

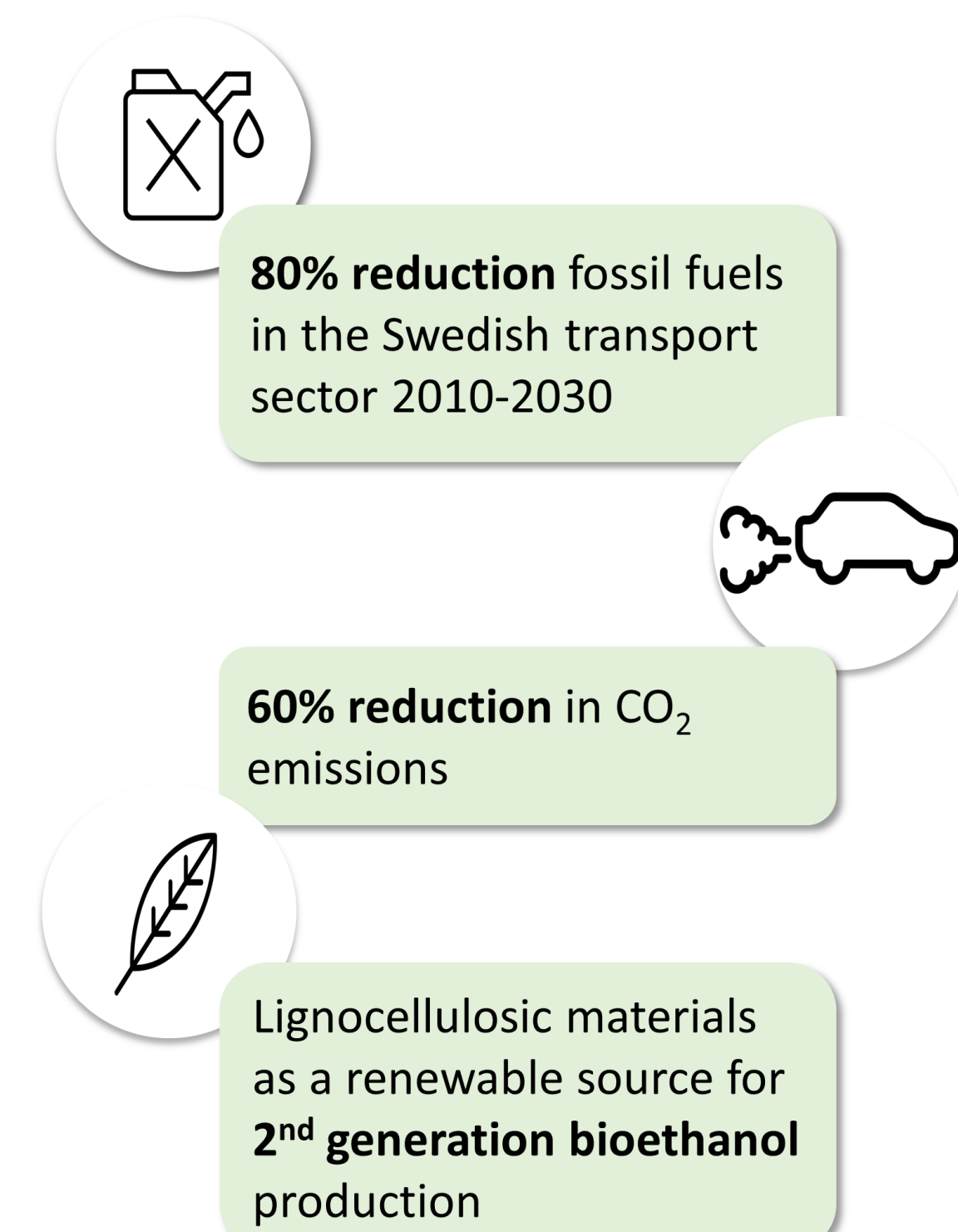
Novel methods for accelerating the development of more inhibitor tolerant yeast strains for cellulosic ethanol production

Elena Cámara, Ignis Trollmann, Lisbeth Olsson and Yvonne Nygård

Division of Industrial Biotechnology, Department of Biology and Biological Engineering - Chalmers University of Technology, Göteborg, Sweden
elenaca@chalmers.se

