

# NOVEL EVOLVED *YARROWIA LIPOLYTICA* STRAINS FOR ENHANCED GROWTH AND LIPID CONTENT UNDER HIGH CONCENTRATIONS OF CRUDE GLYCEROL

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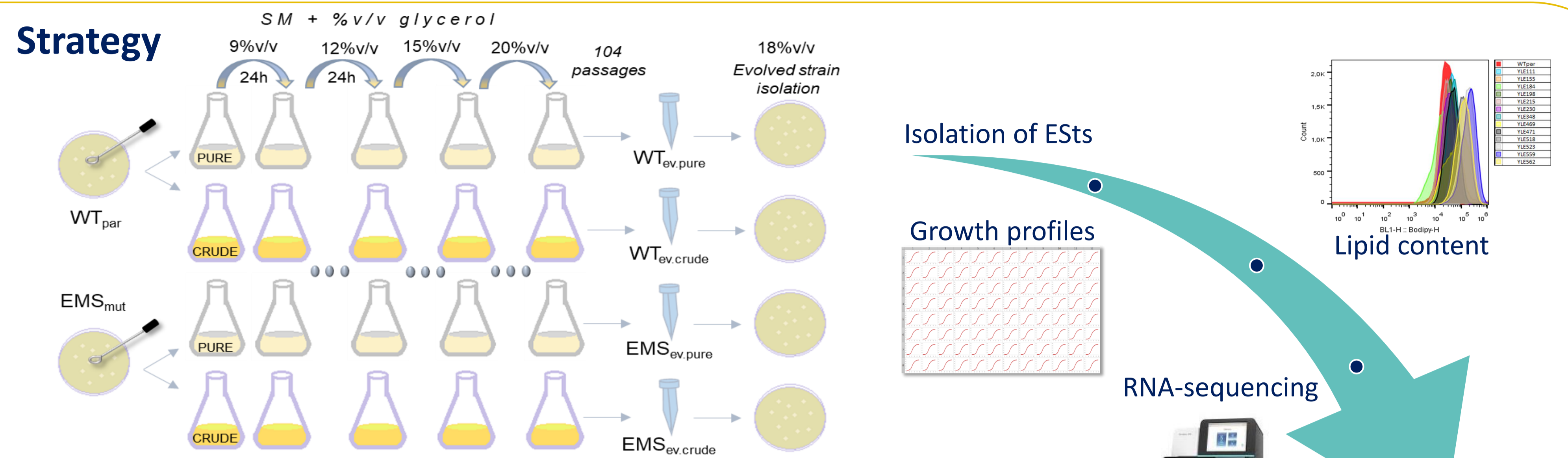
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## Introduction

- Among the oleaginous yeasts, *Yarrowia lipolytica* appears to be a **single-cell oil producer** with great potential.
- Crude glycerol**, derived from biodiesel industry, can be **valorized** as carbon source to develop a **sustainable process** for single-cell oil production.
- Adaptive laboratory evolution (ALE) is employed to **improve the fitness** of *Y. lipolytica* MUCL 28849 while the metabolism rewires under **high concentrations** of pure (PG) and crude glycerol (CrG).
- Dry biomass** and **lipid** concentration of Evolved Strains (ESTs) are evaluated and superior ESTs are studied through **RNA sequencing**.

