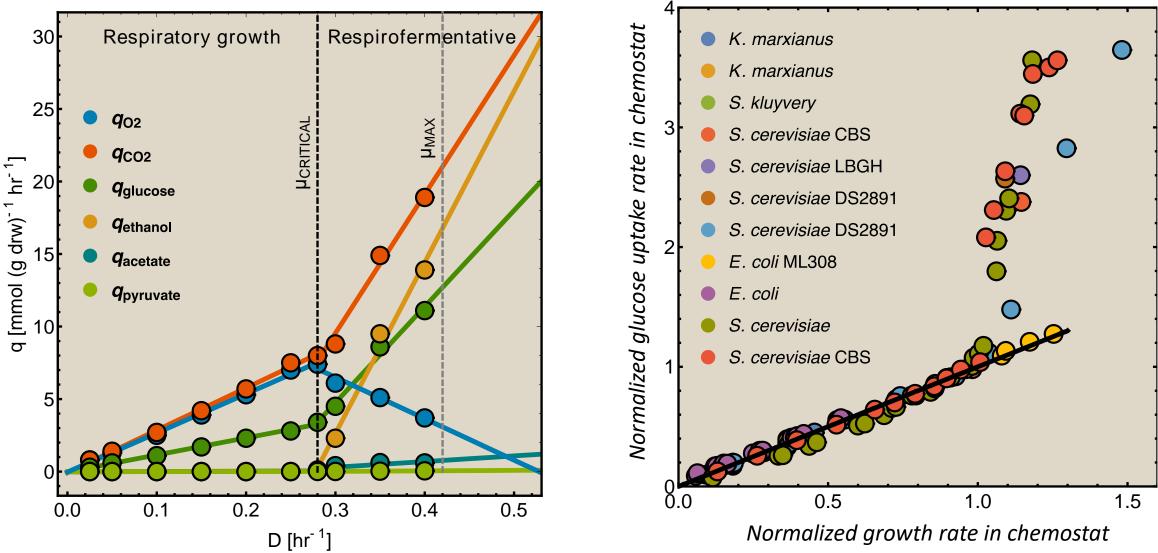
Molecular "hardwiring" of the trade off in E. coli via RNA-pol competition σ-factors are required, transient subunits of RNA polymerase in E. coli



In lab-evolution experiments, growth-vs-stress "rebalancing" mutations were found in sigma factors and RNA pol.

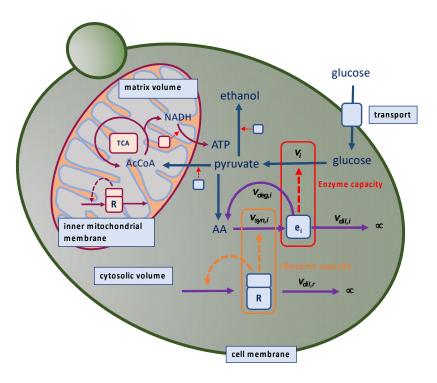
Commonality of overflow metabolism at fast growth for L. lactis example see Goel et al. Molecular Microbiology 2015

S. cerevisiae

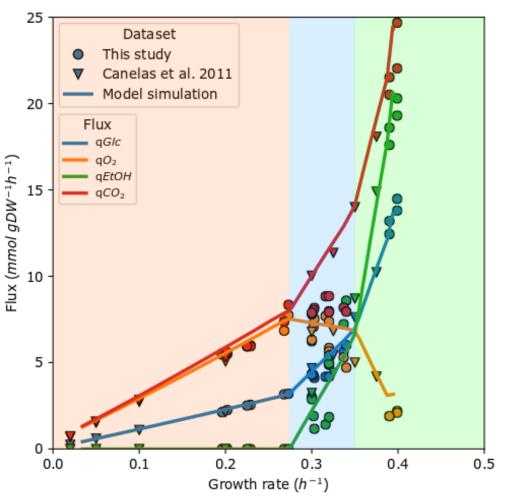


Optimal allocation of biosynthetic resources can explain overflow metabolism at fast growth

