



Aalto University  
School of Chemical  
Engineering

# Yeast 2.0

*Group 2 – Pinja, Sanna, Selina*

# Content

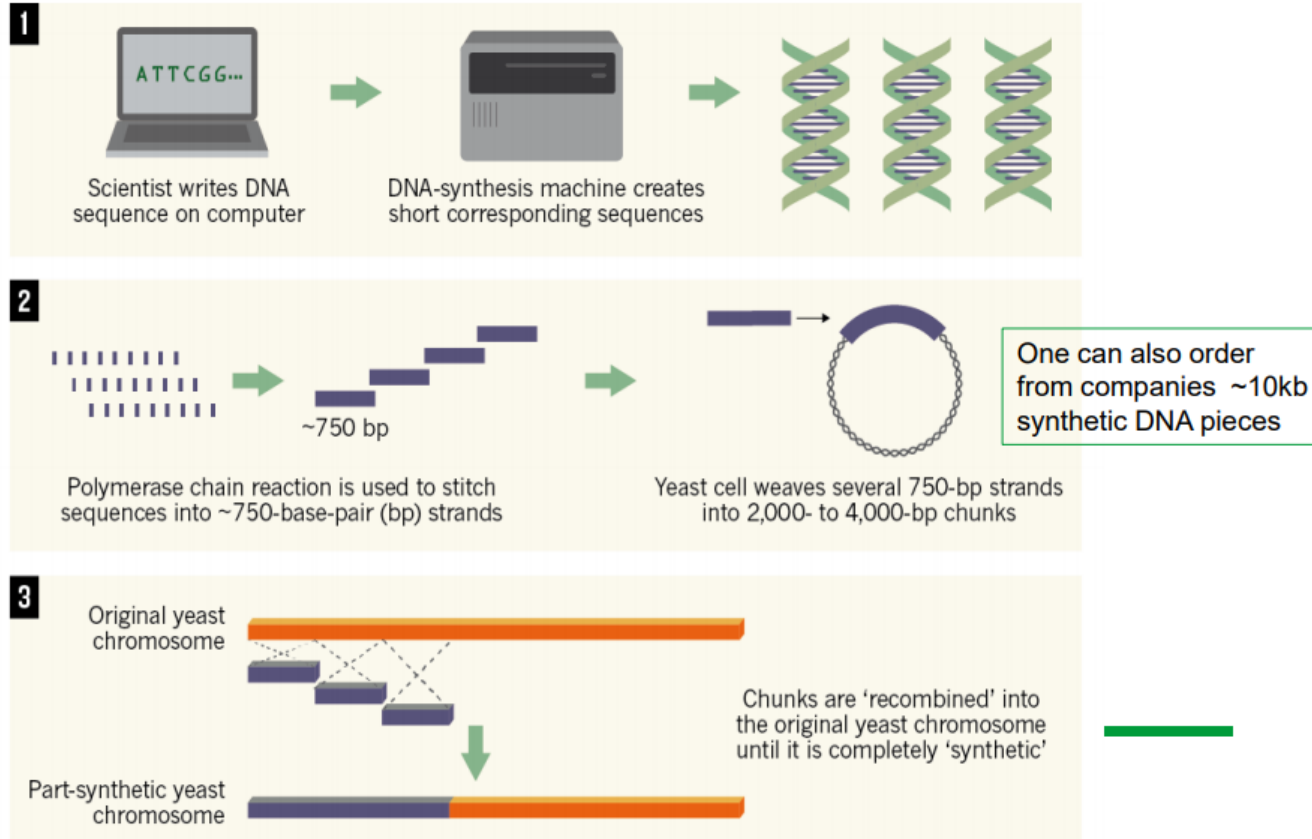
- Introduction
- Construction of yeast 2.0
- Synthetic design and construction of a ~30kb region ('Megachunk')
- Software
- Wet Lab
- SCRaMbLE mechanism
- References

# Introduction

- Synthetic yeast 2.0 is the first attempt to build an artificial yeast (*S. cerevisiae*) genome from a scratch. The synthetic DNA is introduced to the wild-type genome in 30-60 kb pieces by replacing sequences.
- It is called synthetic because all the original pieces are replaced with synthetic ones.
- Alterations that are done: PCR-Tags are incorporated, telomeres are synthesized, introns and non-essential genes are removed, stop codon TAG is replaced with TAA, transposons are deleted, tRNA genes are relocated