Background

Towards a fossil-free transport sector



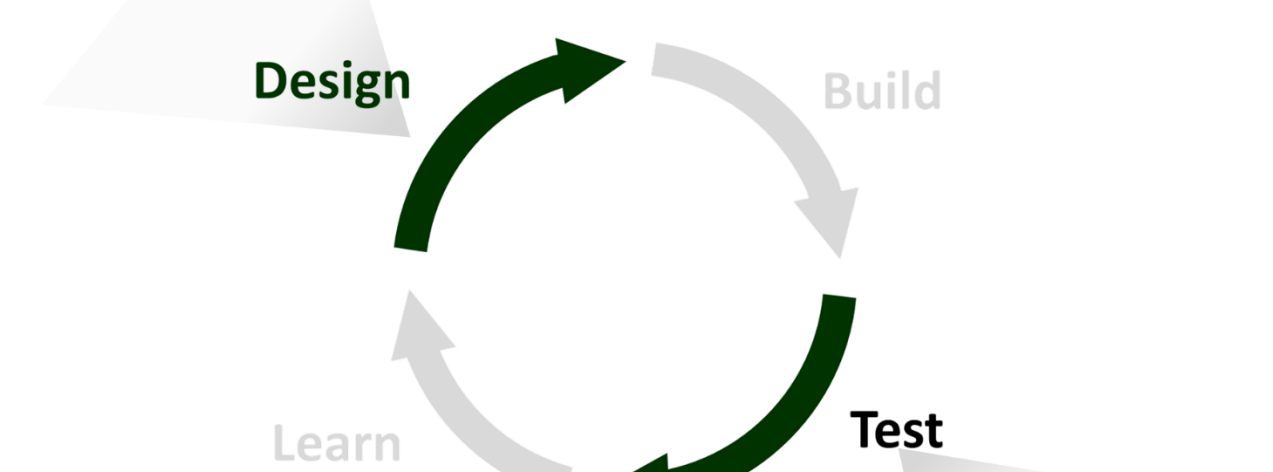
Saccharomyces cerevisiae as a bioethanol production host

- Engineered *S. cerevisiae* is able to ferment glucose and xylose for ethanol production.
- Lignocellulosic hydrolysates contains a broad range of inhibitors for yeast
- Inhibitor composition depends on the type of raw material and pretreatment
- An efficient genome editing strategy for engineering industrial yeast strains is needed

OBJECTIVE

To develop an efficient design-build-test-learn cycle for creating robust production strains

Use of CRISPR(i) based systems as a tool for studying the impact of genetic alterations



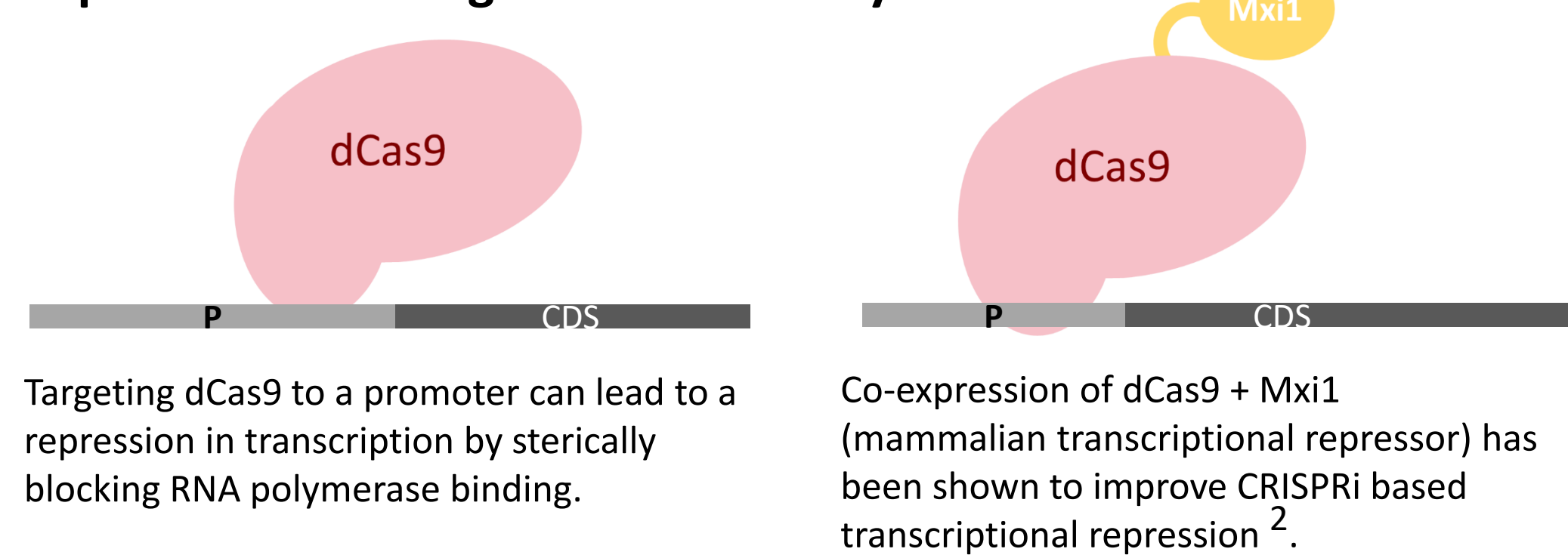
High-throughput analysis of yeast strains during fermentation in lignocellulosic hydrolysates

