

Long term stationary phase in SBW25, REL606 and MG1655: notes from the literature

Saul Pierotti

July 13, 2019

Preliminary notes

- REL606 is supposed to become senescent after 16 days (Książek 2010) (I have not found this in the paper, look deeper), and this has been confirmed by a previous experiment made by Jenna

Abbreviations

- LTSP: long term stationary phase
- GASP: growth advantage in stationary phase

Bacterial aging (Książek 2010)

- Aging is a set of changes that impair the ability to maintain homeostasis
- In human somatic cells aging is manifested as inability to divide (replicative senescence)
 - The maximum number of times a cell can divide is given by the Hayflick limit
 - It does not depend on the chronological time
 - Senescence can be triggered with stressors (SIPS, stress induced premature senescence)
- Also *S. cerevisiae* shows senescence, probably mediated by the accumulation of cytoplasmic factors
- The main way of bacterial replication is binary fission, which is a symmetric process mediated by FtsZ
 - This symmetry has been traditionally considered as a proof that bacteria do not age
 - The symmetry of division in *E. coli* is not reflected at the level of cellular organization
 - One of the daughter cells inherits pre-existing elements from the mother (old pole) while the other synthesizes these *de novo* (new pole)
 - The linear discendence of the old pole shows senescence, and its replicative lifespan is of about 100 divisions
 - The old pole elements are likely damaged DNA and proteins and fragments of cell wall

(Westphal et al. 2018)

- Attenuation of RpoS is strongly selected at the beginning (after 1 day) in *E. coli*
- Mutations in *rho* and *rpoBC* (regulatory proteins) are favoured in LTSP
- The GASP phenotype does not appear in Terrific broth or Super broth (even a disadvantage appears!), but cells aged in them show GASP if transferred to LB

Differences between MG1655 and REL606 (Yoon et al. 2012)

- Only 4% of the genome is strain-specific
- It includes profages and recently transferred islands

- REL606 has an additional set of Type II secretion genes and D-arabinose utilization
- REL606 lacks the cluster *fly* for flagellar biosynthesis and the very short patch repair system
- Different set of genes for the Qin prophage, O-antigen synthesis, catabolism of aromatic compounds, LPS oligosaccharide synthesis
 - REL606 has the *hpa* cluster for catabolism of 3- and 4-hydroxy phenyl acetic acid
 - MG1655 has the *paa* cluster for catabolism of phenyl acetic acid
- There are numerous gene disruptions caused by deletions, frameshifts, IS sequences
- The 2 strains grow similarly in LB but REL606 grows faster in minimal medium
- Negligible differences in the accumulation of byproducts in minimal vs complex medium
- At the trascription level, in REL606 highly expressed genes are those involved in replication, translation and nucleotide metabolism, while in MG1655 genes for motility, transcription and energy production
- Proteins that are more abundant in REL606 are those involved in amino acid biosynthesis and maltose metabolism
- On the contrary, in MG1655 are more abundant protein for amino acid degradation and stress-response
- REL606 releases more proteins in the medium in stationary phase
- REL606 is more susceptible to stressfull conditions caused by osmolarity, pH, salicylate and β -lactam antibiotics

References

- Książek, Krzysztof. 2010. “Bacterial Aging: From Mechanistic Basis to Evolutionary Perspective.” *Cellular and Molecular Life Sciences* 67 (18): 3131–7. <https://doi.org/10.1007/s00018-010-0417-4>.
- Westphal, Lacey L., Jasmine Lau, Zuly Negro, Ivan J. Moreno, Wazim Ismail Mohammed, Heewook Lee, Haixu Tang, Steven E. Finkel, and Karin E. Kram. 2018. “Adaptation of Escherichia Coli to Long-Term Batch Culture in Various Rich Media.” *Research in Microbiology* 169 (3): 145–56. <https://doi.org/10.1016/j.resmic.2018.01.003>.
- Yoon, Sung, Mee-Jung Han, Haeyoung Jeong, Choong Lee, Xiao-Xia Xia, Dae-Hee Lee, Ji Shim, Sang Lee, Tae Oh, and Jihyun F Kim. 2012. “Comparative Multi-Omics Systems Analysis of Escherichia Coli Strains B and K-12.” *Genome Biology* 13 (5): R37. <https://doi.org/10.1186/gb-2012-13-5-r37>.