

Yeast 2.0

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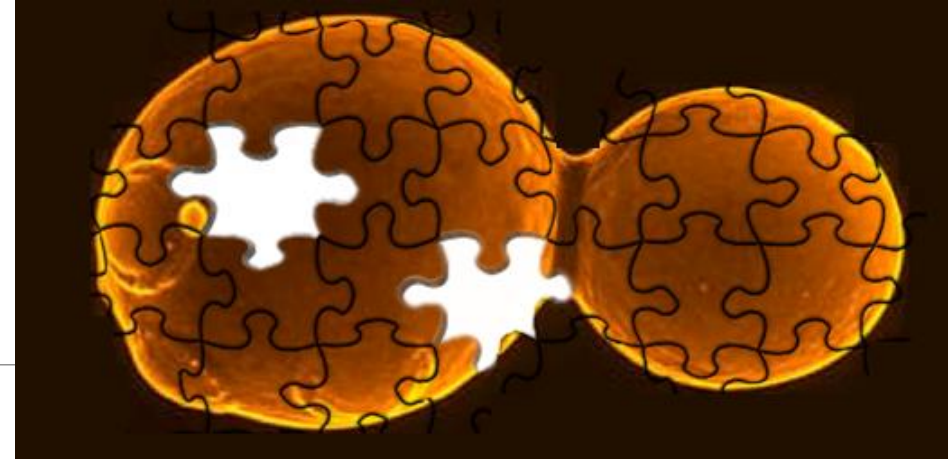
Synthetic yeast: DNA is designed and created by humans

Significance:

- What is the minimum viable genome?
- How do synthetic chromosomes perform in meiosis?
- Which parts in the genome are irreplaceable?
- Studying evolution using SCRaMbLE
- Industrial application

Improvements

- At present several changes are always made at once due to time and funding limits. In an ideal situation we could have hundreds of different versions of the synthetic yeast so that impacts of individual changes could be studied.



Synthetic Yeast construction principles

1. Keep yeastiness
2. Maintain fitness
3. Increase genomic stability -> delete transposons and relocate tRNA genes
4. Increase genetic flexibility -> enable SCRaMbLE
5. Try to minimize genome size -> remove nonessential genes and decrease telomere size
6. Step by step construction

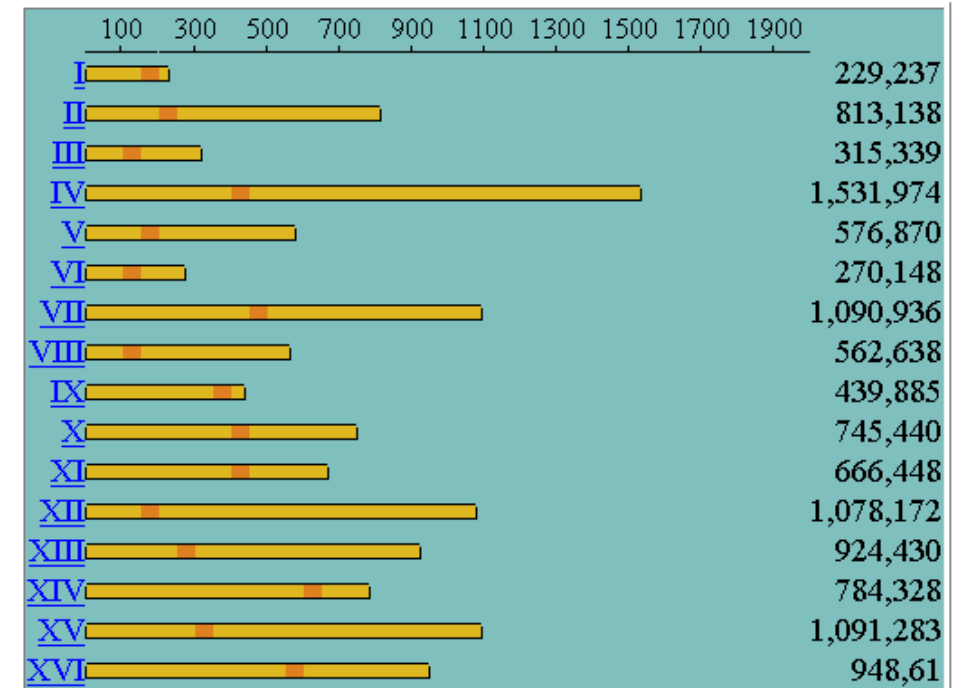
S. cerevisiae chromosome I

- Chr I has not been earlier synthesized
- ~230 kb -> modification from 0 to 30 kb
- No introns, transposons or tRNA genes