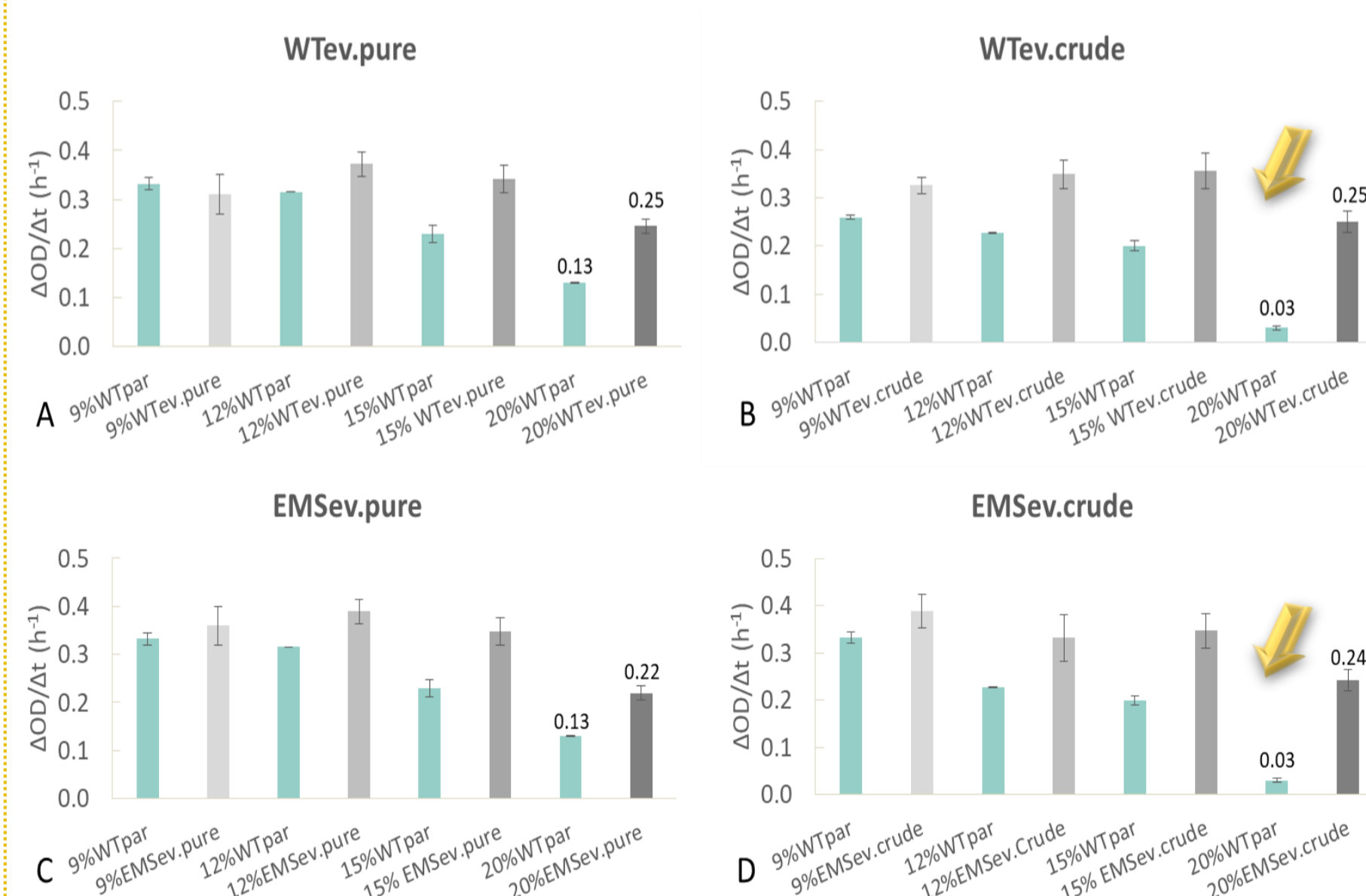
## Strategy



**Figure 1.** Schematic representation of ALE of the yeast *Yarrowia lipolytica*. Four ALE strategies were designed to increase biomass and lipid formation under high Pure Glycerol (PG) and Crude Glycerol (CrG) concentrations. Starting point: WT<sub>par</sub> *Y.lipolytica* 28849 parental strain; EMS<sub>mut</sub> after random chemical mutagenesis with methanesulfonate (EMS) exposure.

