



# Bioprocess scale-up – Tracking the informations relevant for scaling-up by GFP reporter strains

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# Background

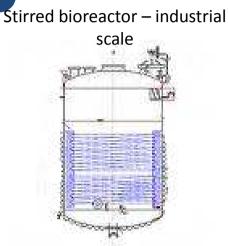
Bioprocess scale-up – general scheme

Stirred bioreactor – lab-scale

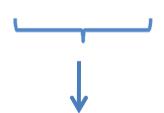
Shaken bioreactors – lab-scale





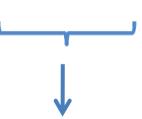


Reactor dimension (D)



Lack of efficieency compared with stirred reactors:

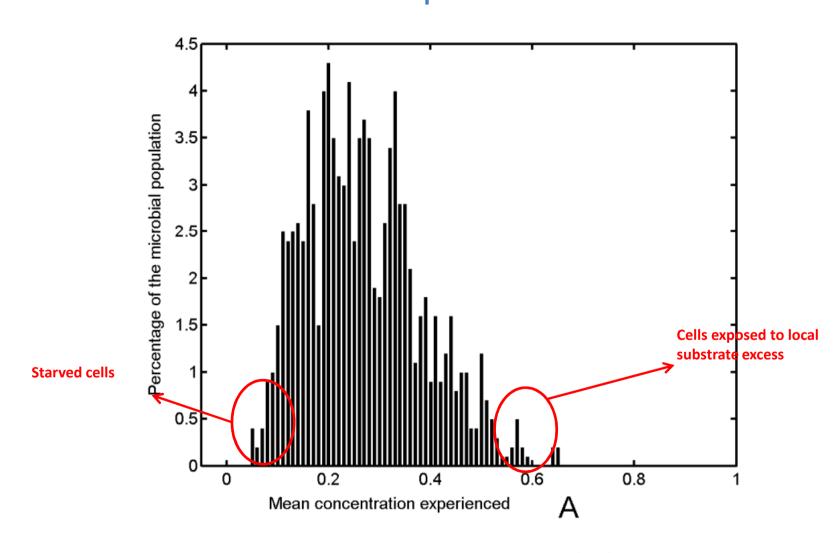
- Lower transfer efficiency
- No regulation of the main environmental variables (pH, dissolved oxygen)



Drop of mixing efficiency when D at constant P/V
Generation of heterogeneities (substrate, dissolved
oxygen, pH, temperature,...)

# Background

Exposure to spatial heterogeneities – hydrodynamic aspects



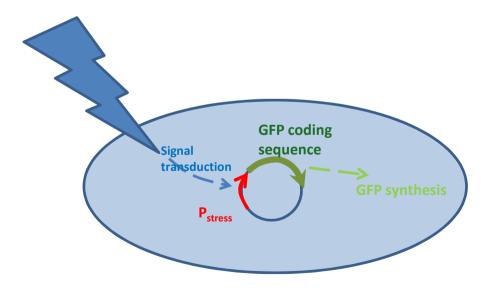
# **Experimental strategy**

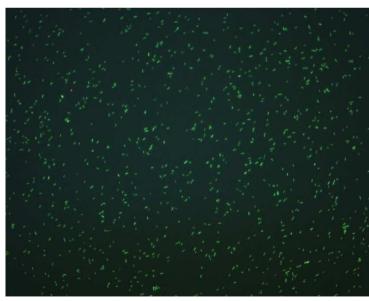
Fluorescent reporter system

#### **Basic principle:**

Using the microbial population as « physiological tracer » for the estimation of the bioreactor mixing and transfer efficiency (potentially capturing the stochasticity linked with the CTD)

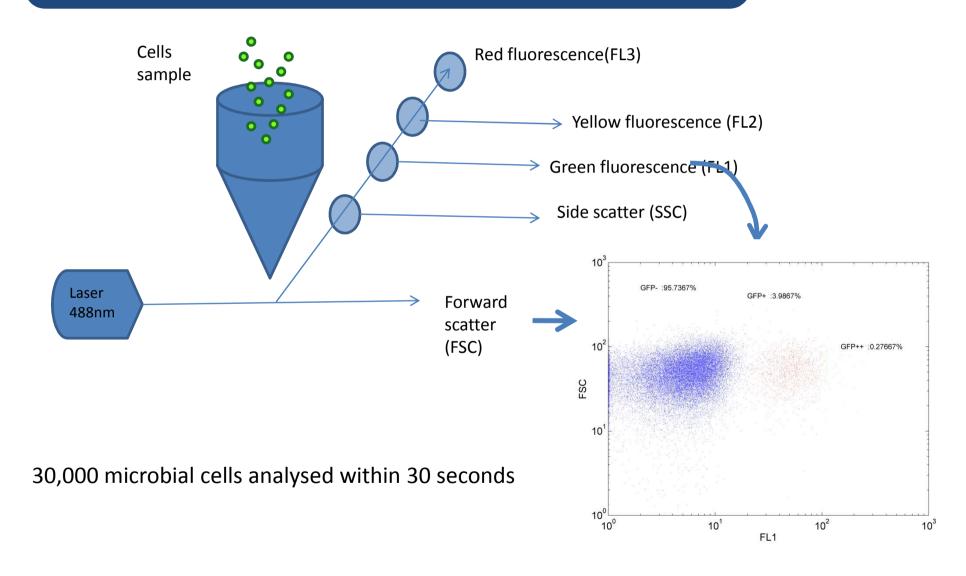
#### Extracellular simuli (S, O2, pH)