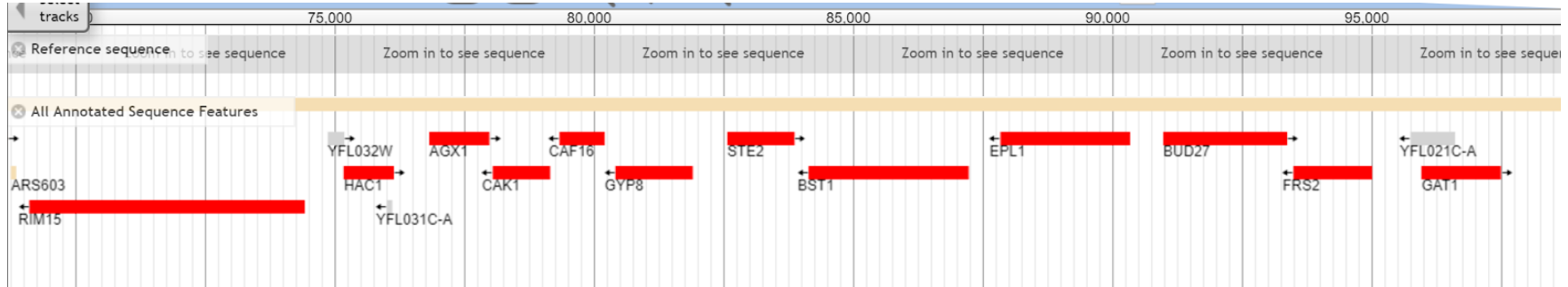
- Yeast 2.0 can be used to answer many questions about chromosomes, genomes structure and evolution, RNA splicing, etc...
- Yeast 2.0 can be industrially significant. It can be genetically engineered to produce useful compounds in greater quantities and to have a better tolerance for stress factors (e.g. pH, temperature, pressure...)
- The artificial yeast could be used to produce biofuels better. This could happen by adding genes to the genome that enhances the production.

# Construction of Yeast 2.0



# Synthetic design of a ~30kb region ('Megachunk')

chrVI:68657..98398 (29.74 Kb)



**Essential genes :** CAK1, EPL1, FRS2

**Non - essential genes:** RIM15, HAC1, AGX1, CAF16, GYP8, STE2, BST1, BUD27, GAT1

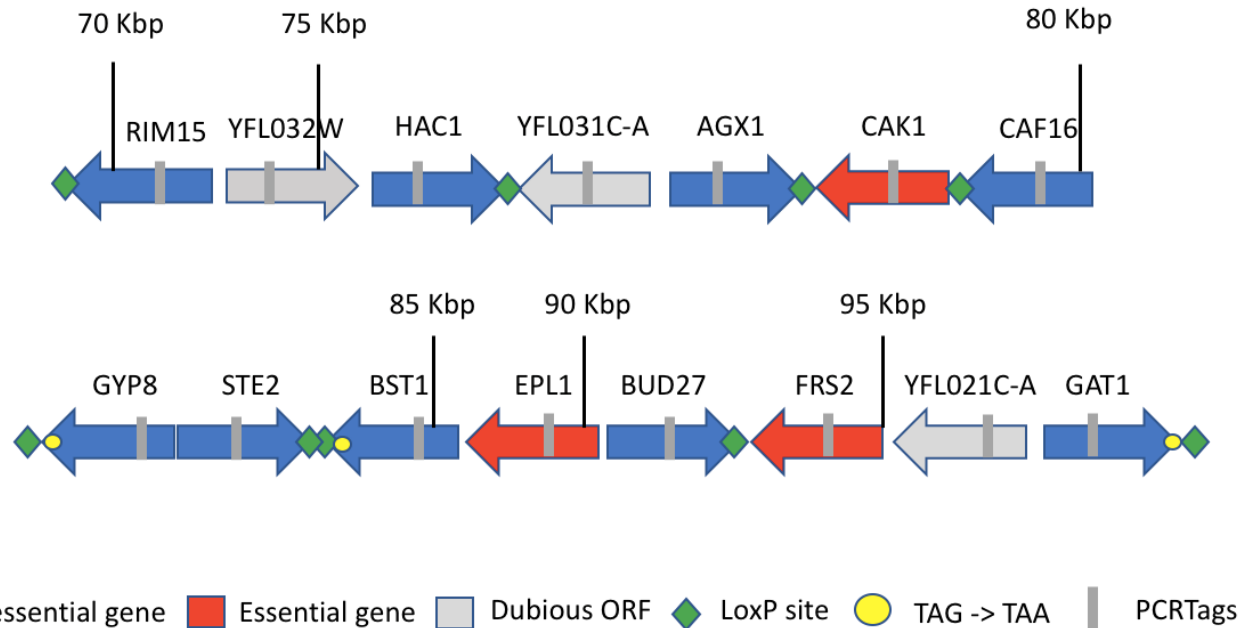
**Dubious ORFs:** YFL031C-A, YFL021C-A

**Autonomously replicating sequence** ARS603

**No introns in this region, no tRNA genes and no transposon**

# Our design of a ~30kb region ('Megachunk')

chrVI:68657..98398 (29.74 Kb)