In order to develop inhibitor tolerant strains, the expression of genes involved in tolerance will be systematically altered using **CRISPR interference (CRISPRi)**. This methodology uses a catalytically inactive, dead Cas9 (dCas9).

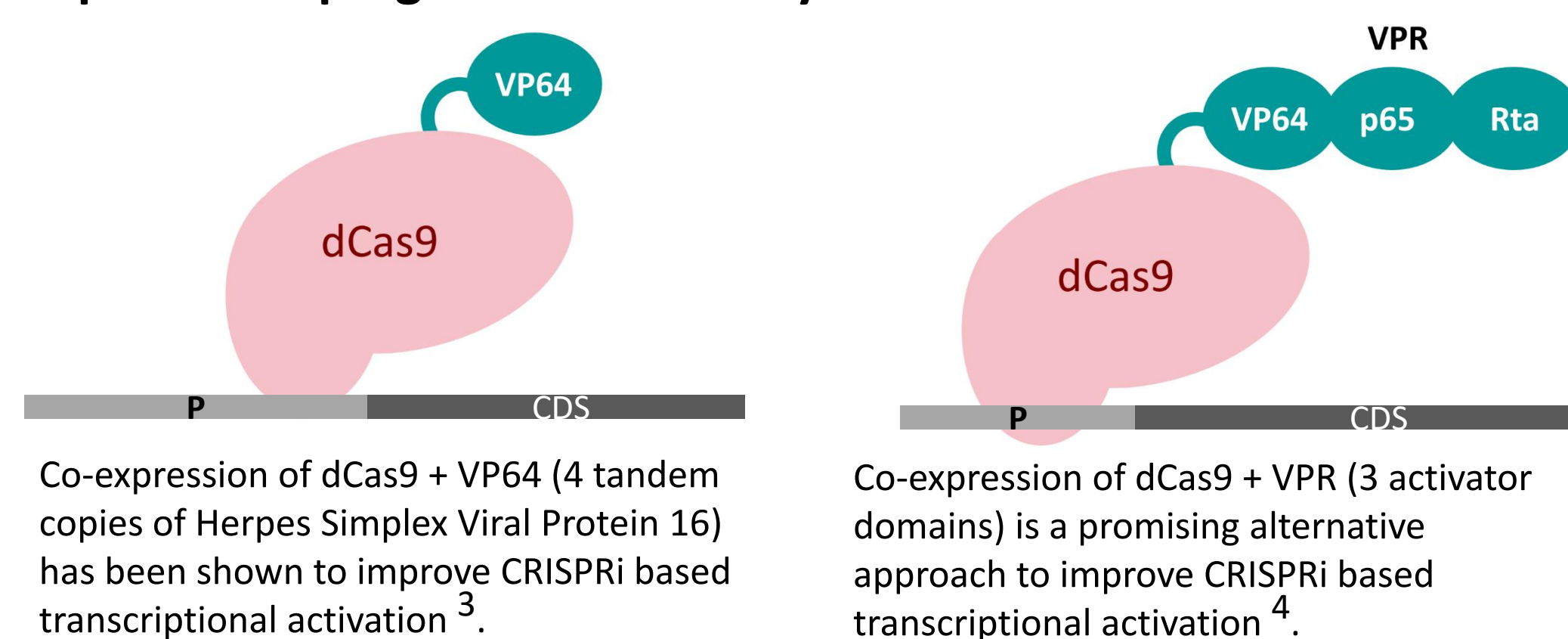
Vectors expressing dCas9+repressor/activator constructs have been constructed using the Moclo Yeast Toolkit ¹.

