EVOLUTION OF THE MUTATION RATE IN VERTEBRATES

AARHUS
UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

EVOLUTIONARY THINKING 2023
WEEK 47

CALIN PANTEA
PHD STUDENT

OVERVIEW

- Mutation rate evolution 12:15 – 12:30

- Paper 12:30 – 13:00 and 13:15 – 13:30
  - + discussion 13:30 – 14:00

MUTATION

- changes in DNA sequence
- point mutations
- DNA damage or replication errors
- DNA repair mechanisms

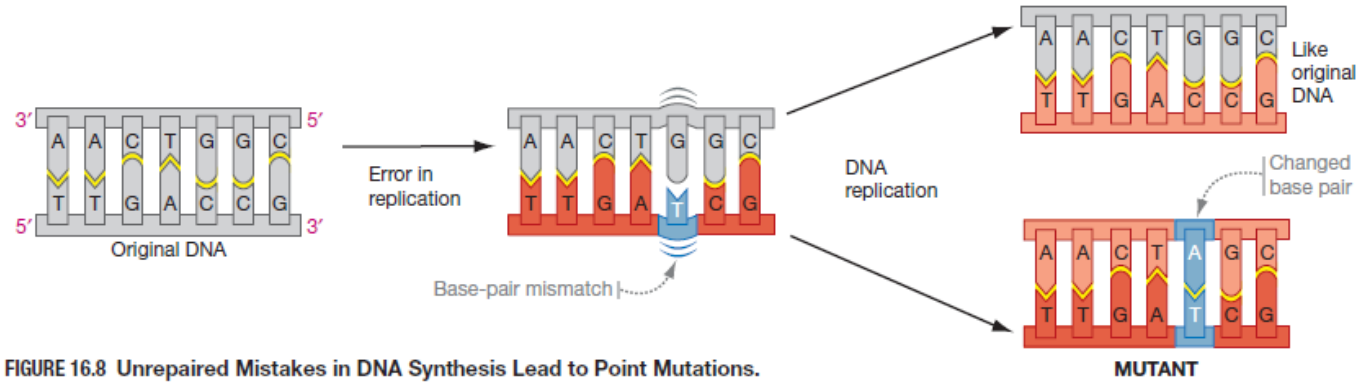
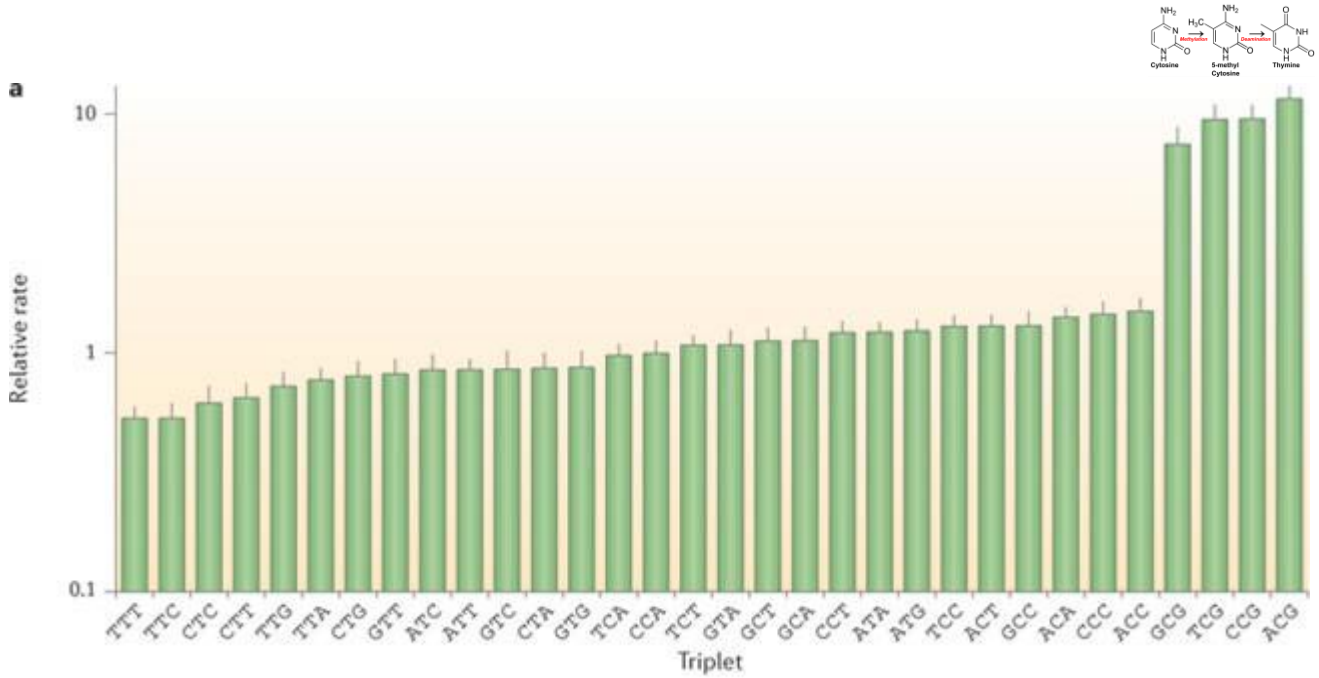


FIGURE 16.8 Unrepaired Mistakes in DNA Synthesis Lead to Point Mutations.