## Results & Discussion

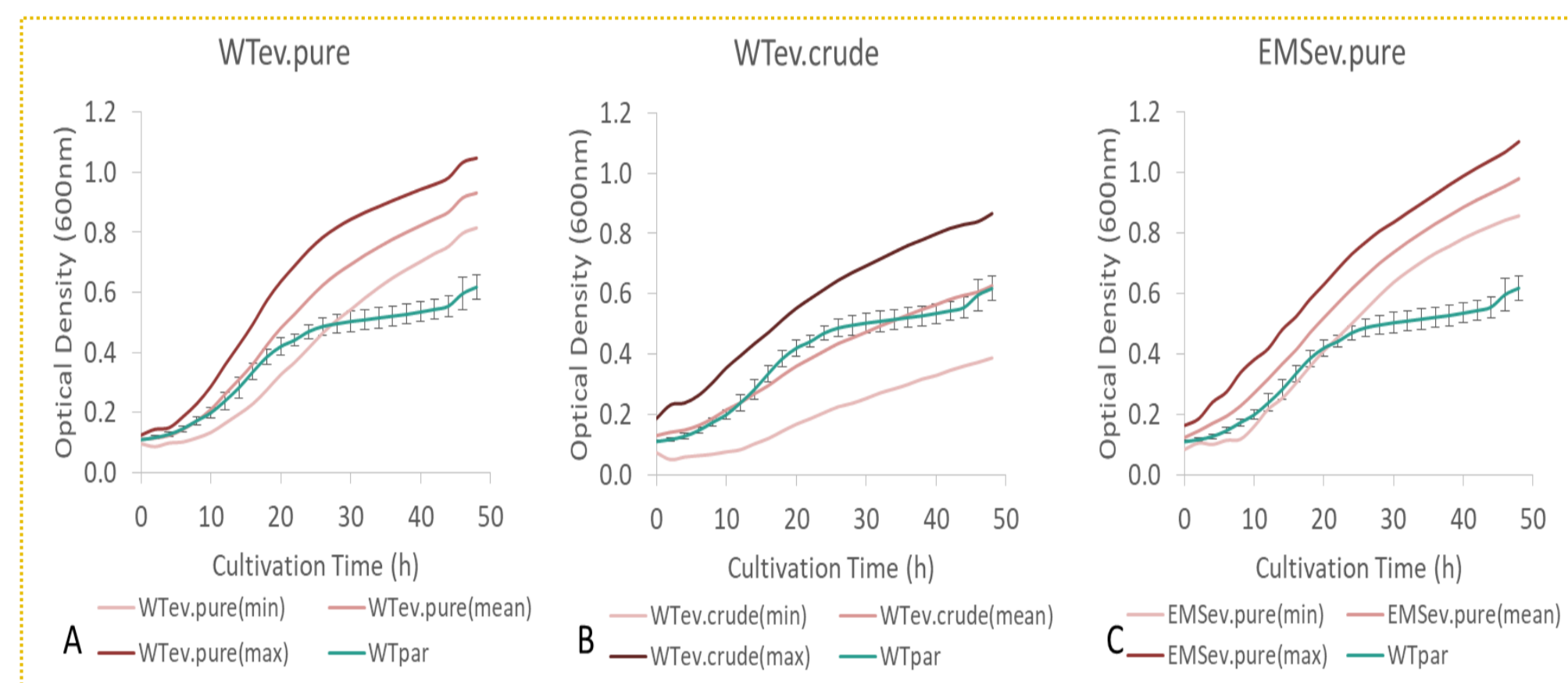
### Monitoring of ALE



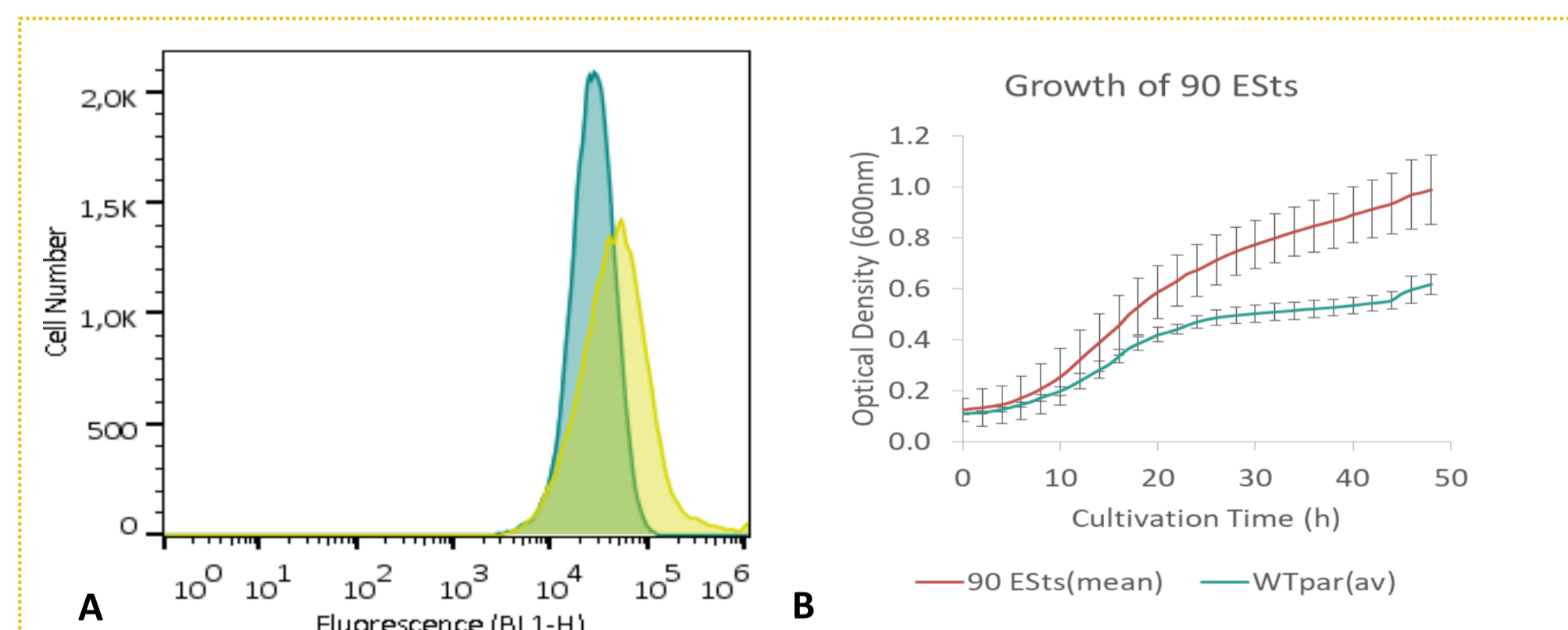
**Figure 2.**  $\Delta OD/\Delta t$  rate during ALE experiment for increasing PG and CrG concentrations. Each graph corresponds to a different population (A. WT<sub>ev.pure</sub>; B. WT<sub>ev.crude</sub>; C. EMS<sub>ev.pure</sub>; D. EMS<sub>ev.crude</sub>); gray shades stand for different glycerol concentrations. Parental strain values are shown in green and error bars indicate standard deviation.

- $\Delta OD_{600nm}/\Delta t$  rate of all Evolved populations (EPs) increased.
- Stable phenotype** was reached for all EPs.

