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► **To cite this version:**

Valentina Baldazzi, Delphine Ropers, Jean-Luc Gouzé, Tomas Gedeon, Hidde de Jong. Resource allocation strategies behind rate-yield phenotypes in *E.coli*. 2023 - Workshop on Advanced School on Quantitative Principles in Microbial Physiology: from Single Cells to Cell Communities, ICTP, Oct 2023, Trieste, Italy. pp.1. hal-04216644

HAL Id: hal-04216644

<https://hal.inrae.fr/hal-04216644>

Submitted on 25 Sep 2023

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Resource allocation strategies behind rate-yield phenotypes in *E.coli*

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July 31, 2023

Microbial growth consists of the conversion of nutrients from the environment into biomass and small energy cofactors (ATP, NADH, NADPH, ...) driving biomass synthesis forward. Two macroscopic criteria for characterizing microbial growth are growth rate and growth yield. The former refers to the rate of conversion of substrate into biomass, and the latter to the efficiency of the process, that is, the fraction of substrate taken up by the cells that is converted into biomass.

Different strains of a microorganism growing in the same environment display a wide variety of growth rates and growth yields. We developed a coarse-grained model, coupling the fluxes of carbon and energy, to test the hypothesis that different resource allocation strategies, corresponding to different compositions of the proteome, can account for the observed rate-yield variability. The model predictions were verified by means of a database of hundreds of published rate-yield and uptake-secretion phenotypes of *Escherichia coli* strains grown in standard laboratory conditions. We found a very good quantitative agreement between the range of predicted and observed growth rates, growth yields, and glucose uptake and acetate secretion rates. These results support the hypothesis that resource allocation is a major explanatory factor of the observed variability of growth rates and growth yields across different bacterial strains. An interesting prediction of our model, supported by the experimental data, is that high growth rates are not necessarily accompanied by low growth yields. The resource allocation strategies enabling high-rate, high-yield growth of *E. coli* lead to a higher saturation of enzymes and ribosomes, and thus to a more efficient utilization of proteomic resources.