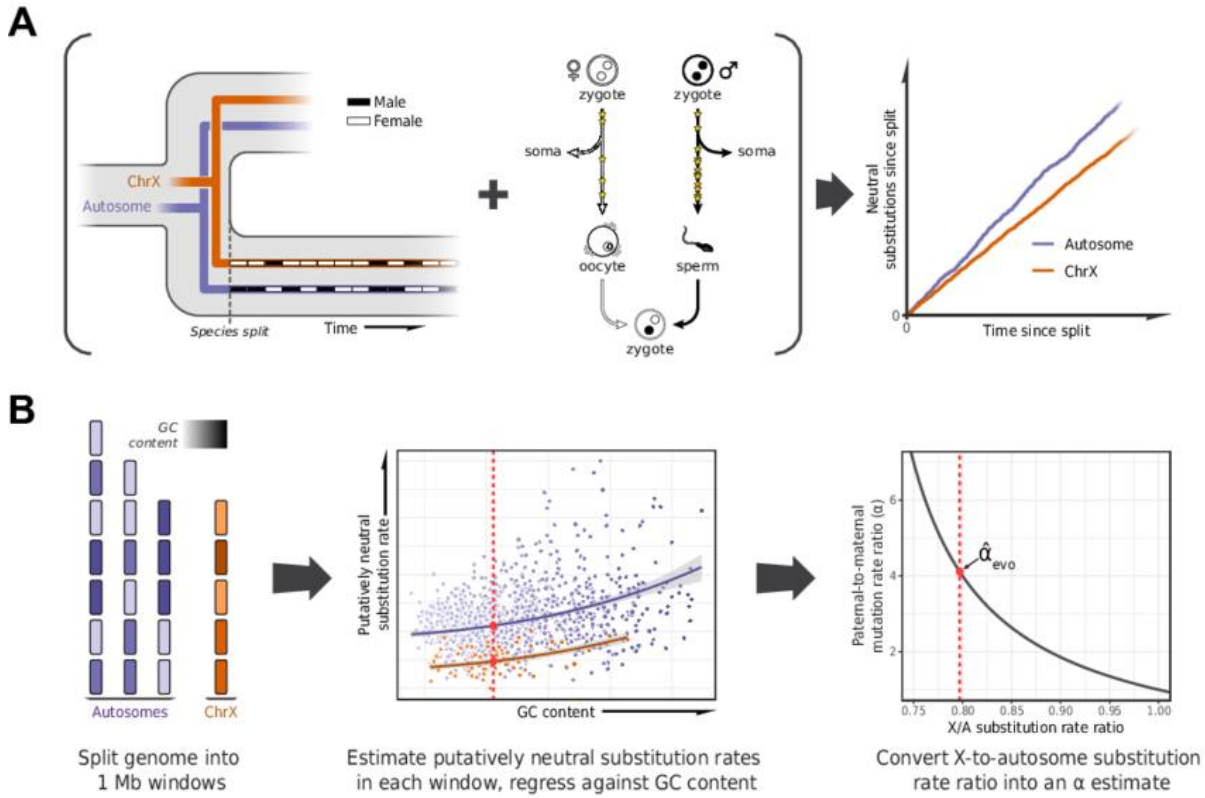
MUTATION RATE VARIATION

- base substitutions only
  - why?
- mutation rate is variable across species and across genomic regions
  - why?



