





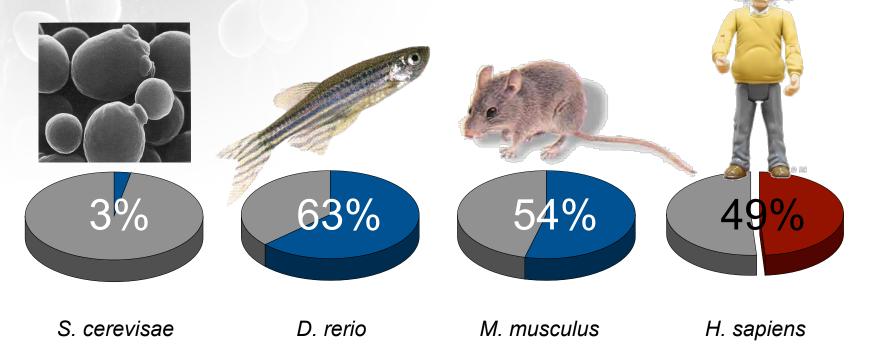
## Tandem Repeats

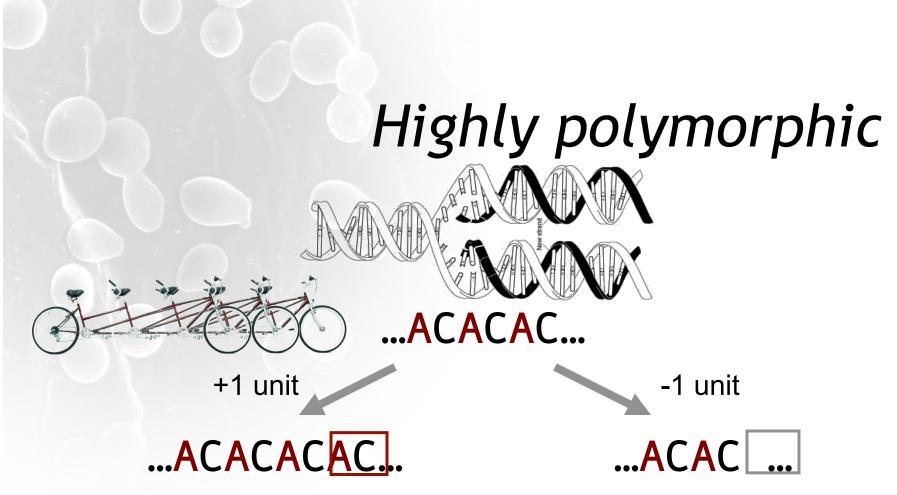
- Consecutive iterations of short sequences of DNA
- "Junk DNA": Previously ignored by genomic researchers
- Highly polymorphic: very prone to errors during DNA replication

...ACACACACAC... ...CCCTAGCCTAGCCTAGCCTA...