### ESTs Phenotype & Selection

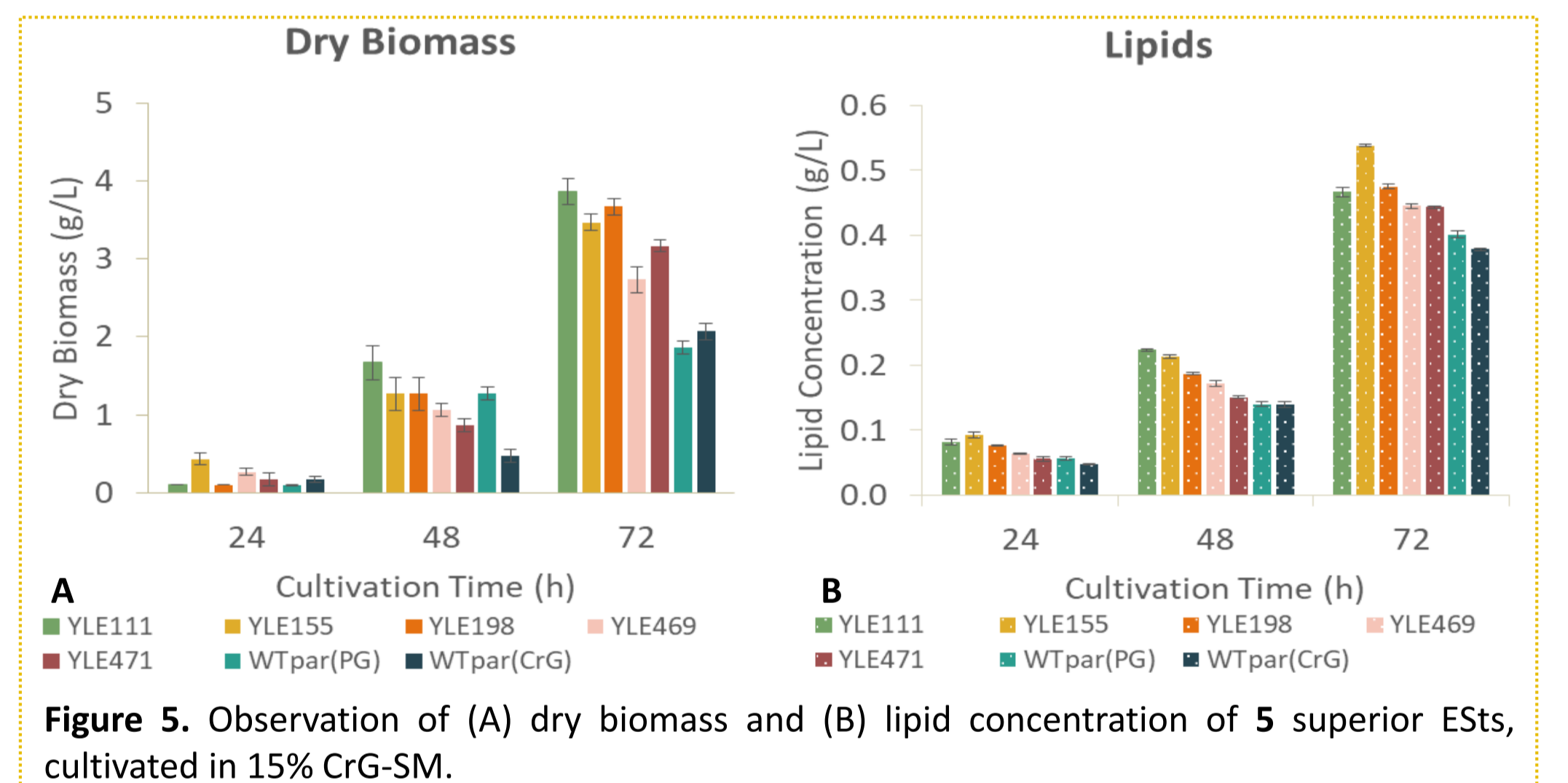


**Figure 3.** Growth profiles of 450 isolated ESTs cultivated in 0.2 mL 15% v/v PG-Synthetic Medium (SM). Graphs depict the average, min and max growth curve of a. WT<sub>ev.pure</sub>, n = 297; b. WT<sub>ev.crude</sub>, n = 53; c. EMS<sub>ev.pure</sub>, n = 100.