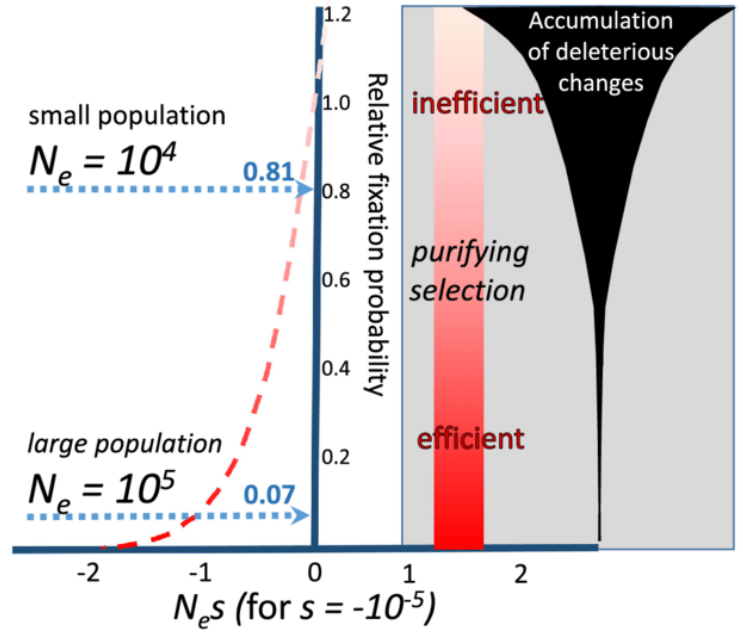
MUTATION RATE EVOLUTION

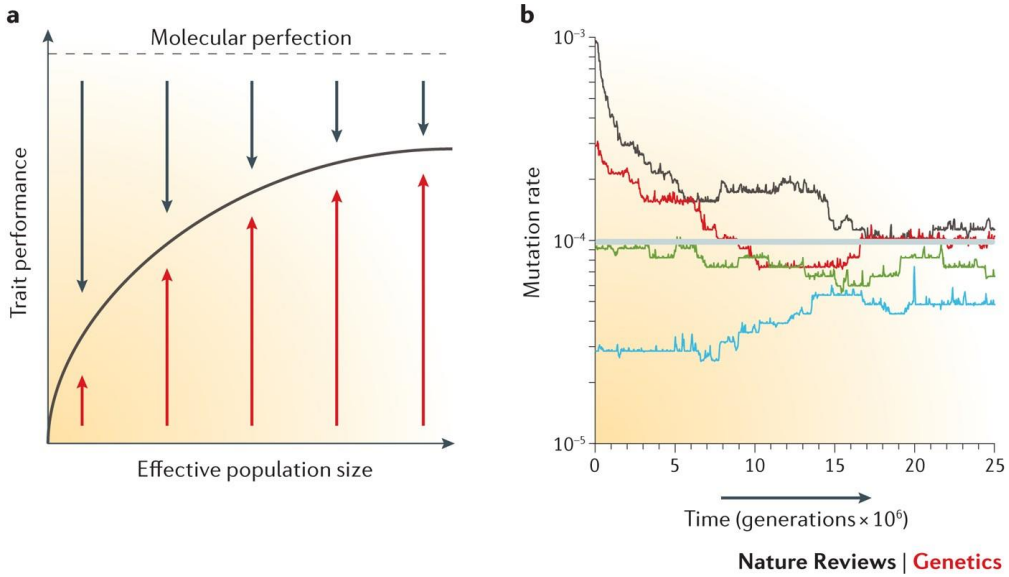
- autosomal vs X mutation accumulation
- selective pressures



DRIFT-BARRIER HYPOTHESIS

- incrementally smaller 'payoff' for trait performance under selection
- selection-drift balance is reliant on N_e
- selective pressure for lower mutation rates due to (mostly) deleteriousness; so advantageous mutations are less impactful over time

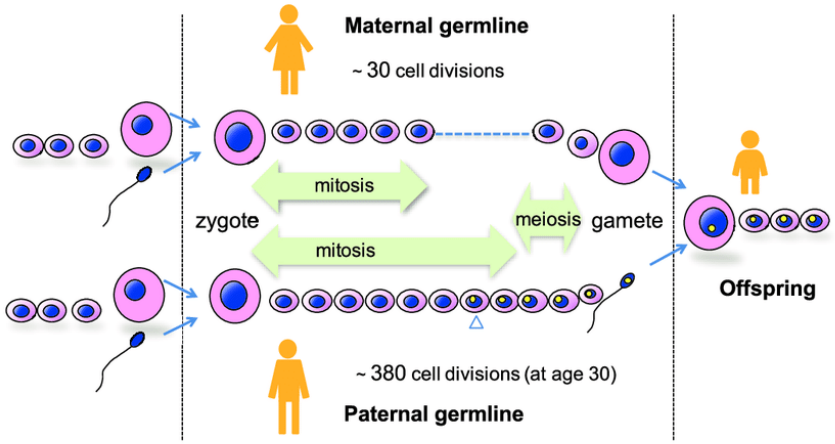


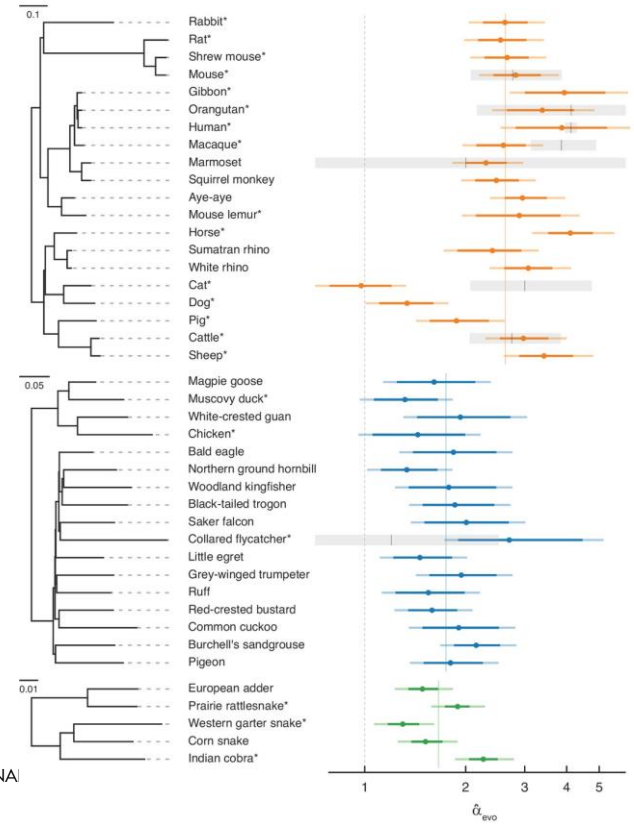


GERMLINE MUTATION BIAS

- due to increase in DNA damage or increasingly defective DNA repair

- present in mammals and birds
  - (also other amniotes)





