
Single-growing units phenotypic heterogeneity in *Streptococcus thermophilus* DSM20617

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Abstract

Microbial cell individuality is a source of phenotypic heterogeneity. This heterogeneity is related to stochastic fluctuations in transcription or translation, despite genetically homogeneous background and constant environment conditions. Heterogeneity at a single-cell level is typically masked in conventional studies of microbial populations, which are based on the average behaviour of thousands or millions of cells. Here we developed a semi-automated protocol to study the growth kinetics parameters of single-growing unit (single cell or single-chain) in the dairy bacterium *S. thermophilus*. The results obtained revealed an unexpected heterogeneity in the lag-phase and max-velocity showing a modal distribution of the measured values. Lag-phase and max-velocity values have been significantly modified by changing the energetic status of the single-growing units before their transfer into a new medium. The approach developed could be useful to set-up the best environmental perturbations able to reduce or increase the phenotypic single-cell heterogeneity in *S. thermophilus* population.

Keywords: single, unit, *S. thermophilus*, phenotypic heterogeneity

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