# **Experimental strategy**

Flow cytometry — an efficient tool to characterize microbial population heterogeneity



# **Experimental strategy**

Choosing the right ORF for my application

E. coli: about 4000 ORFs:

A

Transcriptional network

B

RpoN

OmpR CRP

HNS

FNR

NarLArcA

RpoS

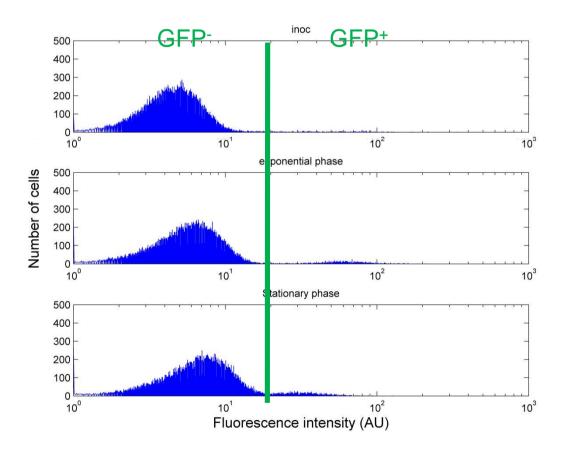
Transcriptional network – hierarchical classification

Ma et al. [2004] BMC Bioinformatics, 5:199

Screening among an E. coli GFP clones library

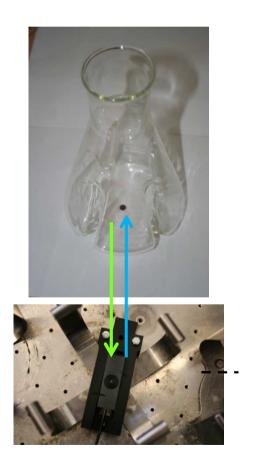
**Cultivation in shake flasks on mineral medium** 

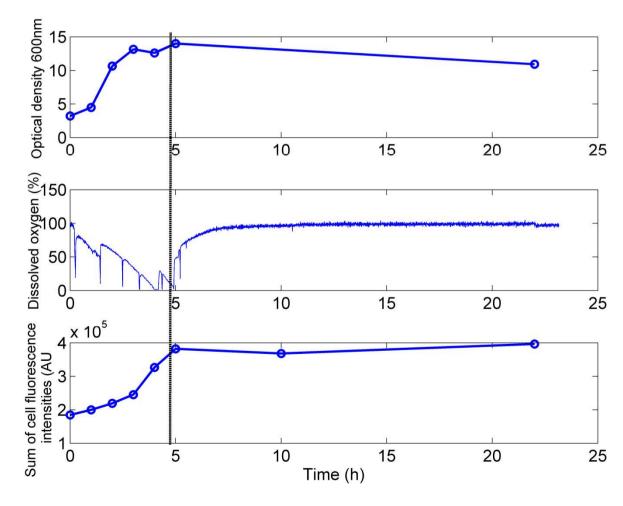
prpoS::gfp



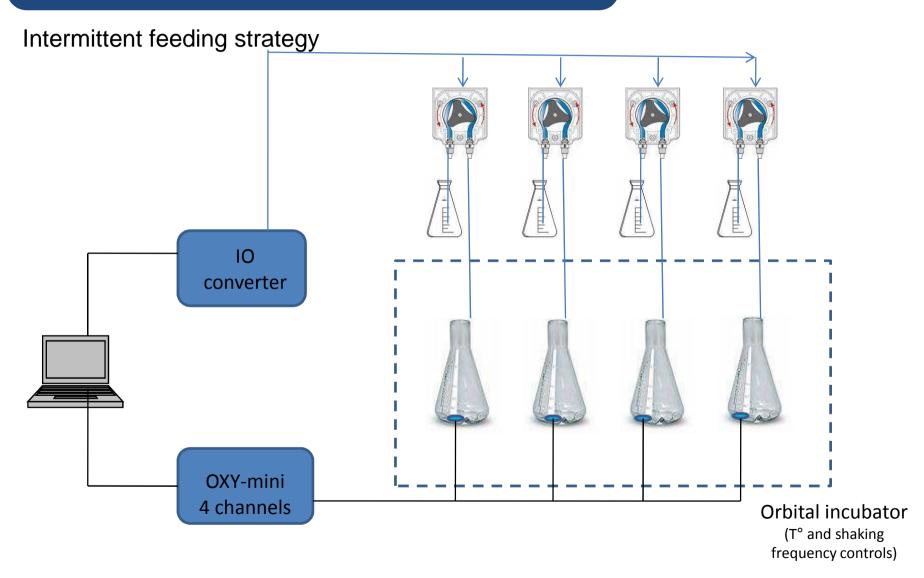
Screening among an E. coli GFP clones library Representativeness of shaken bioreactor

