



Yeast genome duplication

*Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae**

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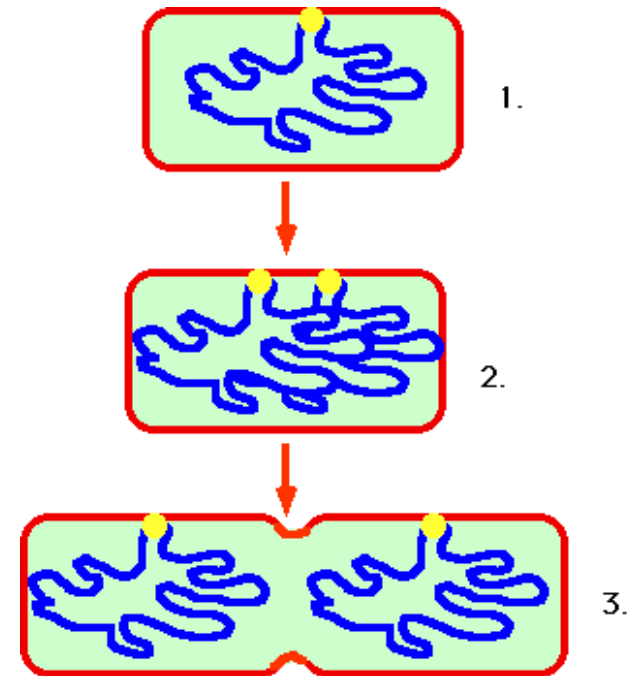
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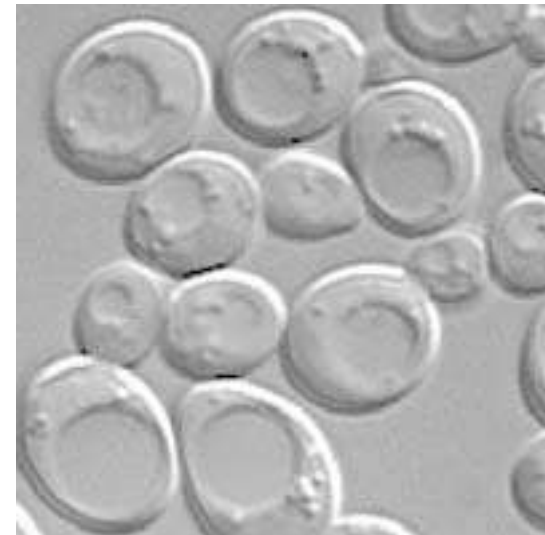
Whole-genome duplication

- Poorly understood
- “Cataclysmic” genomic event
 - Major instability
- Return to normal state
 - Mutations
 - Rearrangements
 - **Gene loss**