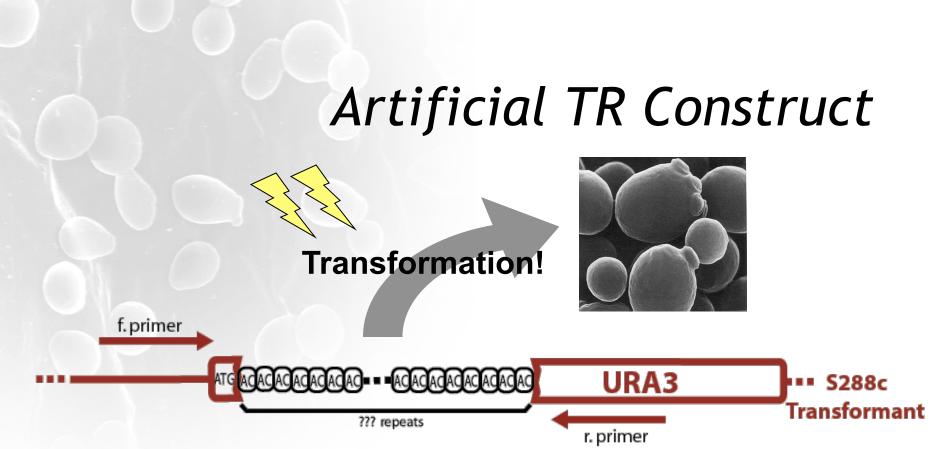
## Abundance in genomes

#### Tandem Repeats are very common in eukaryotic genomes!

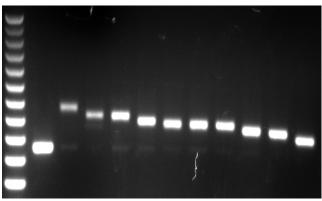




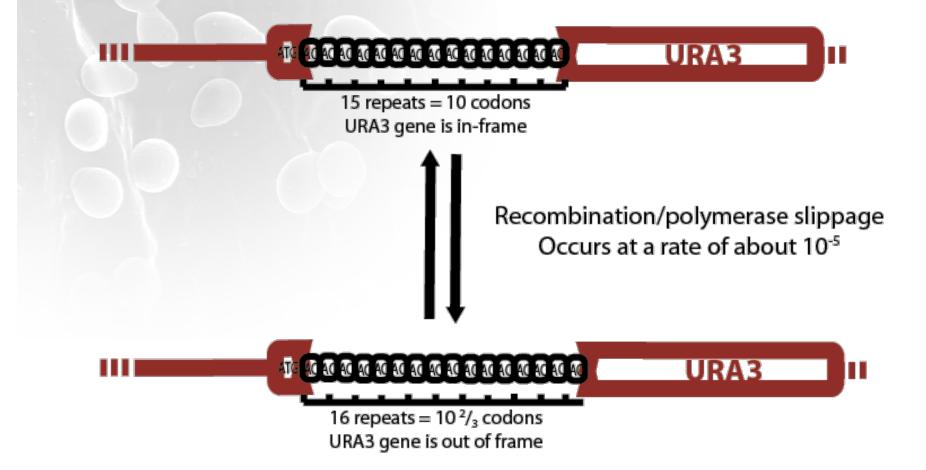
- Occurs 100-1000 times more frequently than other DNA replication errors
- Causes/mechanism for this is unknown.
- Repeat expansion causes a number of human diseases.



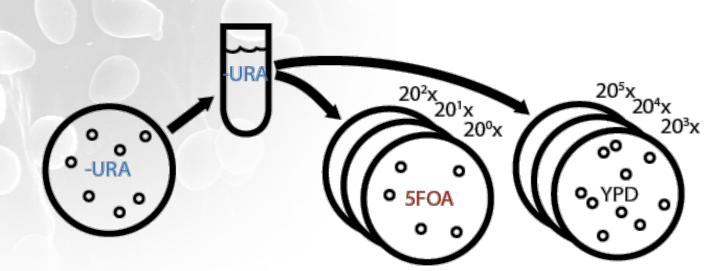
 Artificial tandem repeat was inserted into a marker gene in S. cerevisae