**Shake flask**: easy to handle, well suited to perform parallel cultures, but lack of representativeness compared to the performances of stirred bioreactors



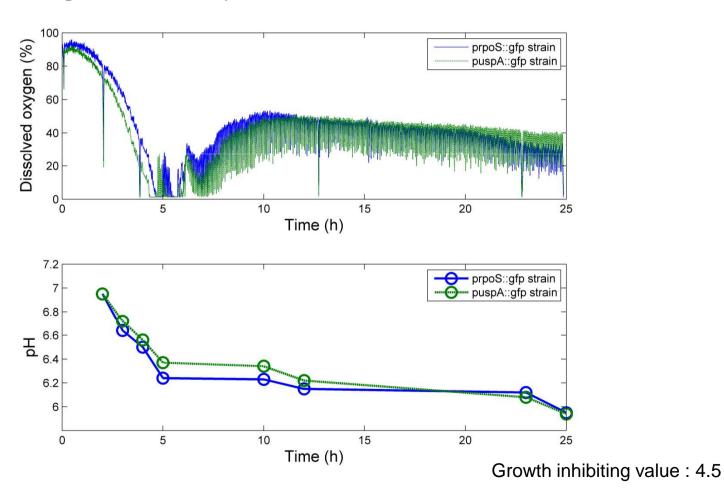


Screening among an E. coli GFP clones library Representativeness of shaken bioreactor

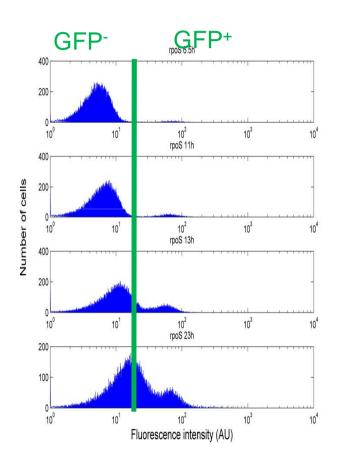


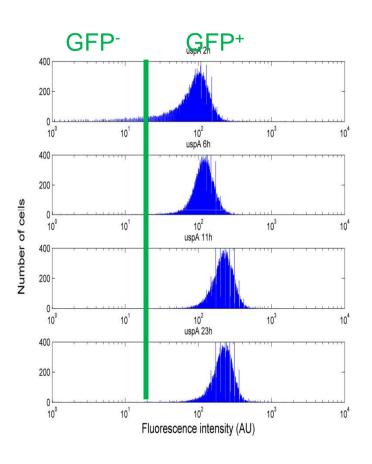
Screening among an E. coli GFP clones library Representativeness of shaken bioreactor

Cultures of GFP clones in shaken bioreactors (1L baffled shake flask : initial working volume : 200mL ; final working volume : 400 mL)



Screening among an E. coli GFP clones library Representativeness of shaken bioreactor



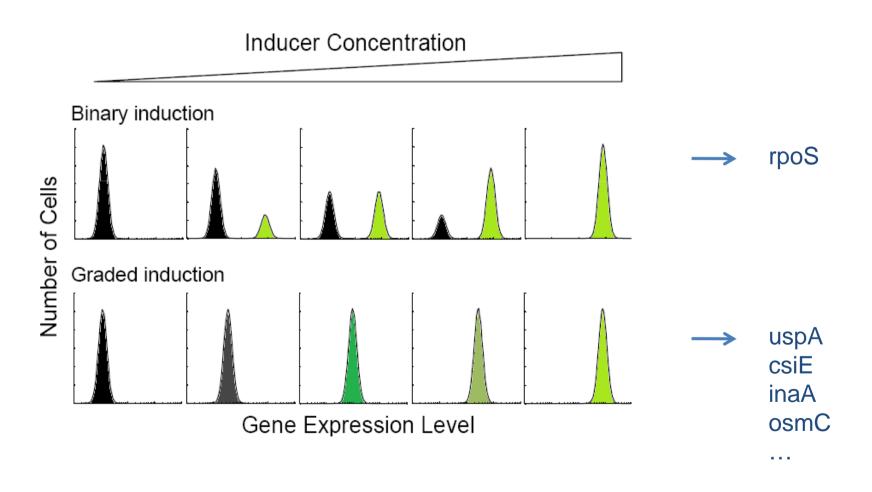


prpoS::gfp

puspA::gfp

Screening among an E. coli GFP clones library

Two modes of expression: binary or graded



Screening among an E. coli GFP clones library

Binary mode of gene expression → sources :