A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers

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PAPER DISCUSSION

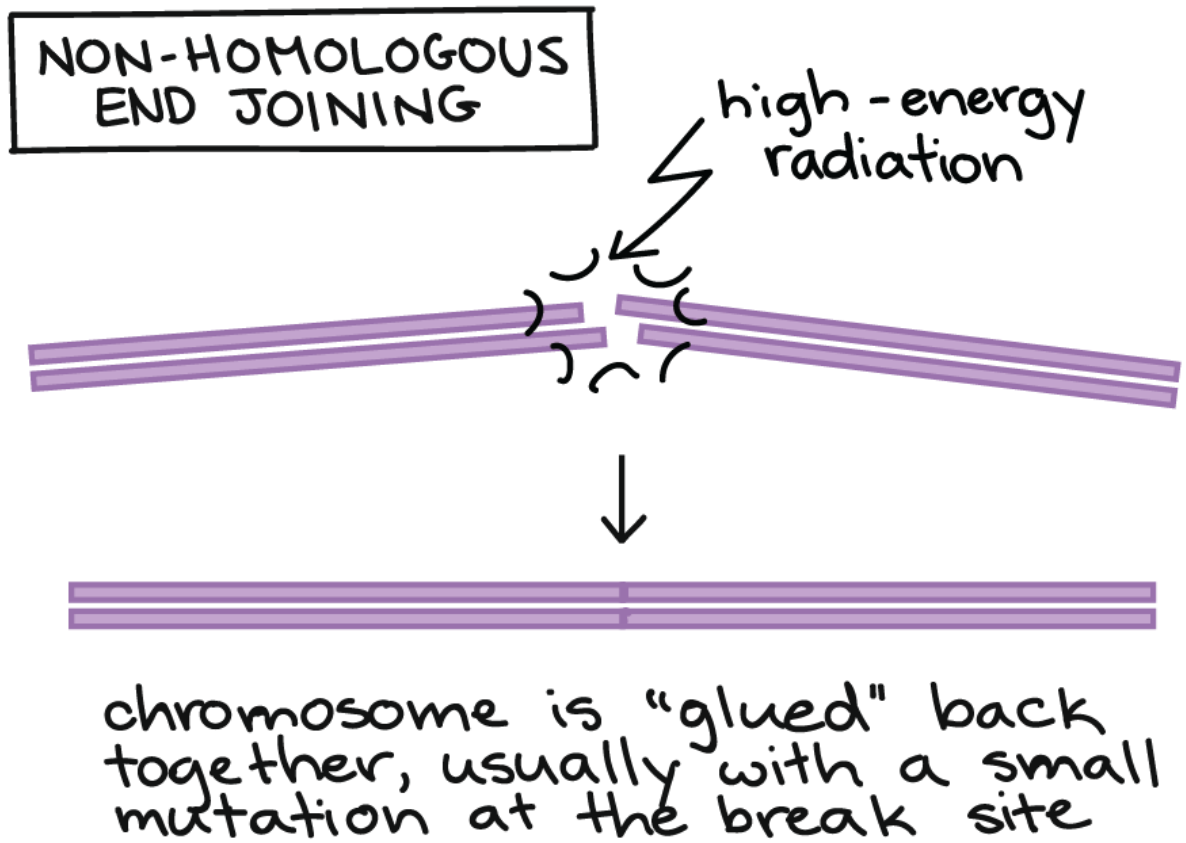
Article | Open access | Published: 01 March 2023

Evolution of the germline mutation rate across vertebrates

Lucie A. Bergeron ✉, Søren Besenbacher, Jiao Zheng, Panyi Li, Mads Frost Bertelsen, Benoit Quintard, Joseph I. Hoffman, Zhipeng Li, Judy St. Leger, Changwei Shao, Josefin Stiller, M. Thomas P. Gilbert, Mikkel H. Schierup & Guojie Zhang ✉

Nature **615**, 285–291 (2023) | Cite this article

DOUBLE-STRAND BREAK (13:00-13:15)