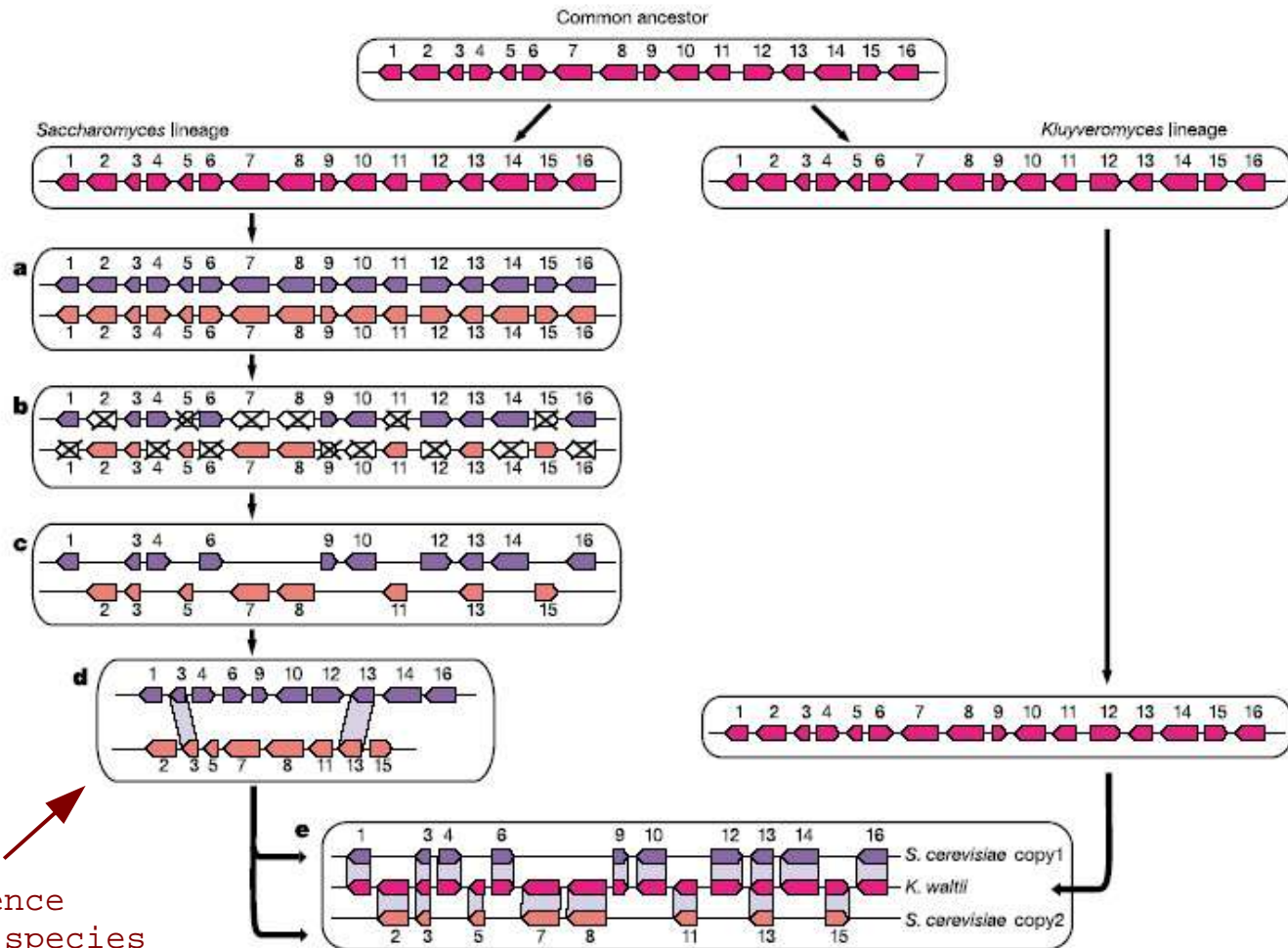


Yeast-genome duplication

- 8 -> 16 chromosomes
- Loss of 90% of duplicated genes
- Paired regions (?) 90% of genome
- ~500 duplicated gene pairs