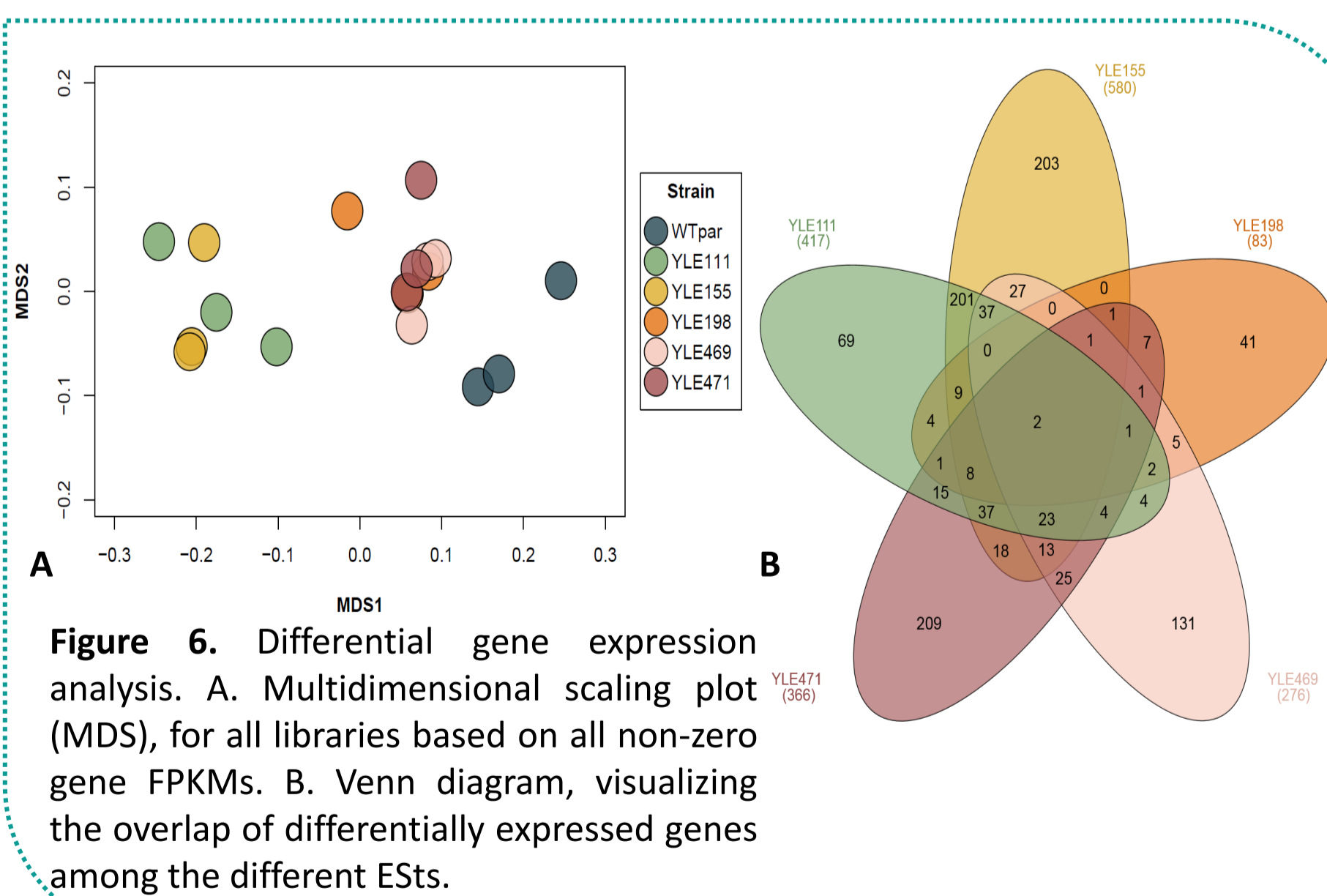
**Figure 4.** A. Comparison of lipid fluorescence and distribution per cell, between YLE155 (green) and WT<sub>par</sub> (blue), using flow cytometry and bodipy dye (493/503nm). B. Growth profiles of 90 isolated ESTs cultivated in 0.2 mL 15% v/v PG-SM. Graph depicts the average growth curve of 58 WT<sub>ev.pure</sub> ESTs, 20 WT<sub>ev.crude</sub> ESTs, and 12 EMS<sub>ev.pure</sub> ESTs.

- ESTs of WT<sub>ev.pure</sub> and EMS<sub>ev.pure</sub> showed from 1.5 to 2-fold higher biomass concentration at 48h, compared to WT<sub>par</sub>.
- Growth profiling differences of ESTs and cell observation through flow cytometry indicate the presence of heterogeneity.
- Multiple selection steps resulted in 5 superior ESTs with enhanced biomass formation while lipid content was slightly increased.
- Culture of YLE155 (in 15%v/v CrG-SM) reached up to 2.4-fold increase of dry biomass in the first 24h.