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NEXT TIME

- Ancient DNA exercise – PCA
- Menti quiz!
- Brief Hand-in III presentation

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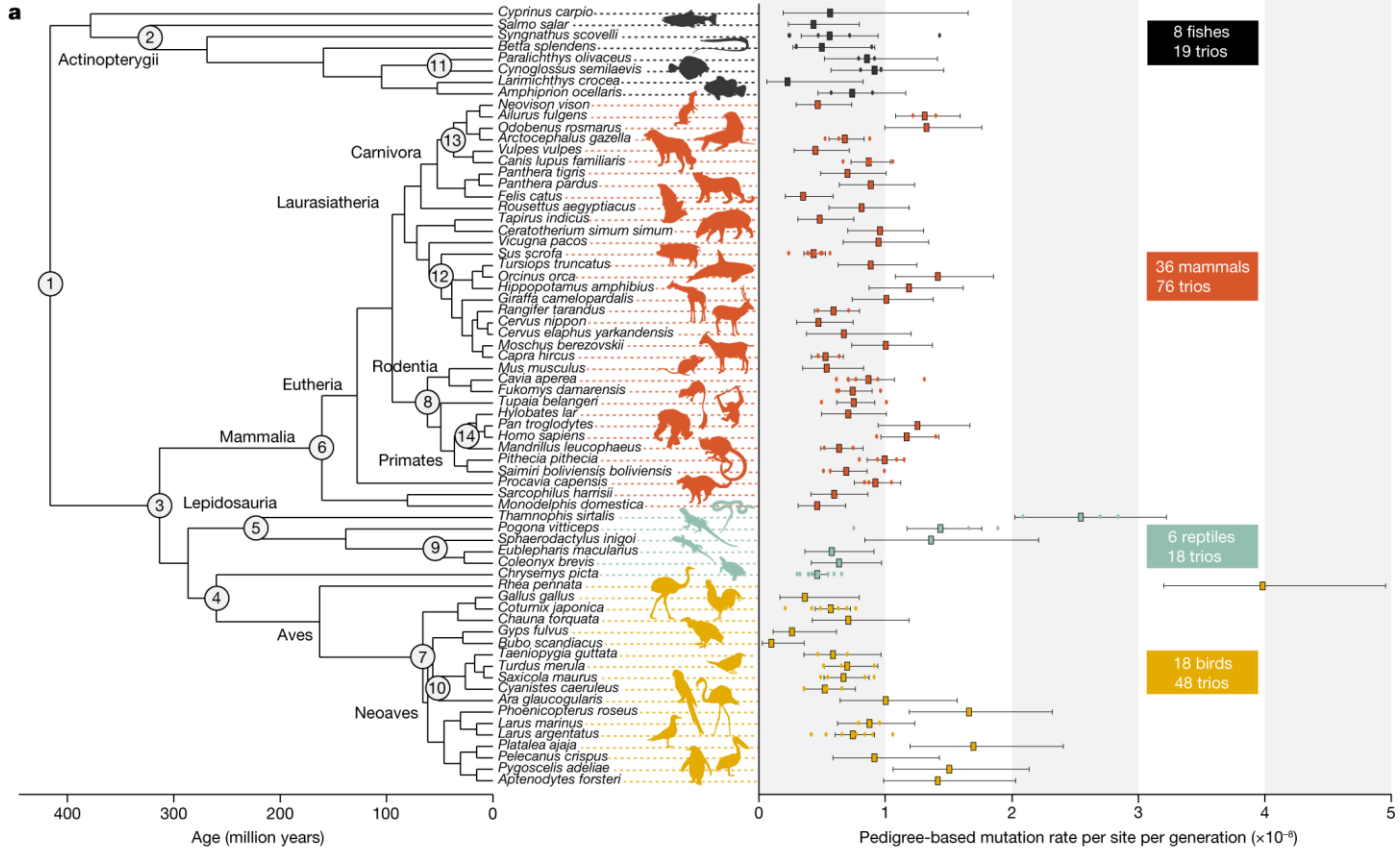

