**Tracking phenotypic traits correlated with glycolytic flux capacity as a strategy for directing cell population**

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**1. Introduction**

Phenotypic diversification has been the focus of intensive researches during the last decade that have led to a coherent mathematical and experimental framework of molecular stochasticity in prokaryotic and eukaryotic systems. This framework has been notably used in order to decipher the impact of regulatory network structure on possible metabolic specialization in clonal population of bacteria upon diauxic shift [1][2], but we are still far from applying these knowledges to more specific case studies, e.g. bioprocess optimization where control of phenotypic diversification is desired [3]. This is partly due to the fact that most of these researches have been conducted at low spatio-temporal resolution, i.e. either on a limited numbers of cells, or focused on given time point. **2. Methods**

Phenotypic diversification dynamics of E. coli strains displaying different glycolytic fluxes (i.e., either wild-type strain E. coli W3110, mutant strains ΔptsG and ΔptsGΔmanX displaying reduced glycolytic flux or mutant strain ΔompC exhibiting increased glycolytic flux) have been investigated based on automated flow cytometry [4]

.**3. Results and discussion**

∆ompC strain, exhibited considerably increased diversification rate in chemostat cultivation. By comparison with the other strains, a correlation between the intensity of the glycolytic flux and the phenotypic diversification rate has been established. Interestingly, this effect was increased when strains were exposed to a succession of diauxic shifts in continuous culture, suggesting the occurence of a cell-decision making process in front of environmental fluctuations.

**4. Conclusions**

Phenotypic diversification rate is correlated to glycolytic flux in E.coli population. This study suggest. a step forward for managing the heterogeneity of microbial systems.

**References [Calibri 10]**

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