Evidence of whole genome duplication



poor evidence
if only 1 species
is analyzed



K. waltii as a proof of genome duplication

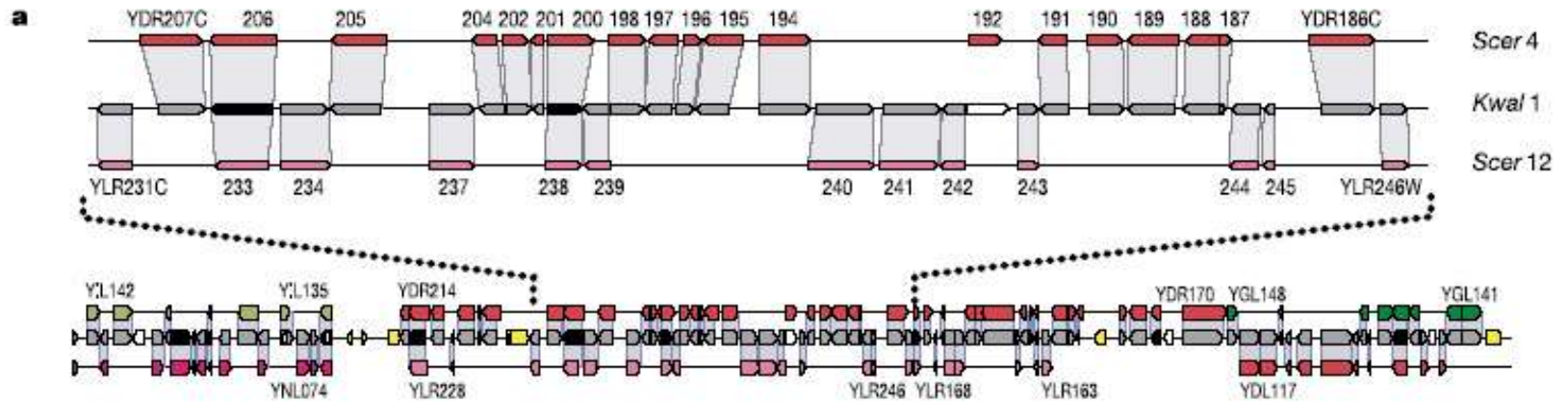
S. cerevisiae

- 5714 genes
- 16 chromosomes

K. waltii

- 5230 genes
- 8 chromosomes
- 7%: no similarity

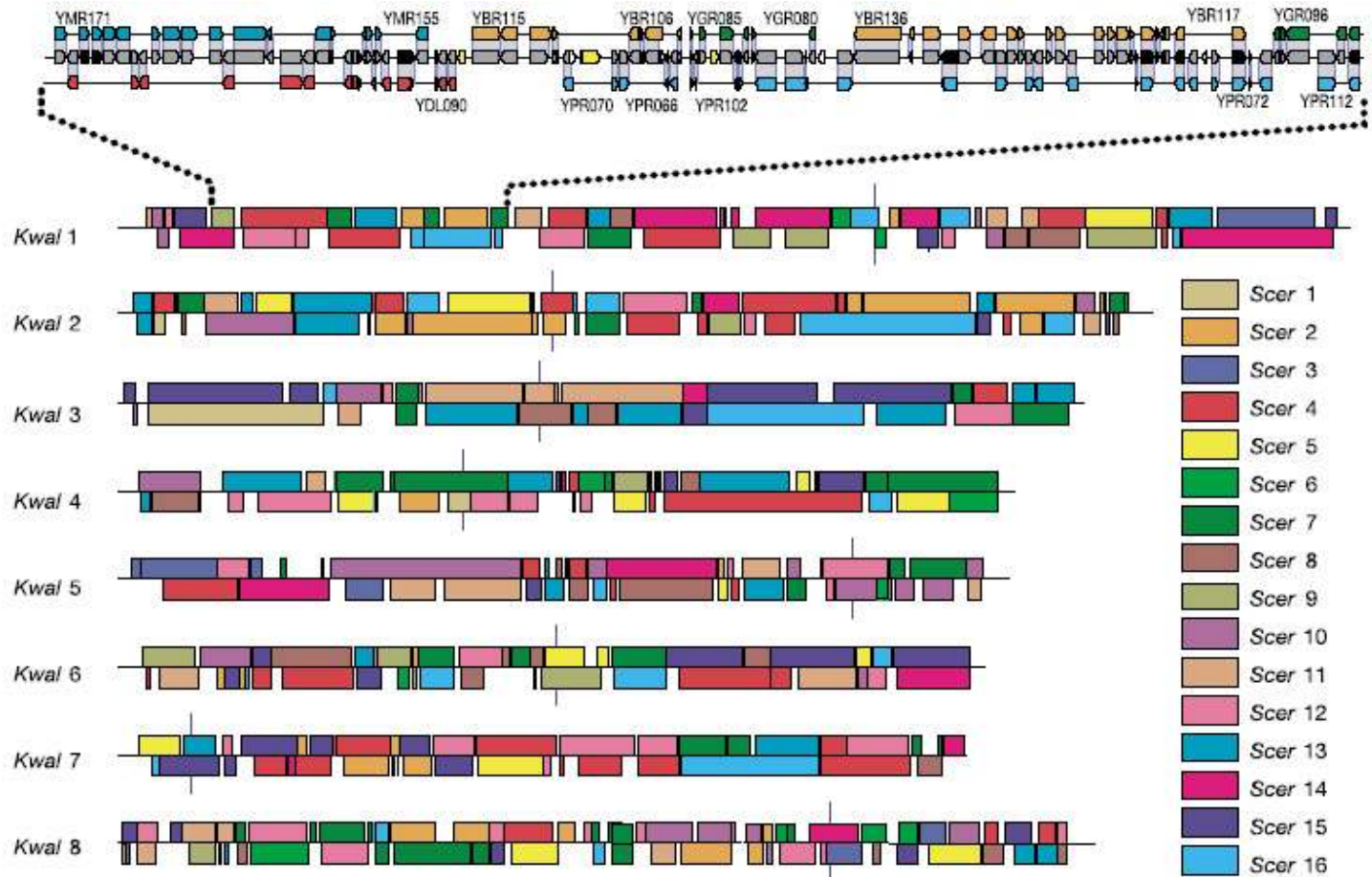
Gene correspondence



Doubly Conserved Synteny blocks:

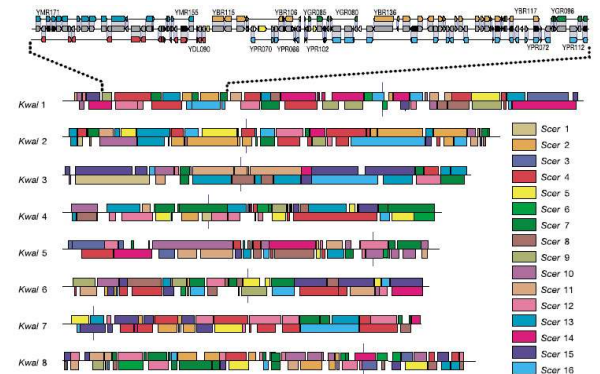
- conserved gene order
- genes less than 20kb apart
- double hits Kw – Sc
- (often) no duplicated genes

Doubly Conserved Synteny blocks

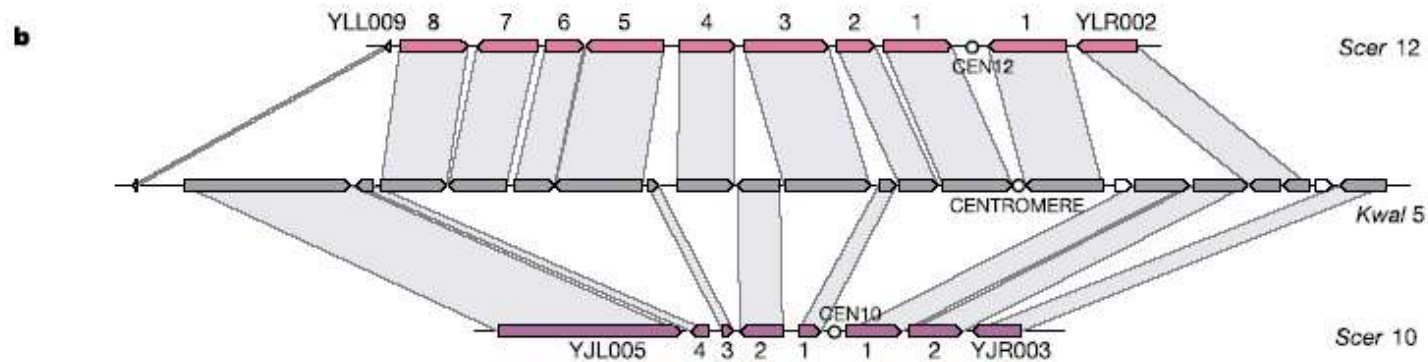


Doubly Conserved Synteny

- 253 DCS blocks
- ~80% coverage of *K.waltii* genome
- Typical DCS
 - Around 27 genes (max 81)
 - Separated by ~3 genes
 - 1% of *Kw* matches >2 blocks in *Sc*