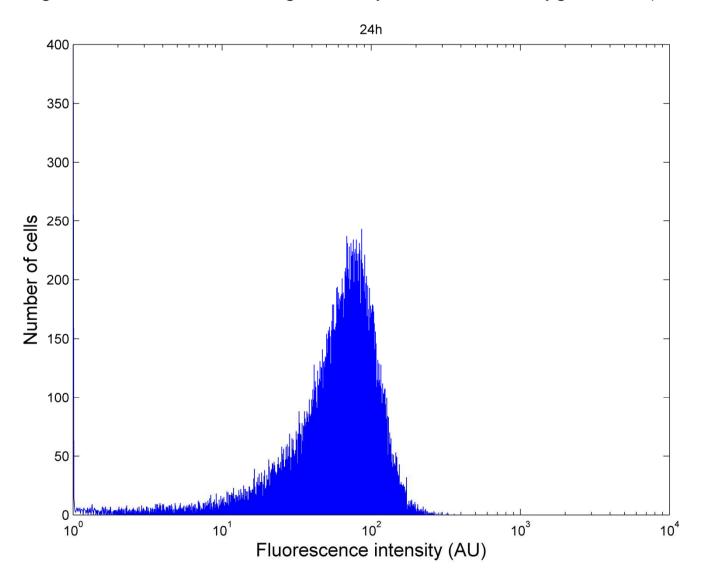
- -Short mRNA and protein half-lives
- -High sensitivity for the detection of the reporter protein

Generally not observed for GFP reporter system considering the high protein stability of this system compared with β-galactosidase and luciferase reporters

This mechanism of gene induction give rise to differentially expressed phenotypes at the protein level. Can potentially be used to gain more sensitivity about the impact of extracellular fluctuations

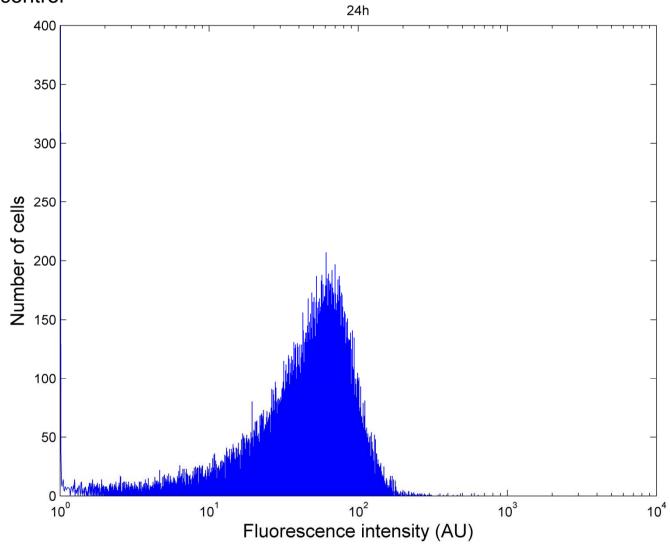
Behaviour of prpoS::gfp strain in fed-batch stirred bioreactor

Regulation of the addition of glucose by the dissolved oxygen level (SP = 30%) PID control



Behaviour of prpoS::gfp strain in fed-batch stirred bioreactor

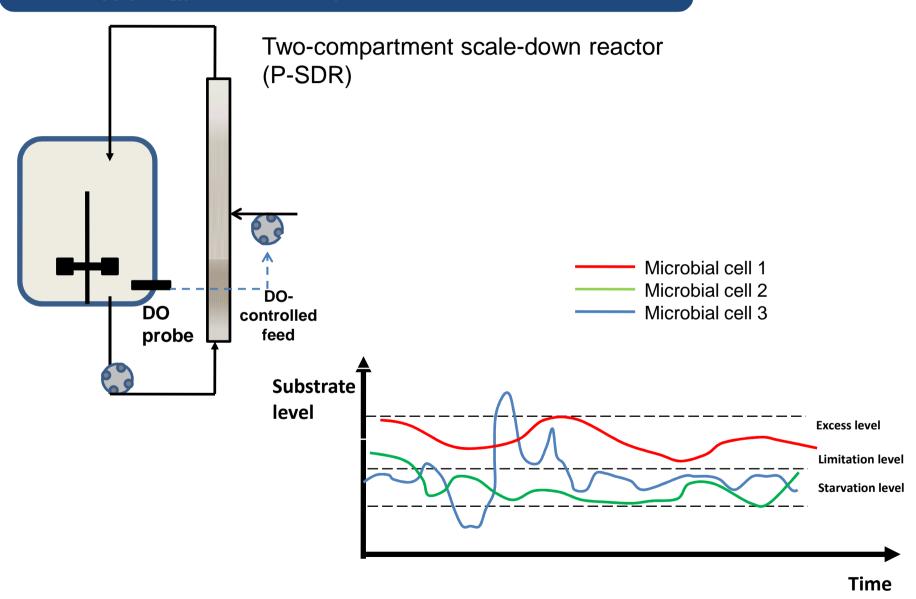
Regulation of the addition of glucose by the dissolved oxygen level (SP = 30%), ON/OFF control