CRISPR will be used to stablish permanently gene modifications successfully tested with CRISPRi.

Expression downregulation driven by:

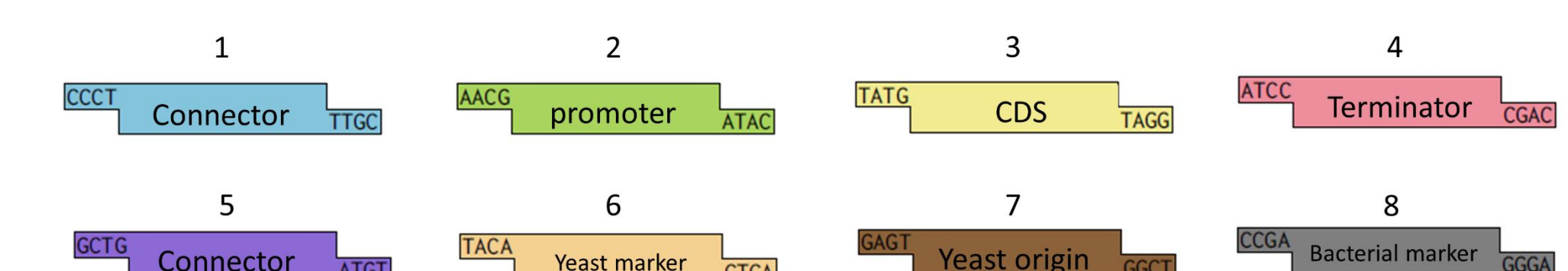


Expression upregulation driven by:

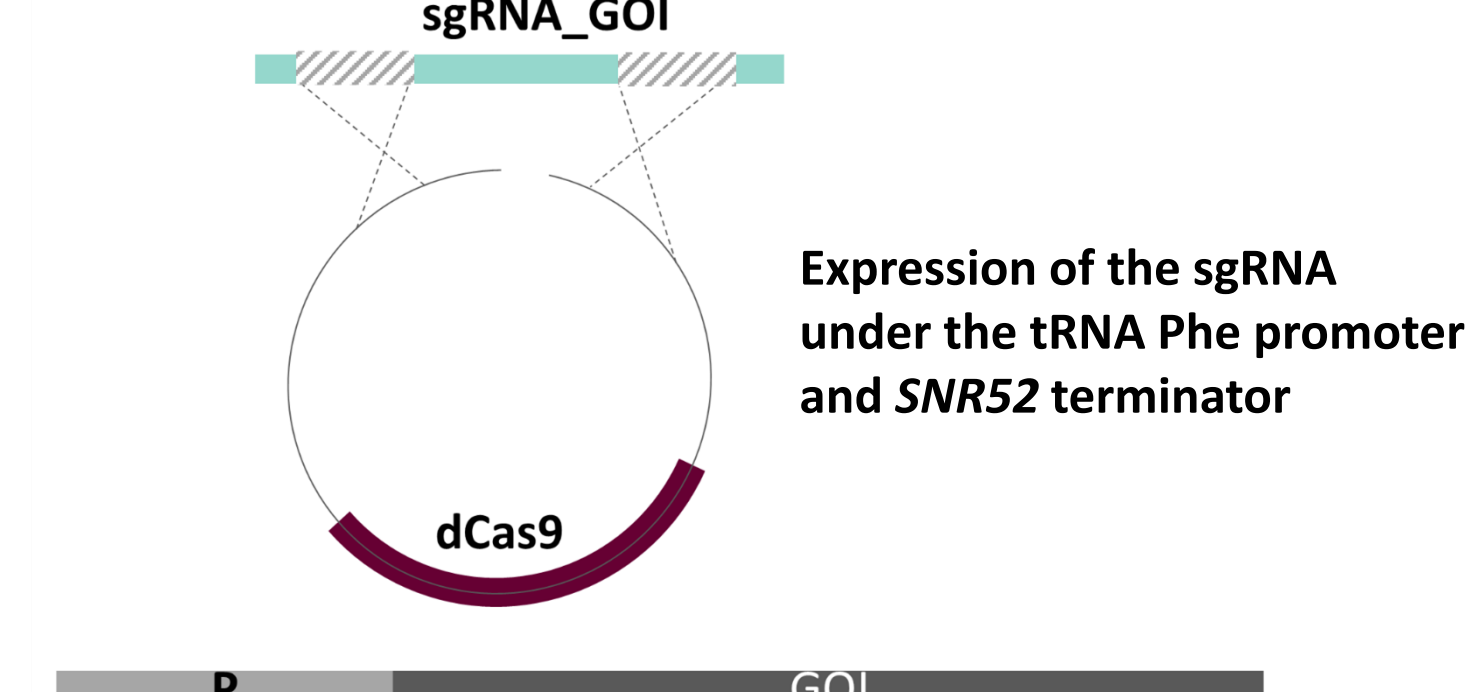


Vector construction

1. Assembly of parts to obtain vectors expressing a CDS or a domain of interest (dCas9 or activator/repressor, respectively).



2. Assembly of a vector containing multiple transcription units, expressing dCas9 + activator/repressor and a cassette for sgRNA expression. The sgRNA is assembly into the vector through *in vivo* homologous recombination.



