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Genome-scale phylogeny and the detection of systematic biases.

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► **To cite this version:**

Matthew J Phillips, Frédéric Delsuc, David Penny. Genome-scale phylogeny and the detection of systematic biases.. *Molecular Biology and Evolution*, 2004, 21 (7), pp.1455-8. 10.1093/molbev/msh137 . halsde-00193019

HAL Id: halsde-00193019

<https://hal.science/halsde-00193019>

Submitted on 30 Nov 2007

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Supplementary Information

Table S1. Character analysis for comparison of NT-coding and RY-coding for the 106-genes (127,026 nucleotides) yeast dataset.

	Standard NT-coding	RY-coding
<i>Stochastic-based tests</i>		
a. Base composition chi-square test	<0.0001	<0.0001
b. Molecular clock test	<0.0001	<0.0001
<i>Magnitude tests</i>		
c. Treeness	0.1176	0.1561
d. Relative composition variability	0.0613	0.0154

Stochastic-based tests include (a.) the base composition chi-square test as implemented in PAUP* and (b.) the molecular clock test (Felsenstein 1988). The magnitude tests include (c.) treeness: the proportion of uncorrected minimum-evolution tree distance attributed to internal (as opposed to external) branches and (d.) relative composition variability (RCV; Phillips and Penny 2003). The chi-square tests and RCV values were determined with constant sites excluded, as these sites buffer against inferring composition bias among the sites that contribute directly to apparent phylogenetic signal.

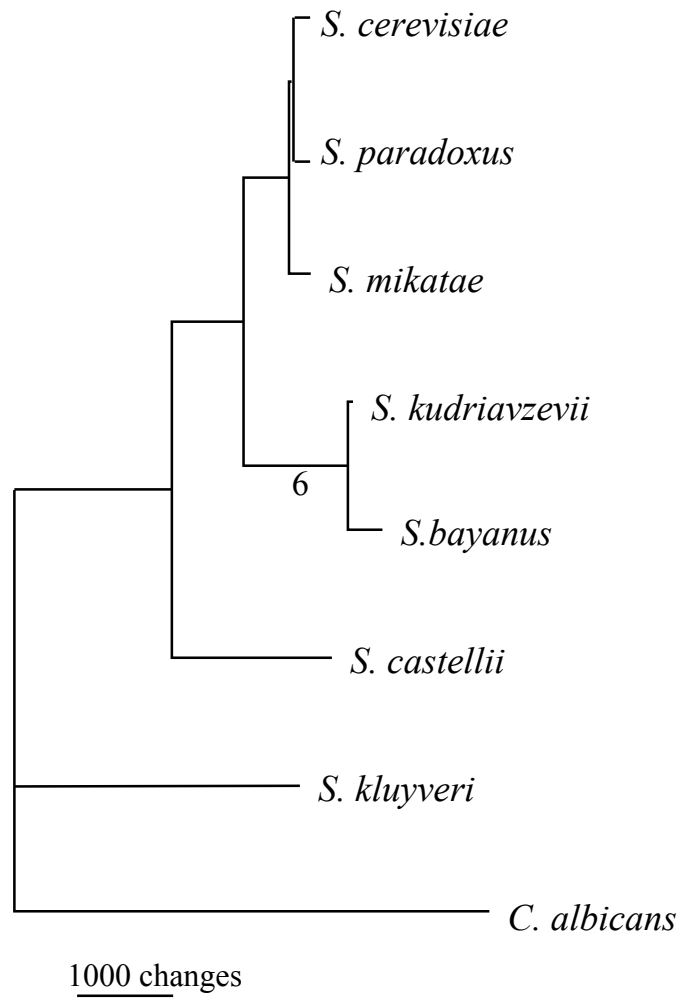


Figure S1. Minimum evolution tree from pairwise AT-GC base-frequency differences. Following Kuhner and Felsenstein (1994) branch-lengths were constrained to be non-negative.

References for Supplementary Material

Felsenstein, J. 1988. Phylogenies from molecular sequences: inference and reliability. *Ann. Rev. Genet.* **22**:521-565.

Kuhner, M. K., and J. Felsenstein. 1994. A simulation of phylogeny algorithms under equal and unequal evolutionary rates. *Mol. Biol. Evol.* **11**:459-468.

Phillips, M. J., and D. Penny. 2003. The root of the mammalian tree inferred from whole mitochondrial genomes. *Mol. Phylog. Evol.* **28**:171-185.