Behaviour of prpoS::gfp strain in fed-batch stirred bioreactor

#### **Basic observations:**

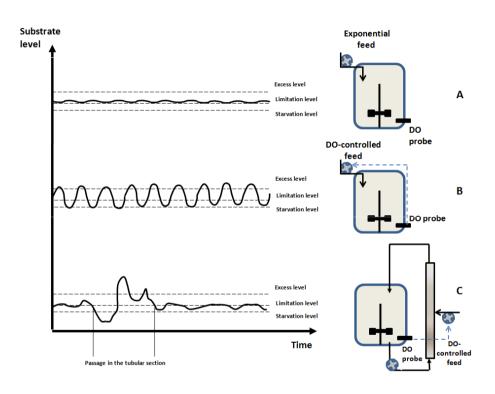
- Binary mode for GFP expression at the end of the batch phase and during the transition from batch to fed-batch phase
- After the induction of the major part of the population (all the cells are in the GFP+ state), graded mode of GFP expression is observed
- Successive glucose excess tends to slow down the binary expression phase

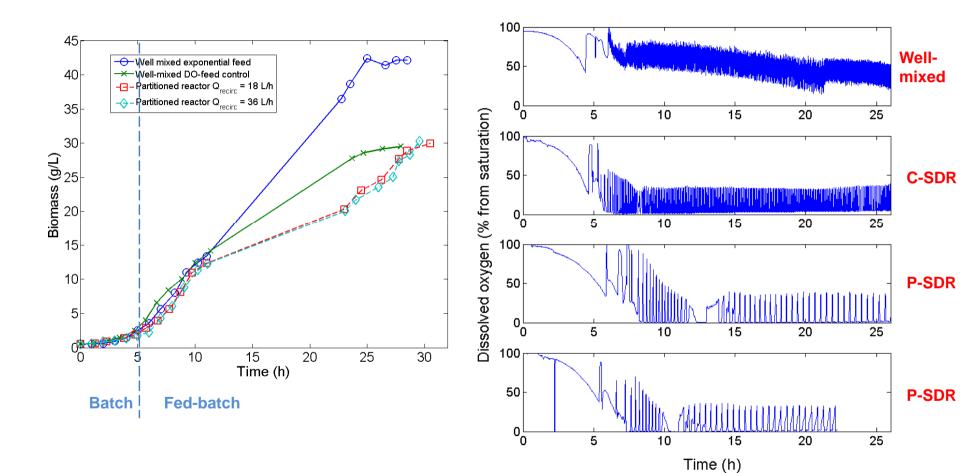


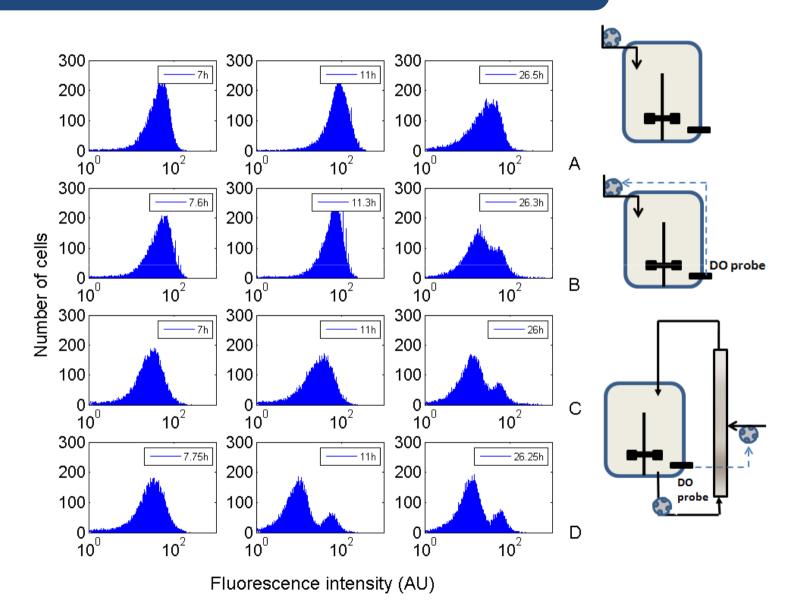
Behaviour of prpoS::gfp strain in two-compartment scale-down bioreactor