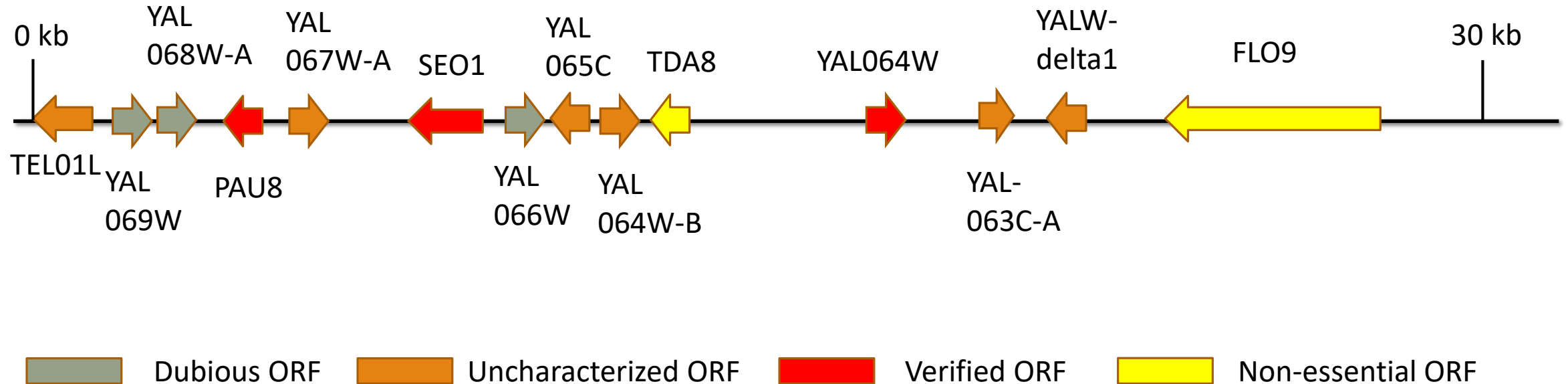
Modifications:

- PCRTag (new coding sequence, same amino acid sequence)
- Telomere cap (simple sequence repeat)
- Removal of non-essential genes
- Stop codons: TAG->TAA (unnatural amino acids)
- Addition of loxPsym sites (all of the ORFs)