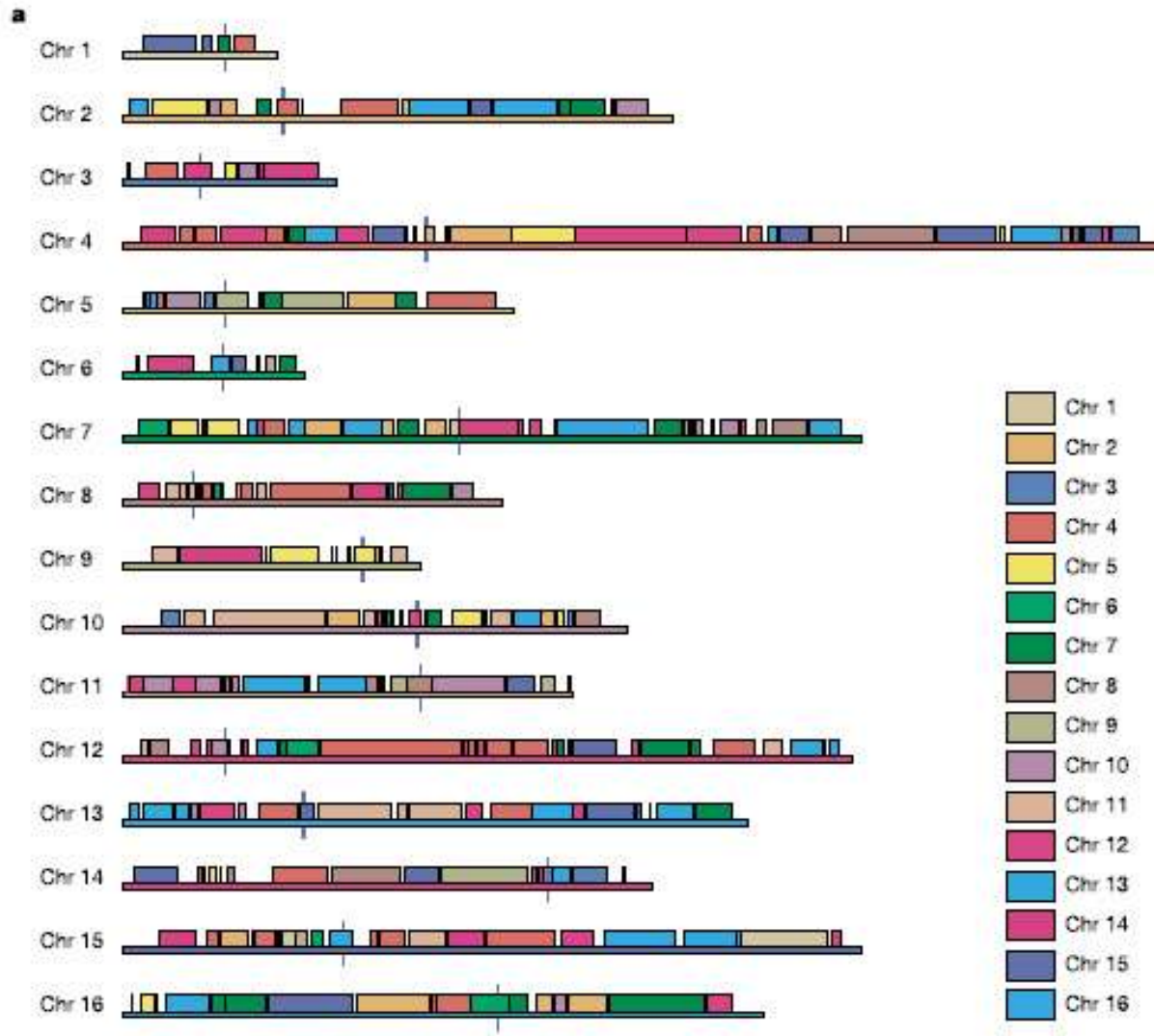


Centromere proof of genome duplication

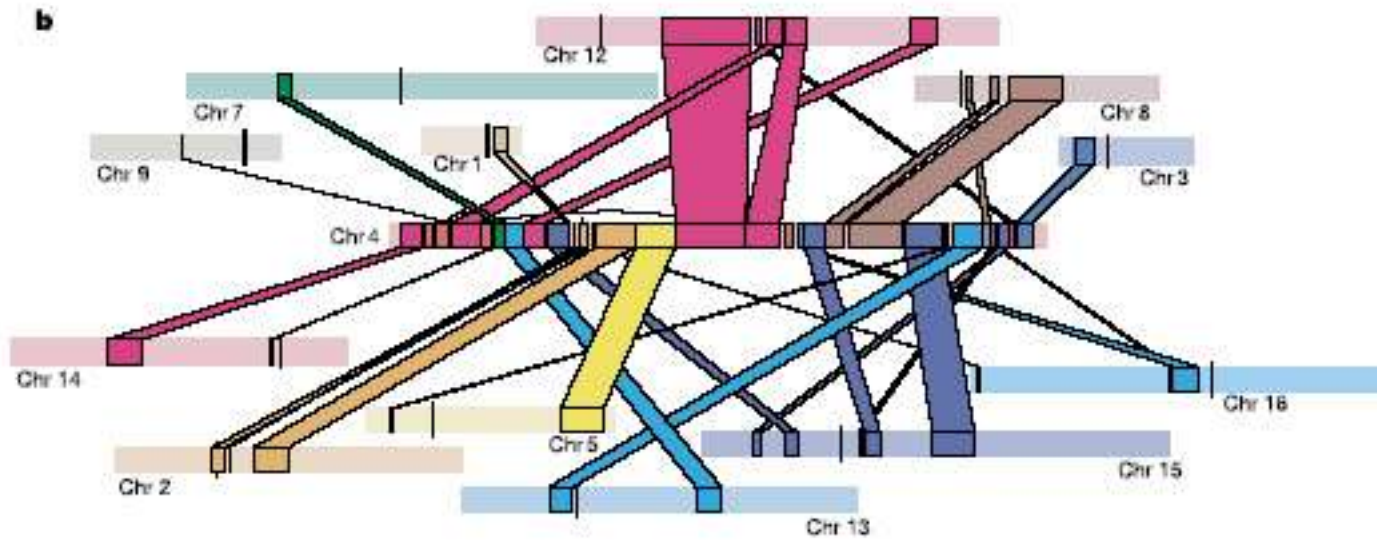


Note! No duplicated genes

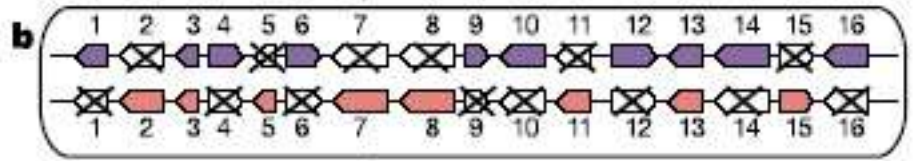
Block pairs: overview



Block pairs: details

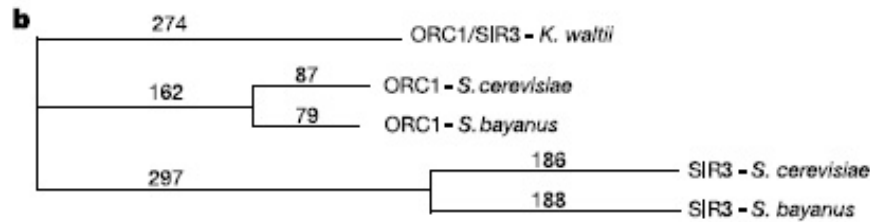


Evolutionary analysis: gene loss



- Genome sizes:
 - Sc 13% larger than Kw
 - 12% paralogous genes
- Pattern of loss:
 - Many small deletions (~2 genes)
 - Balanced between regions
 - No chromosome loss
 - No large segmental deletions

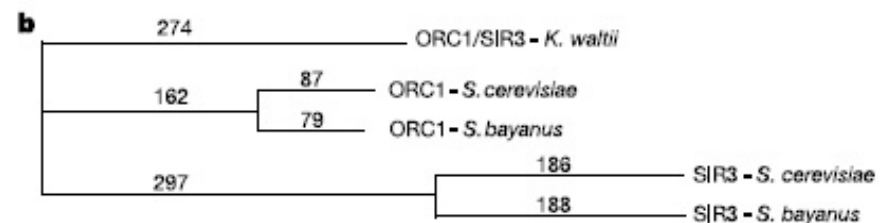
Evolutionary analysis: accelerated divergence



- 500 paralogous pairs
- 80 pairs (17%): accelerated evolution
 - Sc genes which evolve 50% faster than Kw

Old and new functions of duplicated genes