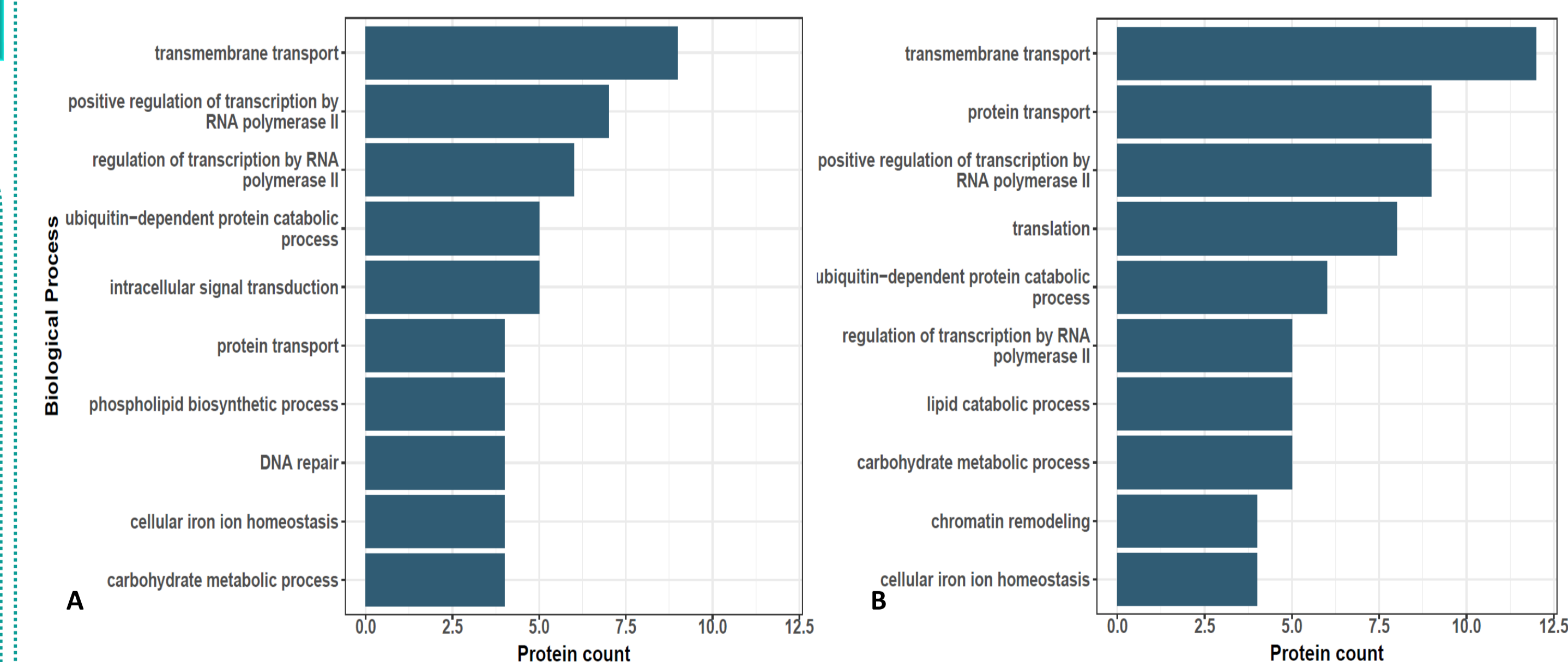


**Figure 5.** Observation of (A) dry biomass and (B) lipid concentration of 5 superior ESTs, cultivated in 15% CrG-SM.

### Differential Gene Expression



**Figure 6.** Differential gene expression analysis. A. Multidimensional scaling plot (MDS), for all libraries based on all non-zero gene FPKMs. B. Venn diagram, visualizing the overlap of differentially expressed genes among the different ESTs.



**Figure 7.** Abundance levels of the most abundant gene ontology (GO) - biological process (BP) terms associated with the differentially expressed proteins in A. YLE111 and B. YLE155.

- Gene ontology annotation** of all 5 ESTs (focused on BP) showed that most differentially expressed (DE) proteins were related to **membrane transport activation**.
- Transcriptome analysis revealed significant differential expression compared to WT<sub>par</sub>, especially in YLE111 and YLE155 ESTs with 417 and 580 DE genes, respectively.

## Conclusions

- Utilization of crude glycerol was favored by applying ALE while growth profiles of ESTs revealed phenotype enhancement in terms of biomass formation.
- Both flow cytometry and lipid concentration analysis verified that intracellular lipid levels of ESTs were slightly increased.
- Initial changes in all derived ESTs affected nucleosomal structure and regulation of transcription. In the more differentiated ESTs, these changes globally affected membrane transport and protein transport processes.
- Gene ontology annotation analysis showed a similar trend in all ESTs even though they originated from different ALE strategies.
- Fermentations in a lab scale bioreactor are currently conducted to determine biomass and lipid yields between selected ESTs and parental strain.

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