Saccharomyces cerevisiae complete genome



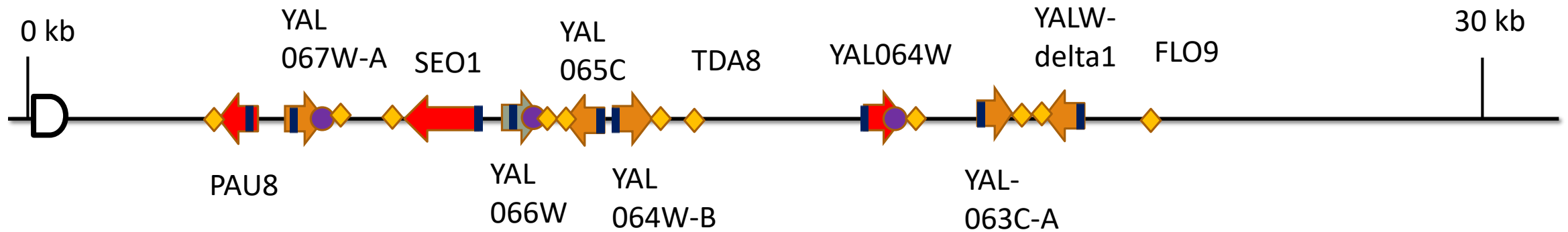
Chromosome I



FLO9: flocculation and adhesion

TDA8: biological role unknown

Synthetic chromosome I



Dubious ORF



Uncharacterized ORF



Verified ORF

Deletion of non-essential genes: FLO9 and TDA8

◆ loxPsym site addition

● Stop codon TAG-> TAA: YAL067W-A, YAL066W, YAL064W

■ PCRTag

D Telomere cap

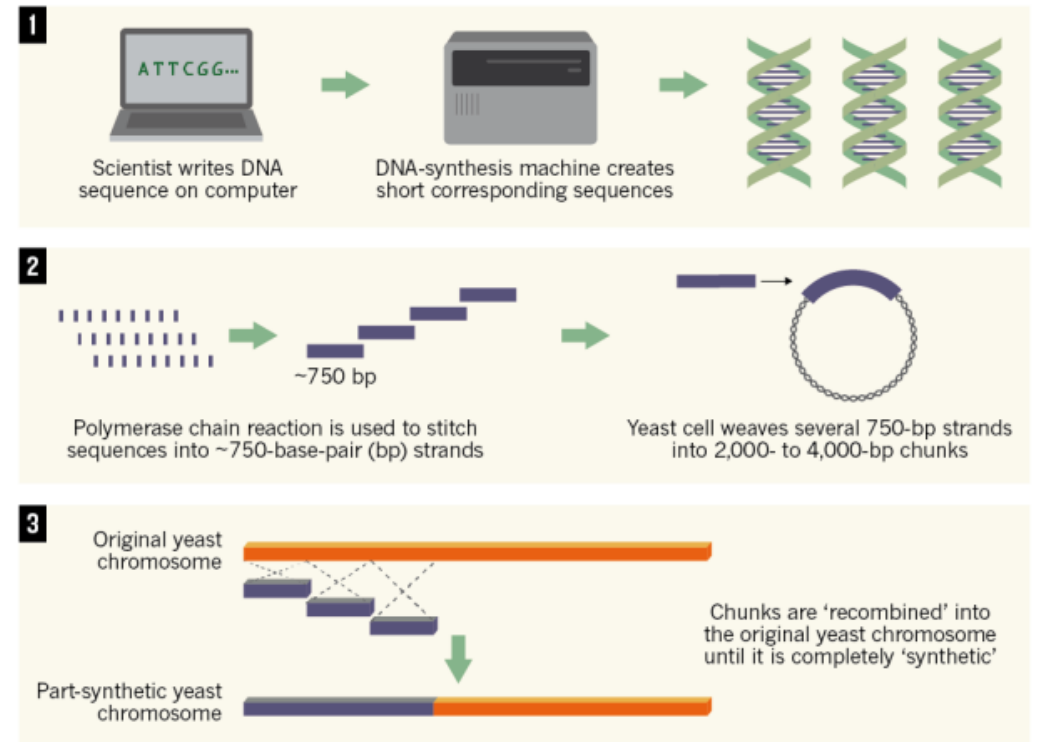
Construction – bottom up approach

- 30-60 kb DNA pieces
- 750 bp building blocks
- 3 kb minichunks
- 10 kb chunks
- Recombination into yeast

After the cycle yeast fitness must be evaluated.

CONSTRUCTING LIFE

Researchers have synthesized a fully functional chromosome from the baker's yeast *Saccharomyces cerevisiae*. At 272,281 base pairs long, it represents about 2.5% of the organism's 12 million-base-pair genome.



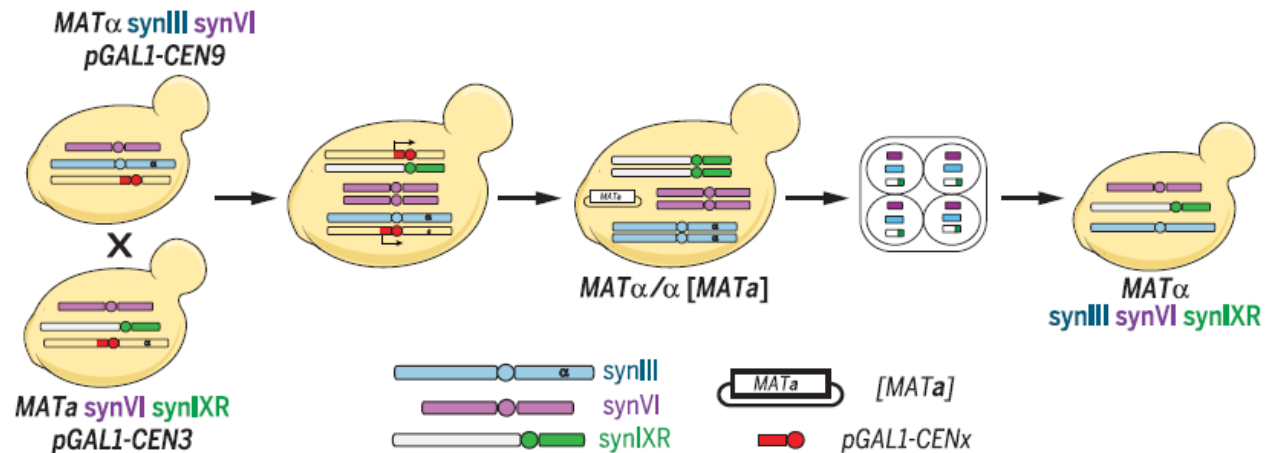
Combining synthetic chromosomes into one strain

- Mating and sporulation of different strains
 - Multiple crossovers challenge the recovery of non-recombinant progeny chromosomes
 - Increase of synthetic chromosomes makes it difficult to find spores that contain entirely full-length synthetic chromosomes
- Endoreduplication intercross can be used to overcome these problems

Endoreduplication intercross

- GAL1 promoter is used to destabilize the chromosome and to make it duplicate
- MATa was introduced to the cell to permit the sporulation

1. Strains are grown in galactose to induce GAL1 promoter
2. Chromosomes are destabilized and duplicated
3. Mating of two different yeast strains
→ intercrossover of chromosomes
4. Sporulation and dissection
→ New strains with multiple synthetic chromosomes



References

Annaluru N, Muller H, Mitchell LA, et al. Total synthesis of a functional designer eukaryotic chromosome. *Science*. 2014;344(6179):55-8.

Ewen Callaway. 2014. First synthetic yeast chromosome revealed. *Nature*.

Richardson, S.M, Mitchell, L.A., Stracquadanio, G., Yang, K., Dymond, J.S., DiCarlo, J.E., Lee, D., Huang, C.L.V., Chandrasegaran, S., Cai, Y., Boeke, J.D., Bader, J.S., Design of a synthetic yeast genome, *Science* 355, 2017, p. 1040-1044.

Syntheticyeast.org. 2019. *Synthetic Yeast 2.0*. [online] Available at: <http://syntheticyeast.org/> [Accessed 19 Mar. 2019].

Yeastgenome.org. *Saccharomyces* genome database. [online] Available at: <https://www.yeastgenome.org/>