## Switching Mechanism

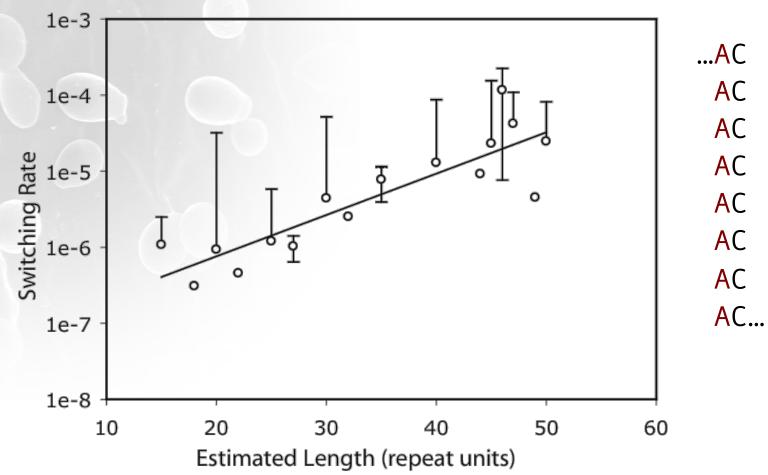


### Measuring switching rate



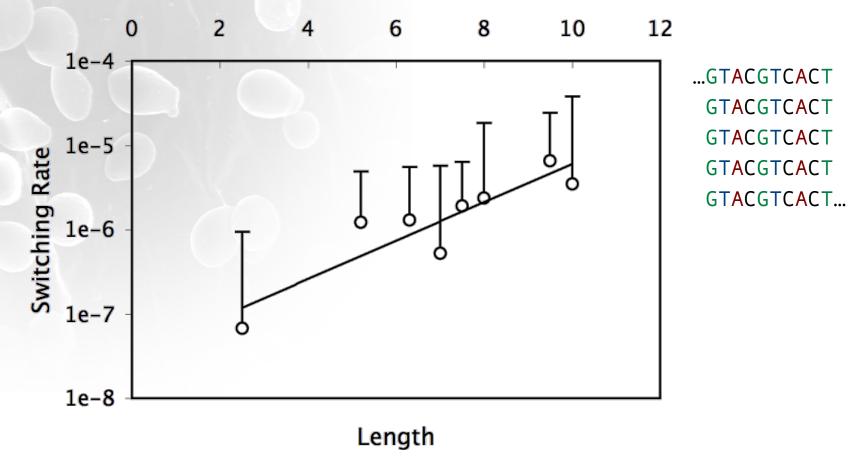
Grow cells in selective liquid medium, e.g., -URA Plate dilution series on the opposite selective medium and YPD. By counting colonies, the fraction of cells that have switched out of frame can be determined.

#### First switching data: Long AC dinucleotide repeats



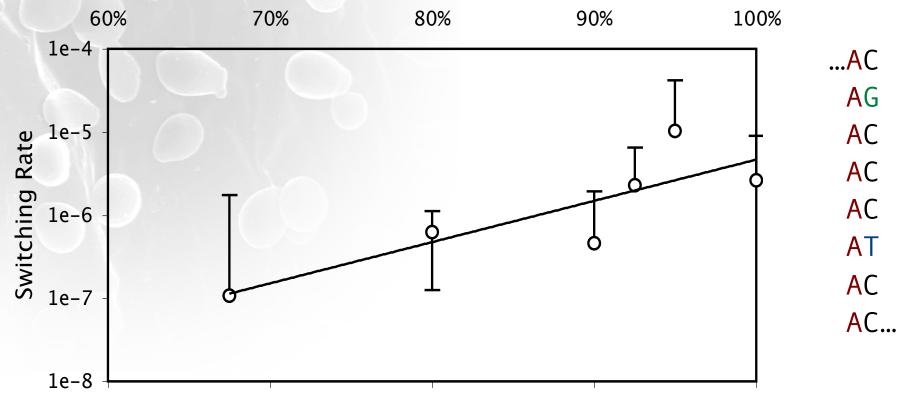
- We first tried a basic AC dinucleotide repeat
- Longer repeats change length faster!

#### Confirming the trend: Long 10mer repeats



Same trend is observed with 10-mers

#### Other trends: Purity in AC dinucleotide repeats



Purity (% bp identity to repeat unit)

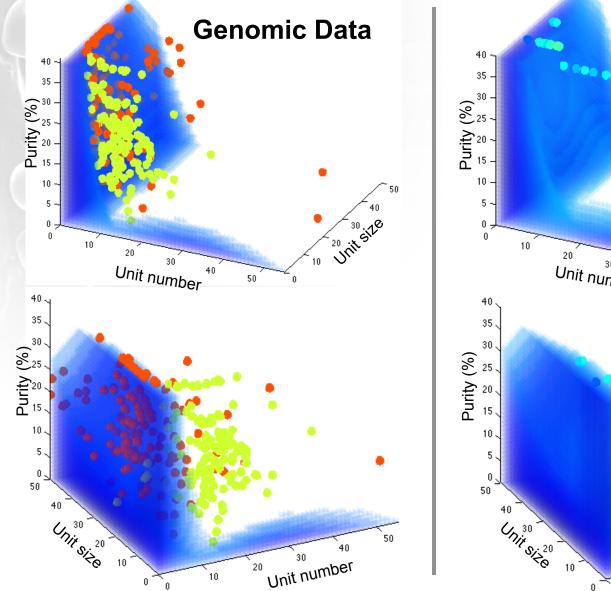
Increasing purity of a dinucleotide tract increases its variability