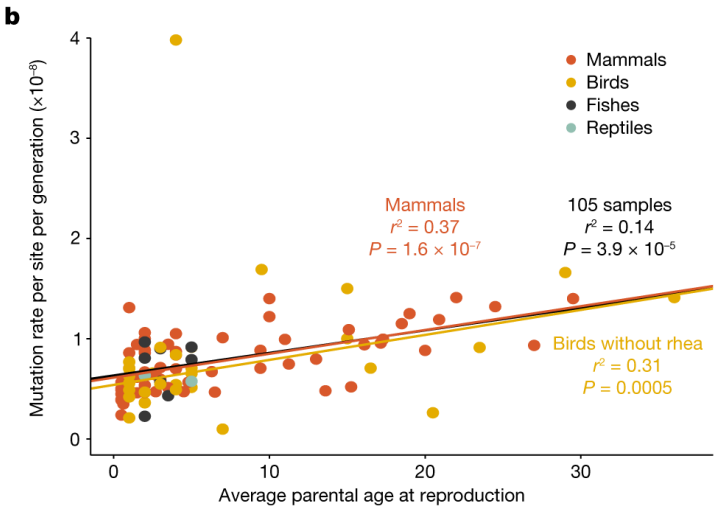

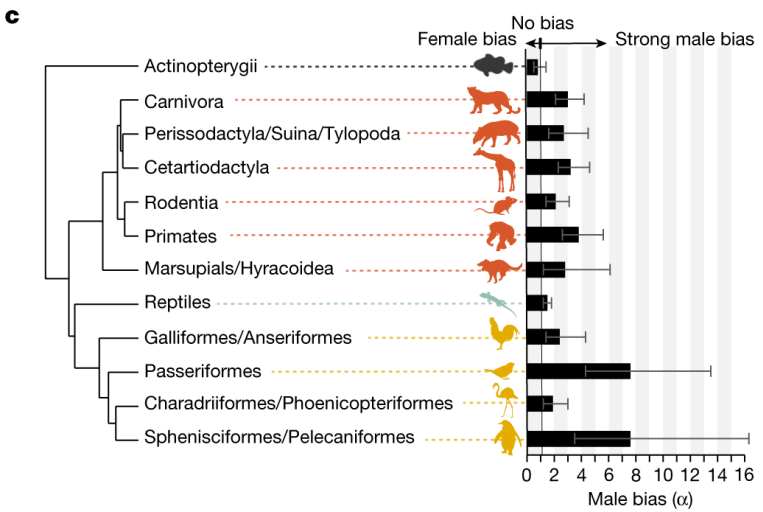

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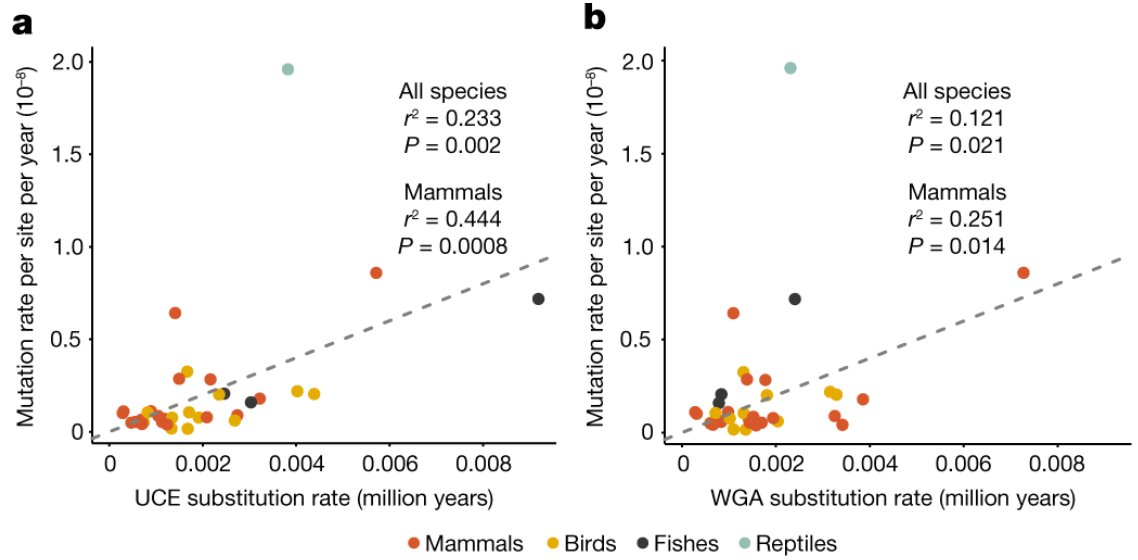
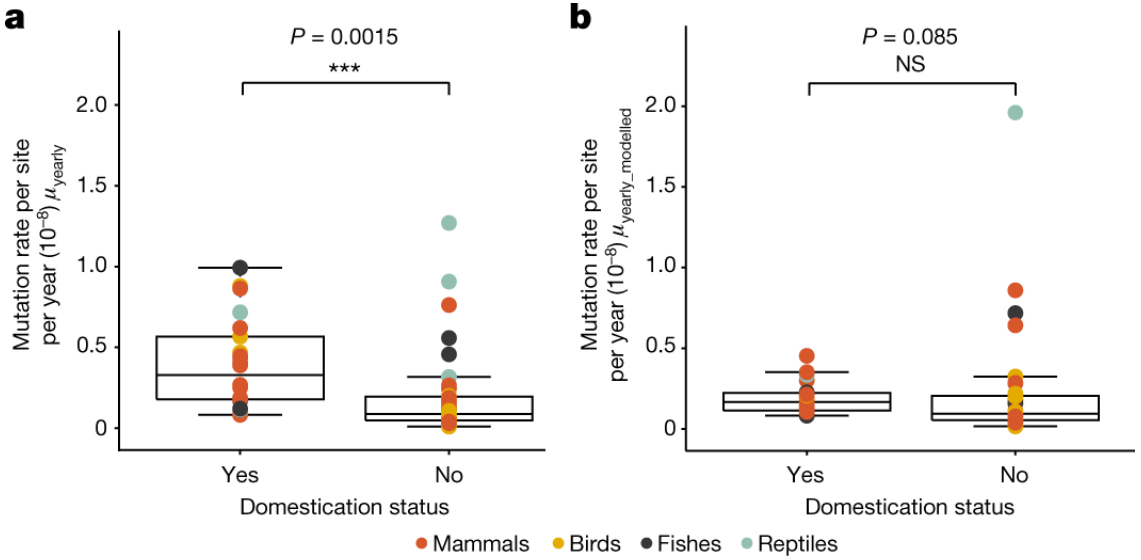