# Softwares

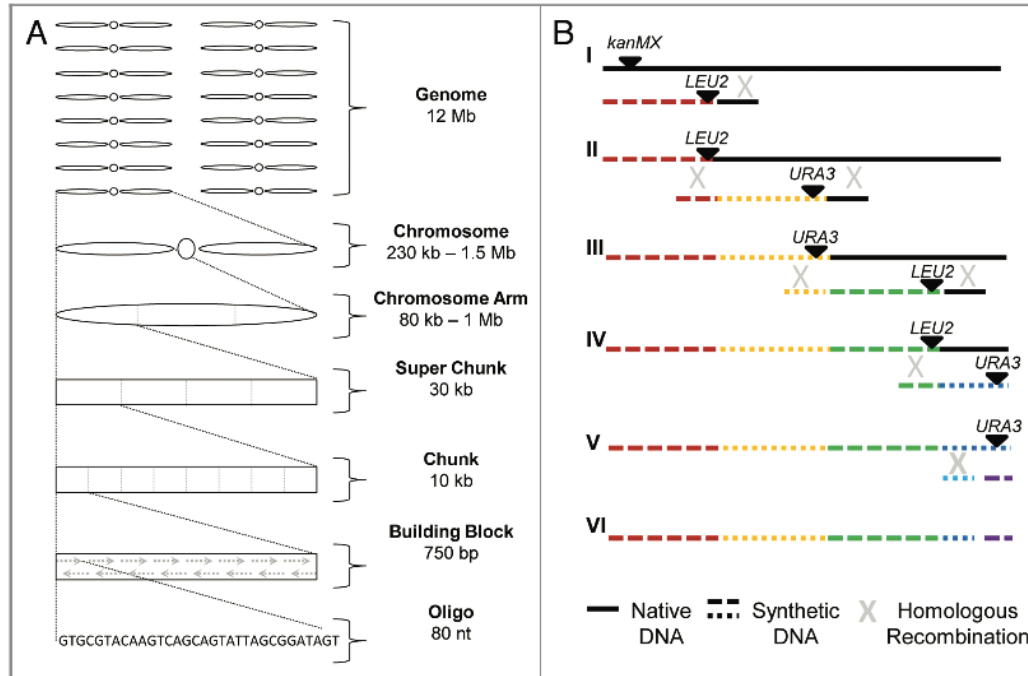
- *Saccharomyces cerevisiae* genome database (SGD)
  - <https://www.yeastgenome.org/>
- SnapGene (planning, visualizing, documenting of molecular biology procedures)
  - <https://www.snapgene.com/>
- ApE - a plasmid editor (free download from multiple websites)
- BioStudio (eukaryotic genome design)
- Database of essential genes
  - <http://www.essentialgene.org/>



# Wet Lab

- Hierarchical assembly plan:
- Construction of building blocks from oligos or buying ready-made chunks
- Smaller chunks are assembled into 'megachunks' (30-60 kb) through restriction enzymes and subsequent ligation
- Integration of 'megachunks' into yeast genome via homologous recombination
- Alternation between two selection markers (LEU2 and URA3)