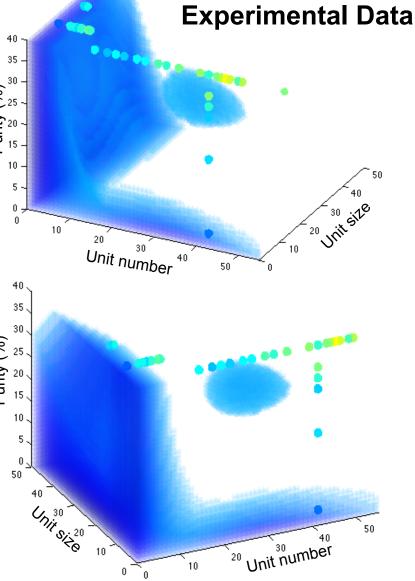
#### Sequence properties alter variability

◆ Several trends have been observed:
◆ More repeat units = ↑ variability
◆ Greater purity of repeat = ↑ variability
◆ Longer repeat units = ↑ variability
So given the above...

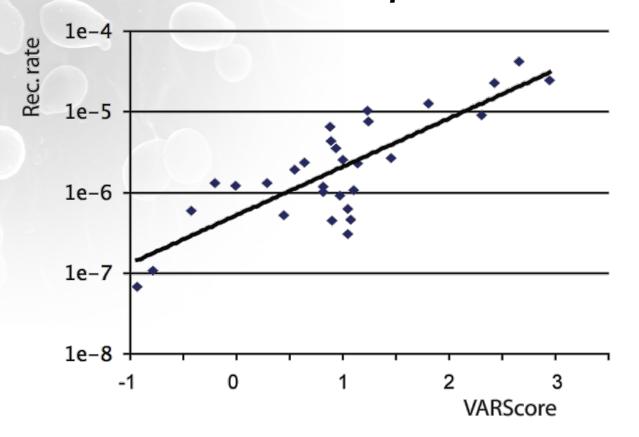
 A model should be able to be constructed that predicts the variability of a repeat based on its DNA sequence.