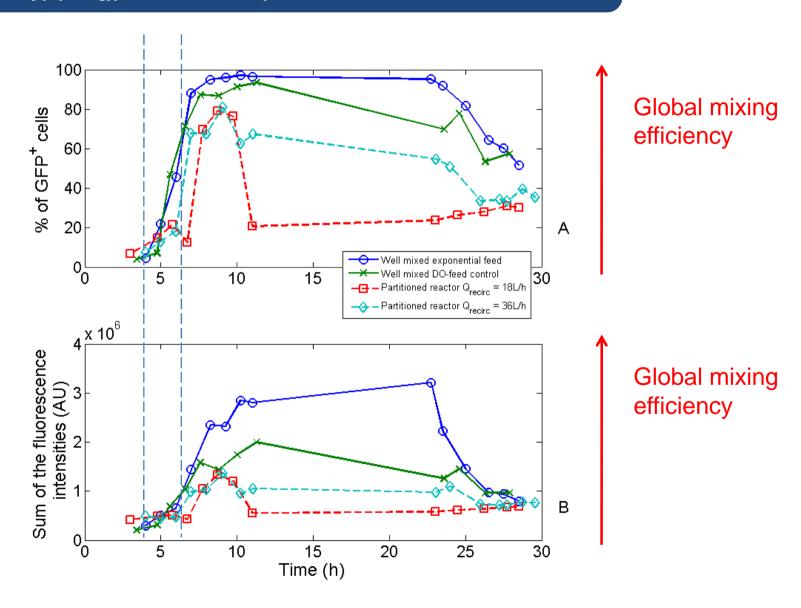
#### **Operating conditions:**

- Stirred bioreactor, working volume 10L
- Mineral medium, glucose as carbon source
- Fed-batch with exponential feed algorithm
- Scale-down approaches with DOcontrolled fed-batch and partitioned reactor



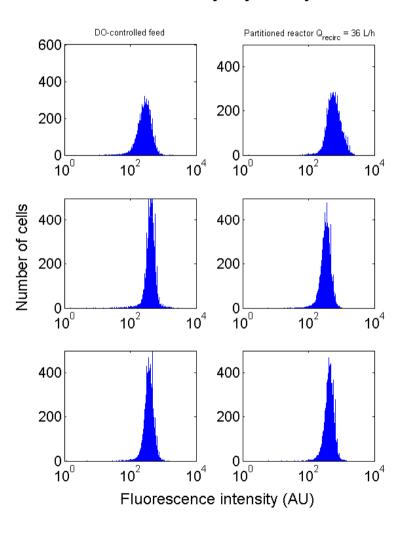




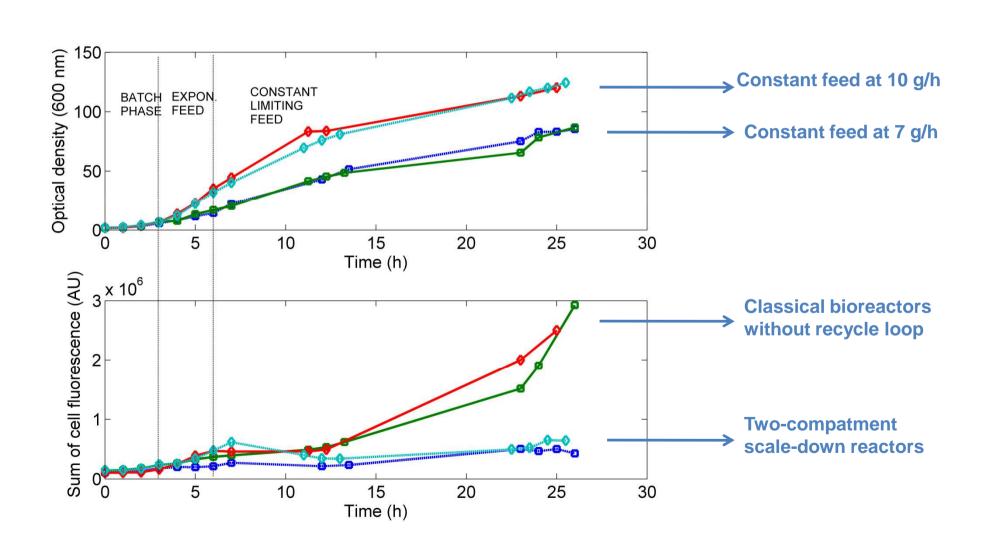


Behaviour of prpoS::gfp strain in two-compartment scale-down bioreactor

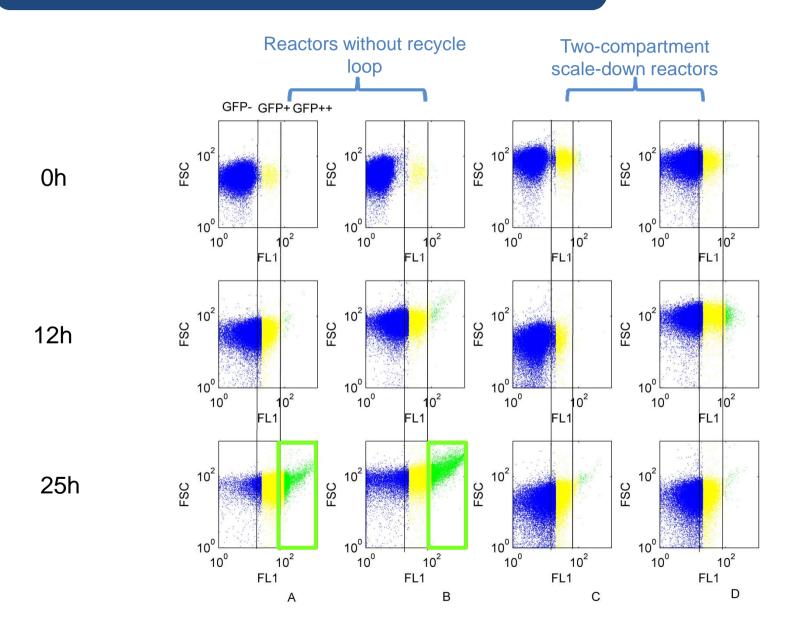
A pcya::GFPmut2 strain is not influenced by hydrodynamic conditions