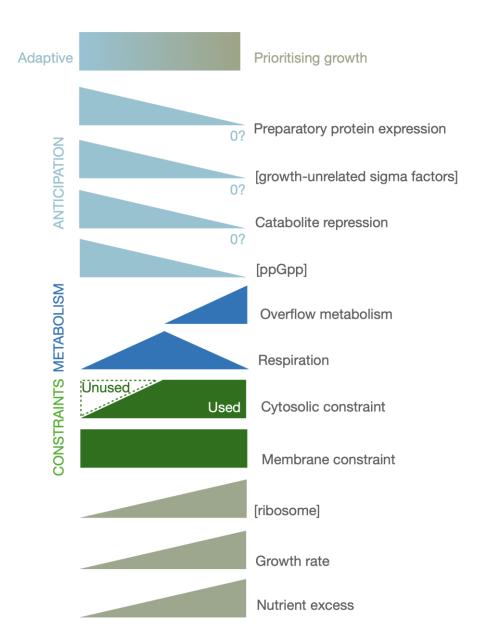
Elsemman, Prado, Griagatis et al, BioRxiv preprint, 2021.



Mathematical model of metabolism, Protein synthesis and protein-expression constraints.



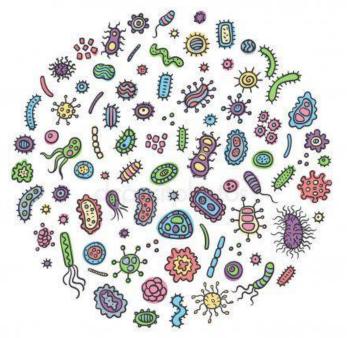
Growth rate is an "order parameter" for E. coli (and likely also for S. cerevisiae)



But not all microorganisms are like E. coli and S. cerevisiae

Commonalities

- ✓ Biochemical kinetics
- \checkmark Biosynthesis
- ✓ Finite biosynthetic resources
- ✓ Fitness measure



Possible differences

- $\checkmark\,$ Protein expression as function of growth rate
- ✓ Absence of overflow metabolism
- $\checkmark\,$ Unneeded protein response of growth rate
- $\checkmark\,$ Anticipation behavior at slow growth

Likely cause:

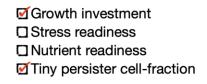
differences in their environment (niches) The field is biased to fast growing microbes in constant conditions.

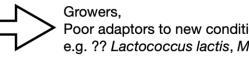
Microbial fitness strategies are likely niche dependent Microbial fitness strategy \cong *Microbial physiology*

Mostly (same) feast environment



Unpredictable environment

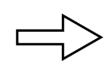




Poor adaptors to new conditions, e.g. ?? Lactococcus lactis, Methanococcus maripaludis

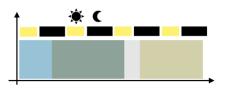


Growth investment Stress readiness **M**Nutrient readiness Phenotypic diversification

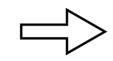


Growers first. Reasonable adaptors Future preparation whenever possible e.g. Escherichia coli, Saccharomyces cerevisiae

Periodic (energy) environment with an unpredictable component

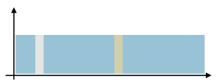


Growth investment Stress readiness **Mutrient** readiness Phenotypic diversification



Growers and storers during the day, Survive during the night Future preparation whenever you can e.g. Synechococcus elongatus

Mostly famine environment



Growth investment Stress readiness Mutrient readiness Phenotypic diversification



Future preparers Good adaptors e.g. many soil bacteria



Famine



Nutrients

Stress

Night

Day

Conclusions

- 1. Commonalities exist across microorganisms.
 - □ Microbes are nearly identical in their basic metabolism, biosynthesis and biochemistry.
 - □ Natural selection selects microbes with the highest average growth rate.
 - □ All microbes suffer from finite biosynthetic resources.
 - □ Expression of proteins is at the expense of others (the growth-stress-adapt trade-off).
- 2. Niche-specific physiological phenomena.
 - Unneeded protein reduces growth rate.
 - Optimal expression of a needed protein maximizes growth rate.
 - Overflow metabolism can result from optimal allocation of finite biosynthetic resources.
 - **E**. coli (and S. cerevisiae?) are opportunistic and prioritize growth over future preparation.
- 3. The physiology (metabolic and stress protein expression) of *E. coli* and *S. cerevisiae* can be predicted by optimal allocation of finite biosynthetic resources to maximize growth rate.
- 4. The physiology of model microorganisms likely still reflects their natural niches such that *E. coli, S. cerevisiae, B. subtilis,* and *S. elongatus* (and *L. lactis*) experience the same protein-expression constraints, but nonetheless behave differently.

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