PHASE 2 – Establishment of a high-throughput screening platform

In order to analyse a large number of strains a rapid, high-throughput system to characterise the performance of new strains in lignocellulosic hydrolysates is essential.

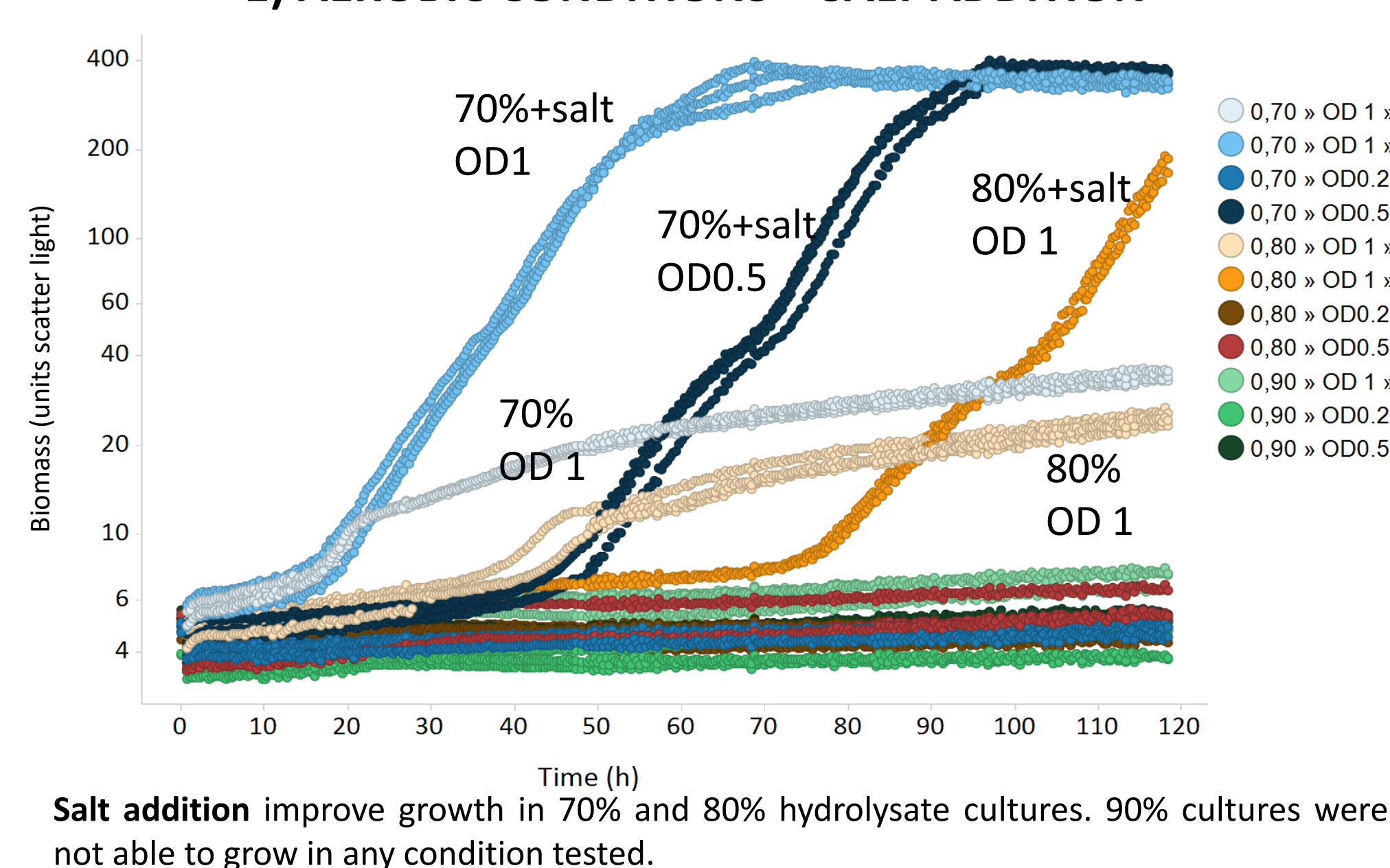
Various culture conditions and parameters have been tested in the Biolector® microbioreactor platform:

- Lignocellulose hydrolysate concentration (% v/v)
- Size of inoculum
- Addition of salt to the medium
- Preculture adaptation
- Aerobic / anaerobic conditions

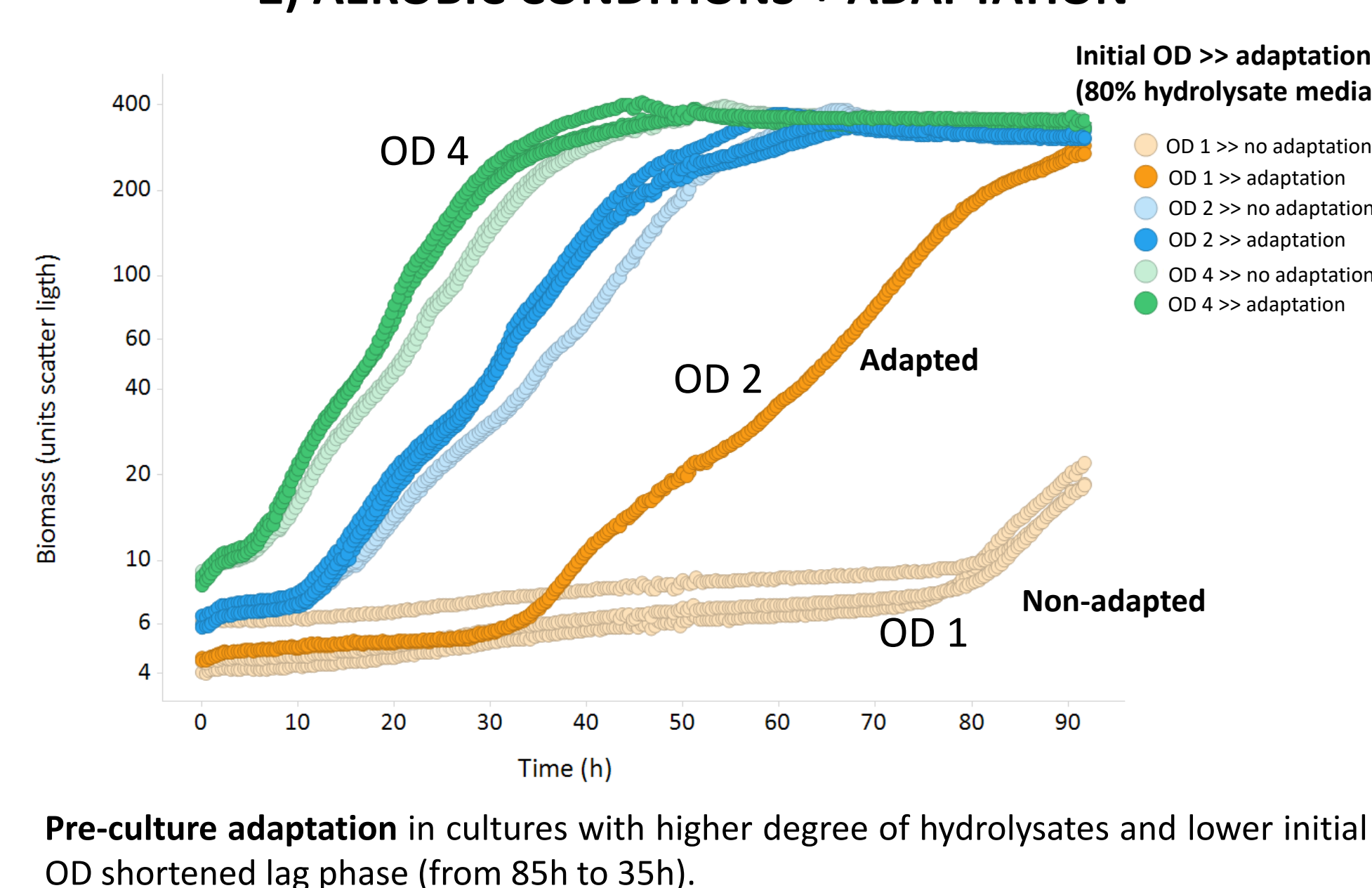
MATERIALS AND METHODS

- Culture volume: 1 mL
- Polyloid industrial strain
- Media: Wheat straw hydrolysate with YPD supplementation (final sugar concentration: 60 g/L glucose + 30 g/L xylose), pH 5.5
- Adaptation in anaerobic conditions was performed by addition of different lignocellulosic hydrolysate concentration (0%, 14% and 40%) in the YPD preculture media, with an overnight incubation

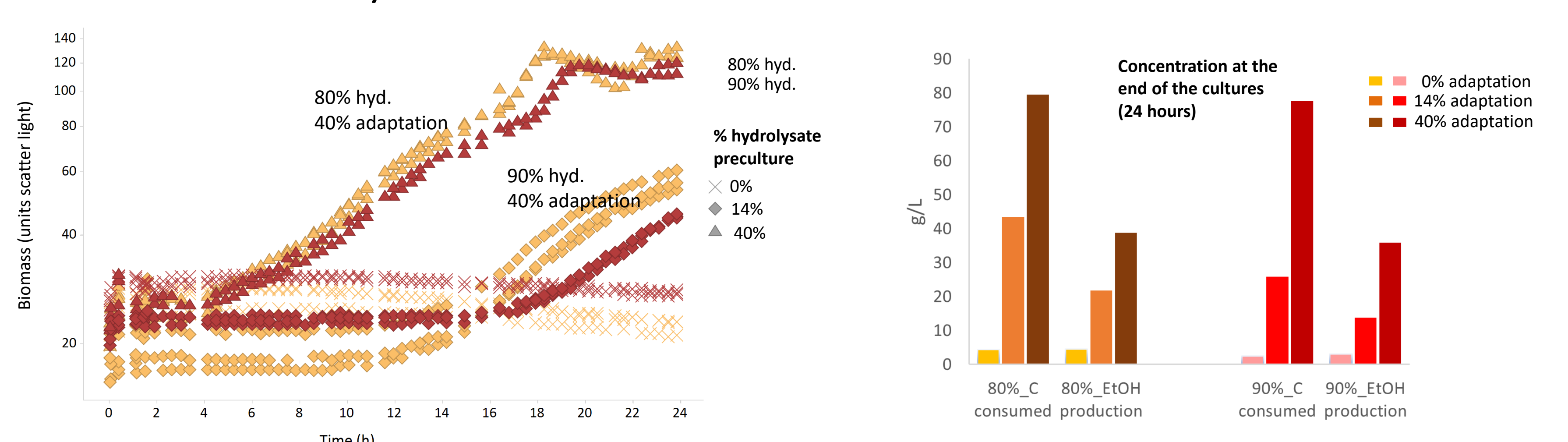
1) AEROBIC CONDITIONS + SALT ADDITION



2) AEROBIC CONDITIONS + ADAPTATION



3) ANAEROBIC CONDITIONS + ADAPTATION LEVELS



Conclusions

- An efficient platform for high-throughput screening of yeast directly in lignocellulosic hydrolysates was established
- Preliminary results showed a reliable correlation in terms of growth with shake flask cultures

References

- Lee, M. E. *et al.* Characterized Yeast Toolkit for Modular, Multipart Assembly. *ACS Synth. Biol.* **4**, 975–986 (2015).
- Gilbert, L. A. *et al.* CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. *Cell* **154**, 442–451 (2013).
- Naranjo, S. *et al.* Dissecting the Genetic Basis of a Complex cis - Regulatory Adaptation. *Plos* **1**–19 (2015).
- Chavez, A. *et al.* Highly efficient Cas9-mediated transcriptional programming. *Nat. Methods* **12**, 326–328 (2015).