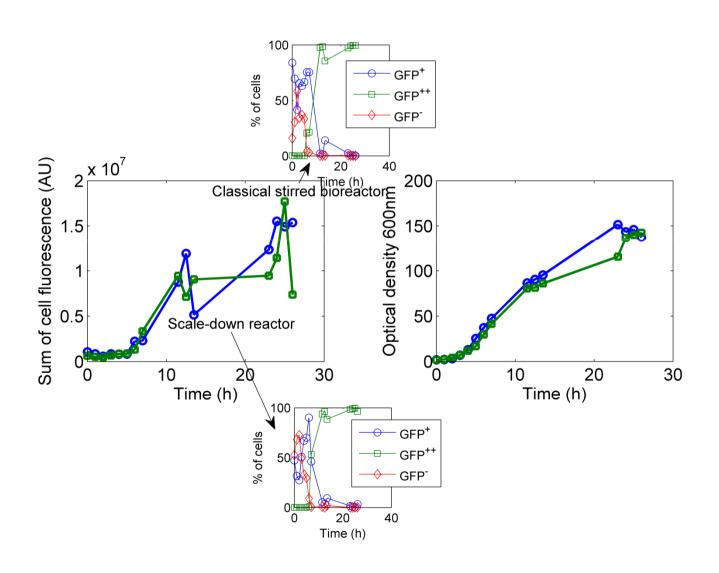
Cultures performed under constant glucose feed



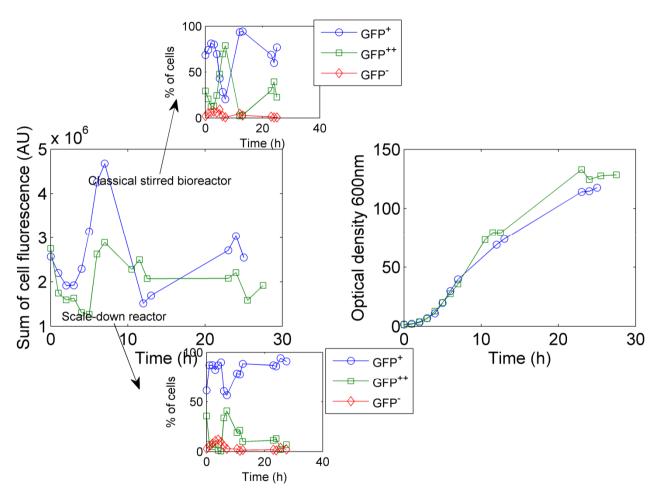
Cultures performed under constant glucose feed



Cultures performed under constant glucose feed : pcsiE::gfp strain



Cultures performed under constant glucose feed: puspA::gfp strain



To be validated by using a DO-controlled feed Prytz *et al* [2003] Biotech bioeng **83**:595-603

Synopsis: relation between GFP expression level and cell density

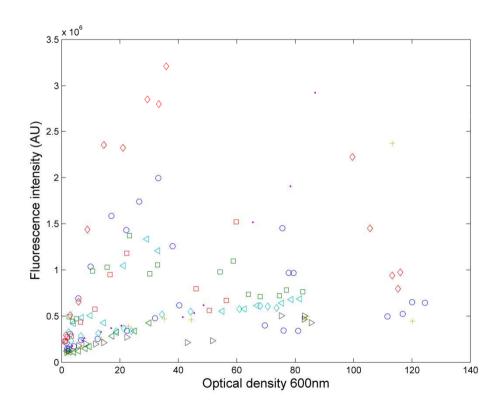
Two main mechanisms proposed to regulate rpoS in high cell density cultures:

- Cell density

DeLisa and Bentley [2002] Microbial cell factories, 1:5

- Decreasing growth rate

Ihssen and Egli [2004] Microbiology, 150:1637:1648



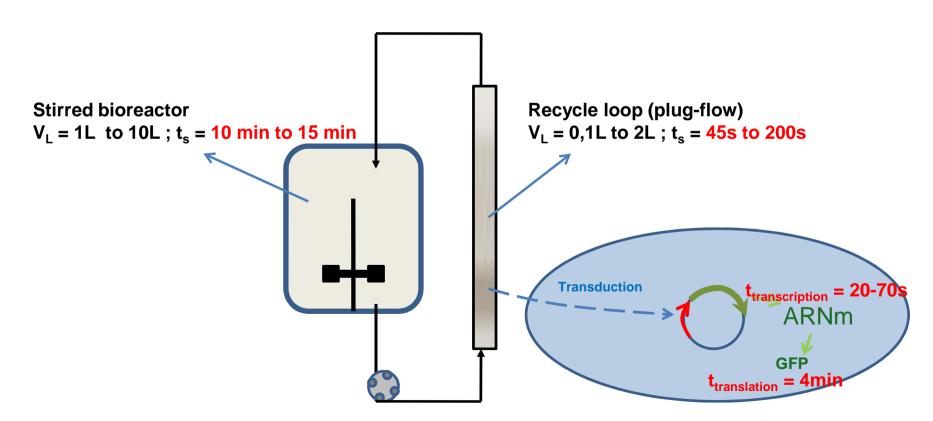
prpoS::GFP strains seems to react to the degree of homogeneity inside the bioreactor :