- Only 1 gene accelerates (95% of cases)
 - one copy preserves the function
 - the other copy is **free to diverge**
- Functions derived from ancestral ones
 - silencing of Sir3 comes from origin-of-replication Orc1
 - Spatio-temporal differentiation



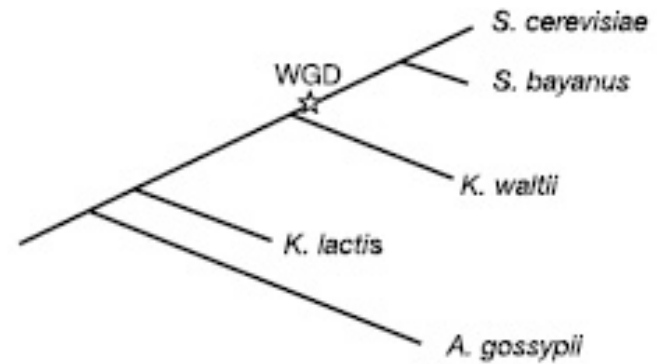
Knocking-out duplicated genes

- KO of paralogue
 - ancestral: lethal (20%)
 - derived: not lethal
- Derived function is not essential in a rich medium
- Derived copy (sometimes) lose essential aspects of its original function



Summary

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- Genome duplication is followed by:
 - massive gene loss (90% of new genes)
 - gene specialization
- Tiny footprints of duplication (genome +10%)
- Only one of paralogues accelerates