#### **Predictive Computational Model**



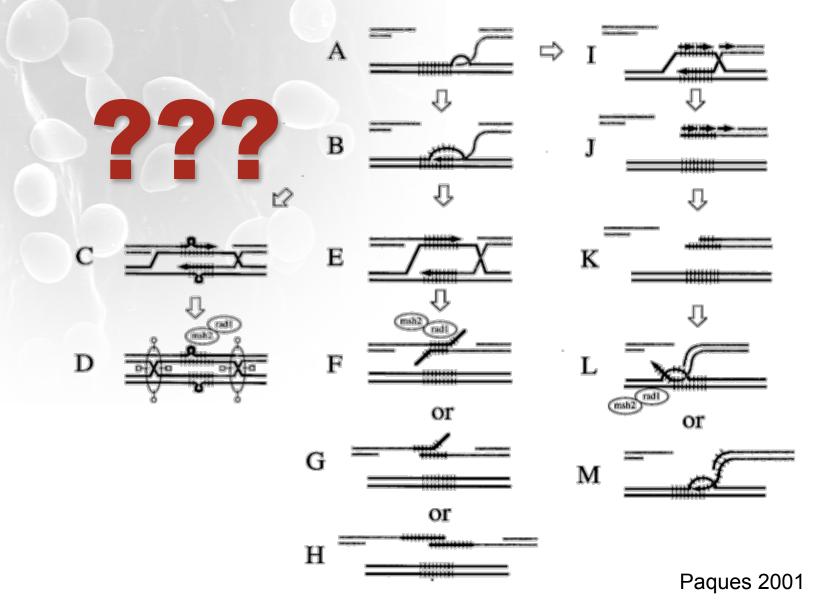


## Correlation between model and experimental data



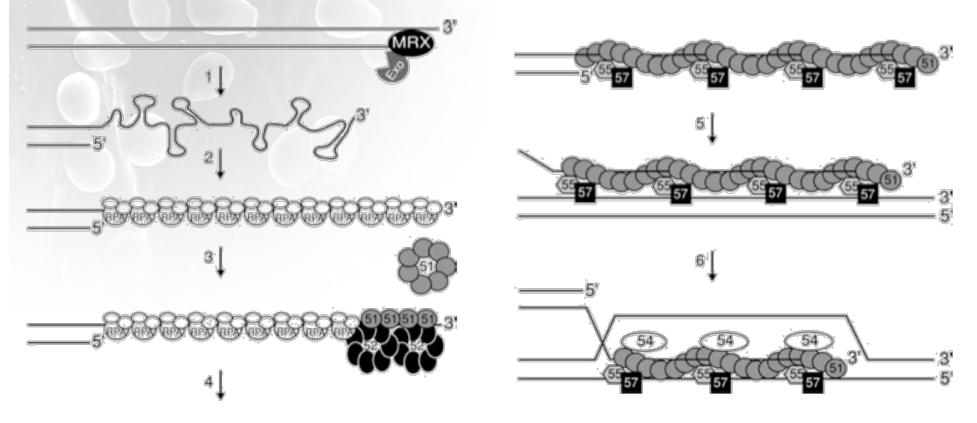
Matthieu Legendre, Nathalie Pochet, Theodore Pak, and Kevin J. Verstrepen. **Sequence-based estimation of minisatellite and microsatellite repeat variability.** Genome Res. doi:10.1101/gr.6554007

## Switching Mechanism?



## **Recombination Proteins**

RAD genes, the MRE complex



Krogh 2004

## Future directions

 Delete genes in the recombination pathway and examine effects on variability

#### OR

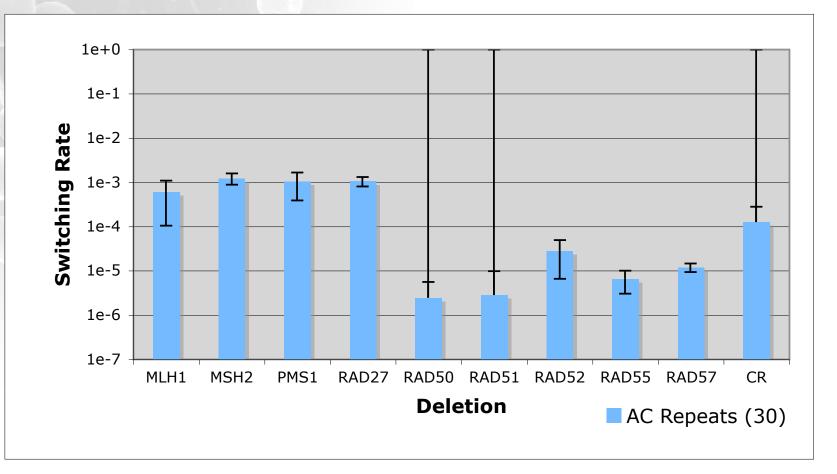
 Attempt to create a more sophisticated model for Tandem Repeat variability based on experimental data

## Acknowledgements

Kevin J. Verstrepen, PI Matthieu Legendre, Nathalie Pochet Marcelo Vinces, Chris Brown The Verstrepen Lab My labmates Chen, Bianca, Amy, Barry, Bena... HURS, HCRP, PRISE The FAS Center for Systems Biology

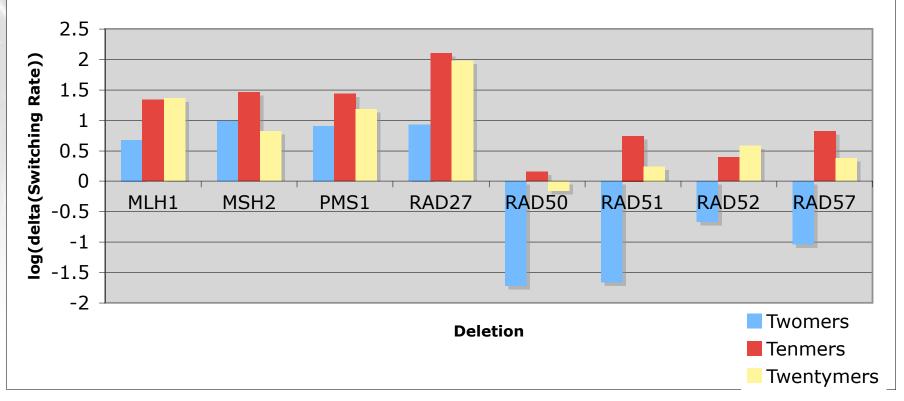


#### Mechanisms? Long dinucleotide repeats w/ deletions



Deleting genes related to the recombination pathway appears to affect switching rates.

#### Unit number makes a difference



- Examine REC pathways, hypothesize why this might be the case
- Additional genes. THO complex required for transcription of repeats?