Homogenous reactor: GFP+

Inhomogenous reactor: GFP-

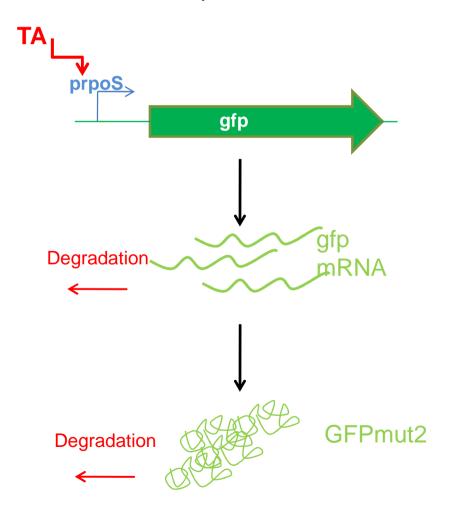
Two questions have to be raised:

- Flow cytometry combined with  $P_{stress}$ ::GFP expression  $\rightarrow$  impact of extrinsic fluctuations
  - What about the intrinsic fluctuations?
- Characteristic times of hydrodynamic mechanisms compared with those of the biological processes behind GFP synthesis



#### Complex phenomena:

- Two sources of noise (extrinsic and intrinsic)
- Very different characteristic time constants (physical and biological pocesses)
- $\rightarrow$  A model is required



$$\begin{array}{c} \overset{k_1}{\rightarrow} TA \\ TA + DNA \overset{k_2}{\rightarrow} TA\_DNA \\ TA\_DNA \overset{k_3}{\rightarrow} TA + DNA \\ TA \overset{k_4}{\rightarrow} \emptyset \\ TA\_DNA \overset{k_5}{\rightarrow} TA\_DNA + RNA \\ RNA \overset{k_6}{\rightarrow} RNA + GFP \\ RNA \overset{k_7}{\rightarrow} \emptyset \\ GFP \overset{k_8}{\rightarrow} \emptyset \end{array}$$

### Reaction scheme: **Exposure to** glucose excess $= f(t_m, t_c)$ $TA + DNA \xrightarrow{k_2} TA\_DNA$ $TA\_DNA \xrightarrow{k_3} TA + DNA$ $TA \stackrel{k_4}{\rightarrow} \emptyset$ $TA\_DNA \xrightarrow{k_s} TA\_DNA + RNA$ $RNA \stackrel{k_6}{\rightarrow} RNA + GFP$ $RNA \stackrel{k_7}{\rightarrow} \emptyset$ $GFP \stackrel{k_g}{\rightarrow} \emptyset$ **Generation time:** $k8 = log(2)/t_a$

#### ODEs system:

$$\frac{dTA}{dt} = k_1 - k_2.TA.DNA - k_4.TA + k_3.TA_DNA$$

$$\frac{dTA_DNA}{dt} = k_2.TA.DNA - k_5.TA_DNA - k_3.TA_DNA$$

$$\frac{dDNA}{dt} = k_3.TA_DNA - k_2.TA.DNA$$

$$\frac{dRNA}{dt} = k_5.TA_DNA - k_6.RNA - k_7.RNA$$

$$\frac{dGFP}{dt} = k_6.RNA - k_8.GFP$$

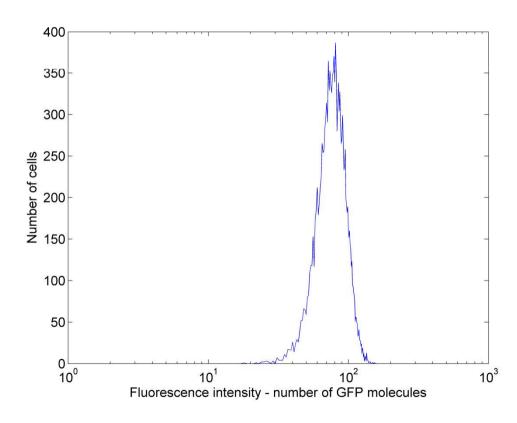
$$GFP_{steady-state} = RNA_{steady-state}. \left(\frac{k_6}{k_6}\right)$$

8 rates (including the characteristic time constants) to specify

These equations can be used in the classical deterministic formalism (ODEs solver), but more interestingly in the stochastic formalism :

Probablity that reaction  $\mu$  occurs at time  $\tau$  (Gillespie algorithm)

Gillespie [1977] J. of physical chemistry, 81:2340-2361



Example: simulation of 30,000 cells after 6 hours of induction

# Thank you

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