# Wet Lab

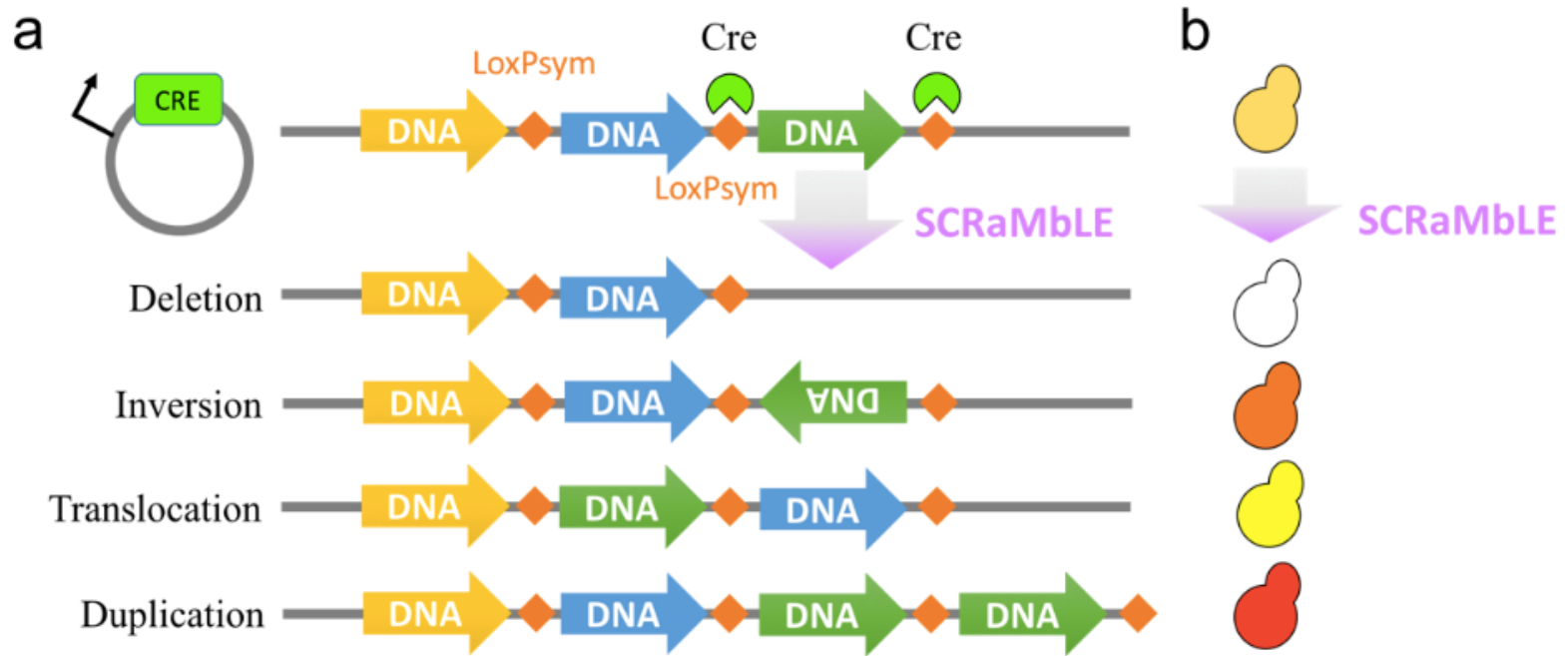


## Genome modularity and integration of synthetic DNA

# SCRaMbLE mechanism

- **S**ynthetic **C**hromosome **R**ecombination and **M**odification **b**y **L**oxP-mediated **E**volution
- Cre recombinase can recombine a pair of short target sequences called the *LoxP* sequences (both derived from bacteriophage P1)
- Recombination between loxPsym sites could lead to genome rearrangements
- Introduction of around 5000 symmetrical loxP sites 3 bp after the stop codon of nonessential genes and at major landmarks
- Inducible evolution and genome minimization
- Production of strains with a large genotypic diversity
- Cre expression control through galactose or estradiol induction

# SCRaMbLE mechanism



SCRaMbLE leads to diversity generating desired phenotypes

# Possible problems

- Harmful to humans
  - Harmful to environment
  - Harmful dual-use e.g. bioterrorism
- 
- Reduced fitness of the yeast
  - Instability of the genome

# References

- Dymond, J. & Boeke, J. The *Saccharomyces cerevisiae* SCRaMbLE system and genome minimization. *Bioeng. Bugs* 3, 168–171 (2012).
- Richardson, S. M. *et al.* (2017) 'Design of a synthetic yeast genome', *Science*, 355(6329), p. 1040 LP-1044. doi: 10.1126/science.aaf4557
- Foo J.L., Chang M.W. (2018). Synthetic yeast genome reveals its versatility. *Nature* 557 (7707) : 647-648. ScholarBank@NUS Repository. <https://doi.org/10.1038/d41586-018-05164-3>
- Jia, B. *et al.* (2018) 'Precise control of SCRaMbLE in synthetic haploid and diploid yeast', *Nature Communications*, 9(1), p. 1933. doi: 10.1038/s41467-018-03084-4.
- Merja Penttilä, Synthetic yeast 2.0, Synthetic Biology (CHEM-E8125), Aalto University, School of Chemical Engineering, 2019, (course material)
- Synthetic Yeast 2.0, <http://syntheticyeast.org/> 25.03.2019
- *Saccharomyces cerevisiae* Genome Database, <https://www.yeastgenome.org/> 25.03.2019
- [https://www.genscript.com/synthetic\\_yeast\\_genome.html](https://www.genscript.com/synthetic_yeast_genome.html) 25.03.2019

Any questions?