

Approach to the sequencing of *Aspergillus niger*

Approach *A. niger* sequencing

- Strain: natural derivative of NRRL 3122
- Sequencing approach: random or structured?

Random

- Shotgun
- Unpositioned contigs
- High coverage at end

Structured

- Ordered library
- Positioned contigs
- High coverage from start

- *A. niger*: combined approach

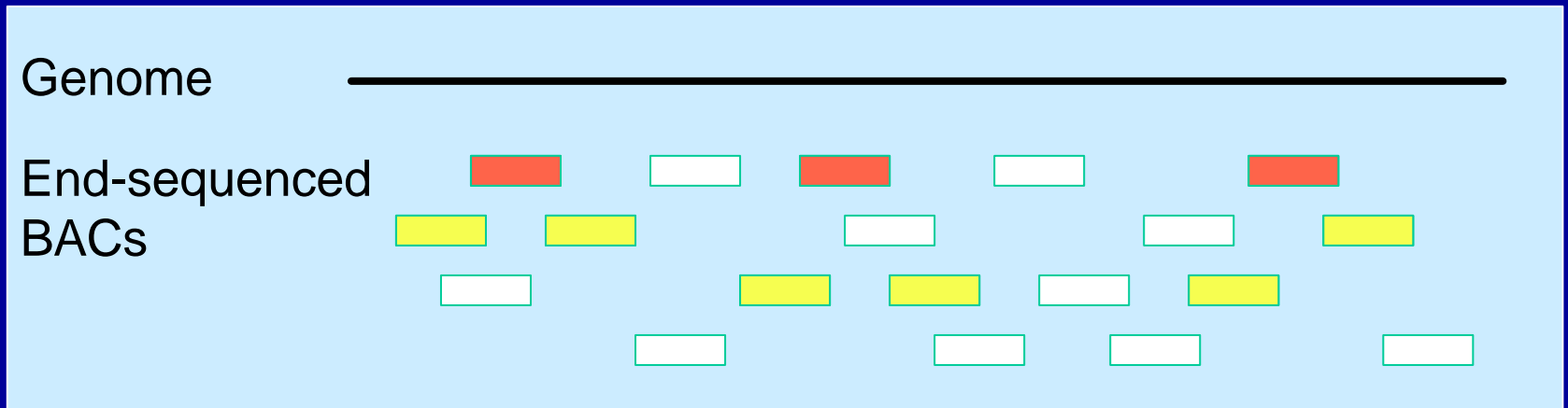
Approach *A. niger* sequencing (II)

- Cut genome in large  fragments (60 – 110 kb)
- Clone fragments in Bacterial Artificial Chromosomes (BACs)



- Sequence ends of the BACs
 - short sequence of ~500 bp per BAC end

Approach *A. niger* sequencing (III)



- Start the sequence analysis with a number of randomly selected BACs ('seed BACs')
 - BACs are sequenced using shotgun approach
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- Compare seed BACs to end-sequences and select BACs with minimal overlap ('BAC-walking')

From BAC ends to Supercontigs