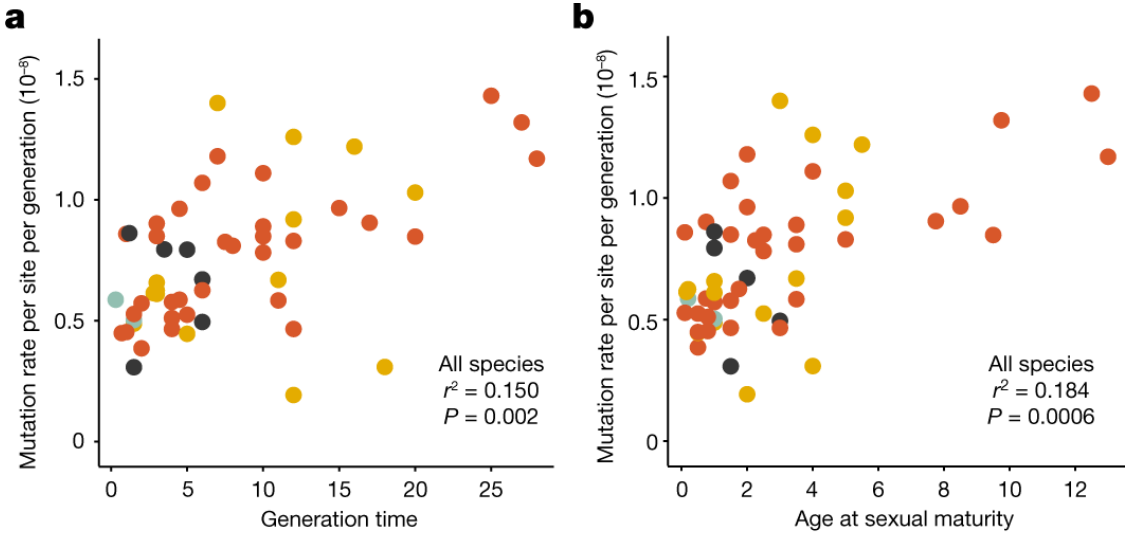
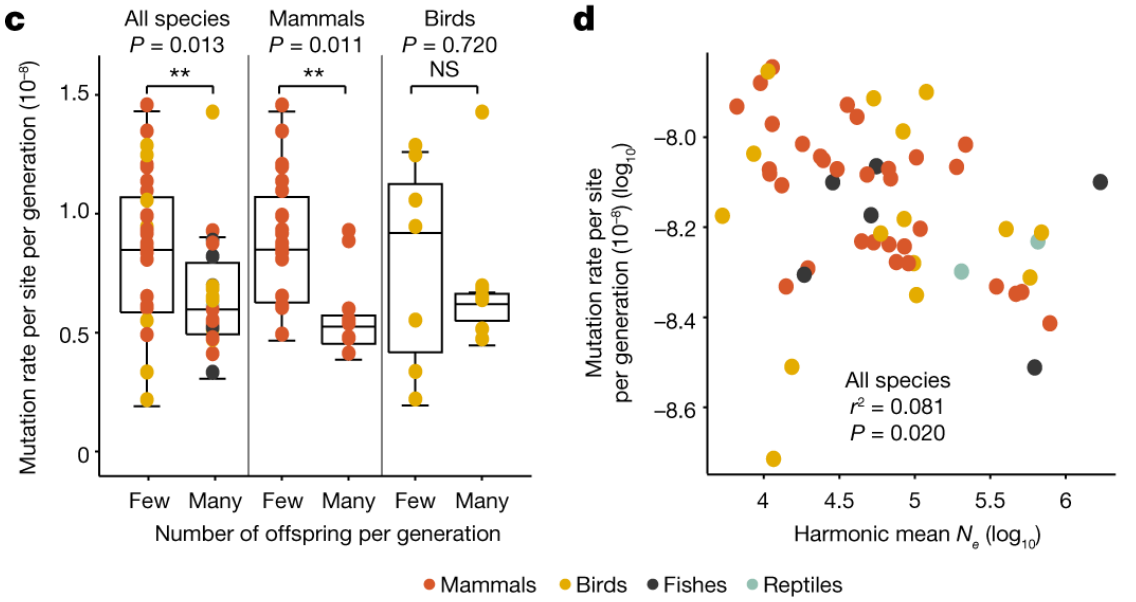
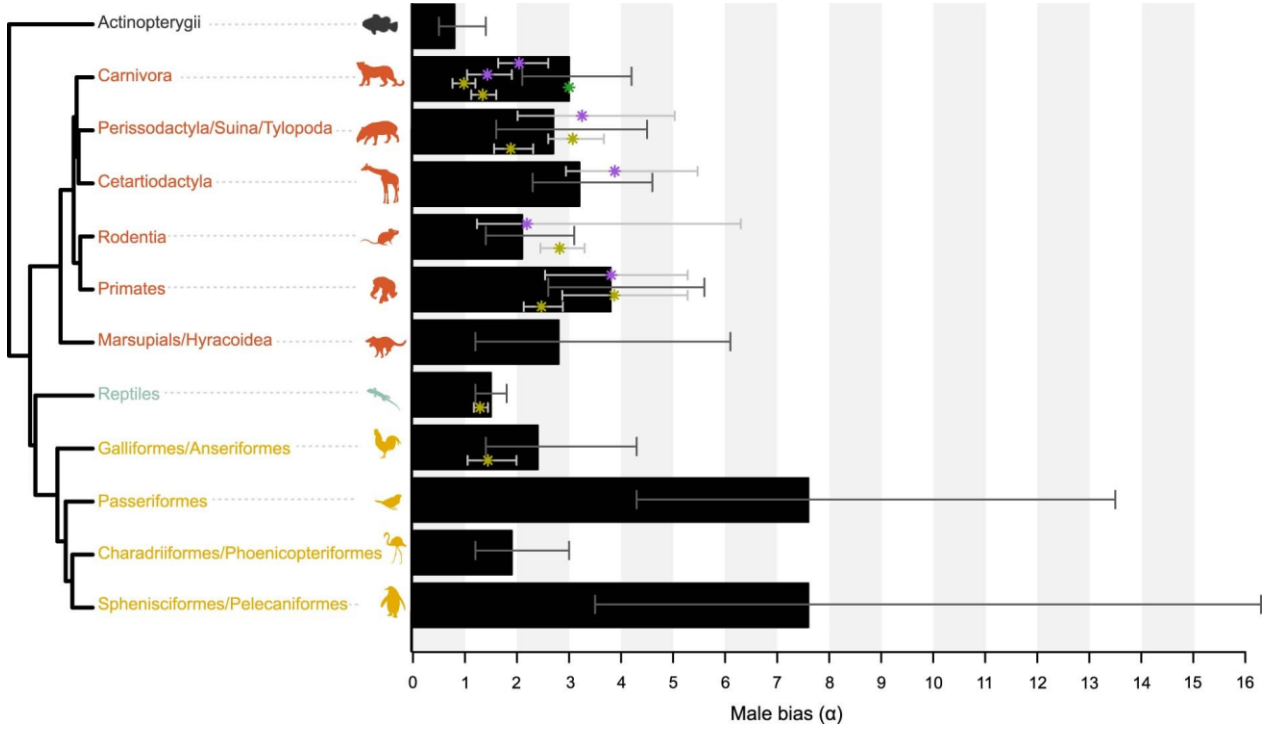
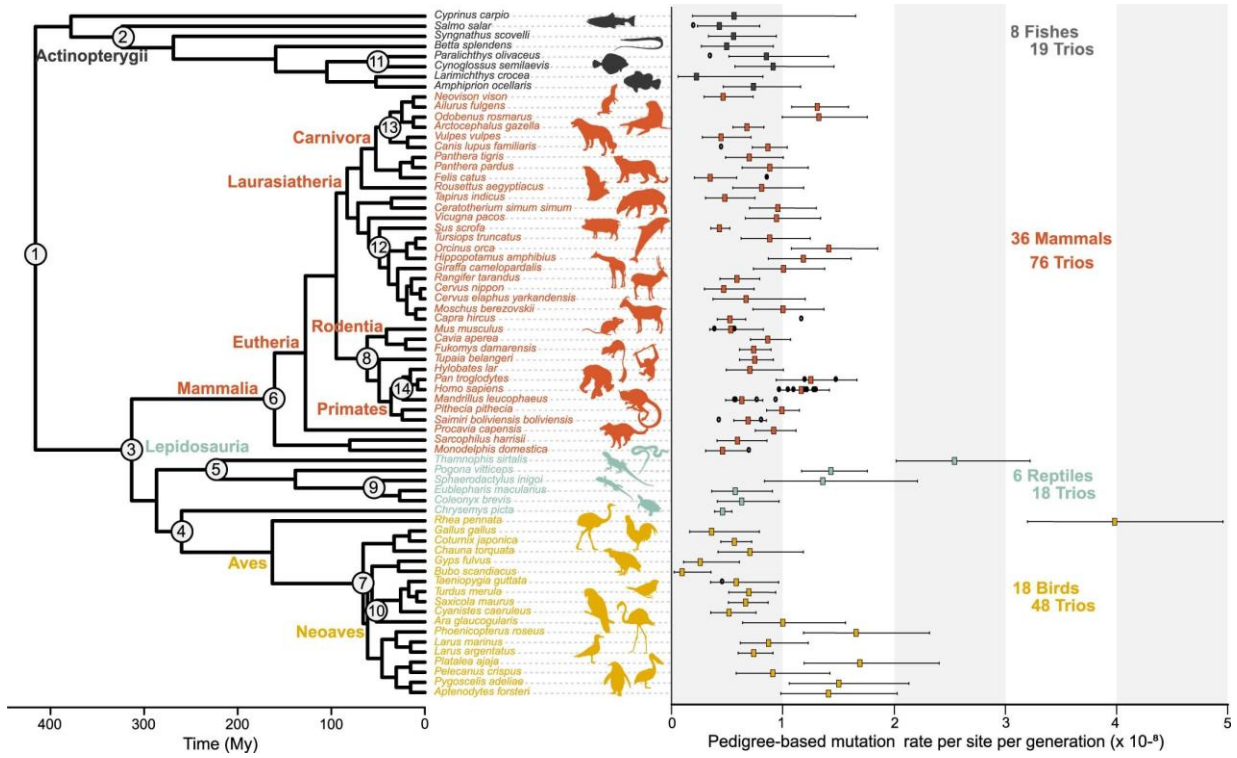

a
b
Mutation rate per site per year (10^{-8})
All species
r^2 = 0.233
P = 0.002
Mammals
r^2 = 0.444
P = 0.0008
UCE substitution rate (million years)
All species
r^2 = 0.121
P = 0.021
Mammals
r^2 = 0.251
P = 0.014
WGA substitution rate (million years)
Mammals
Birds
Fishes
Reptiles

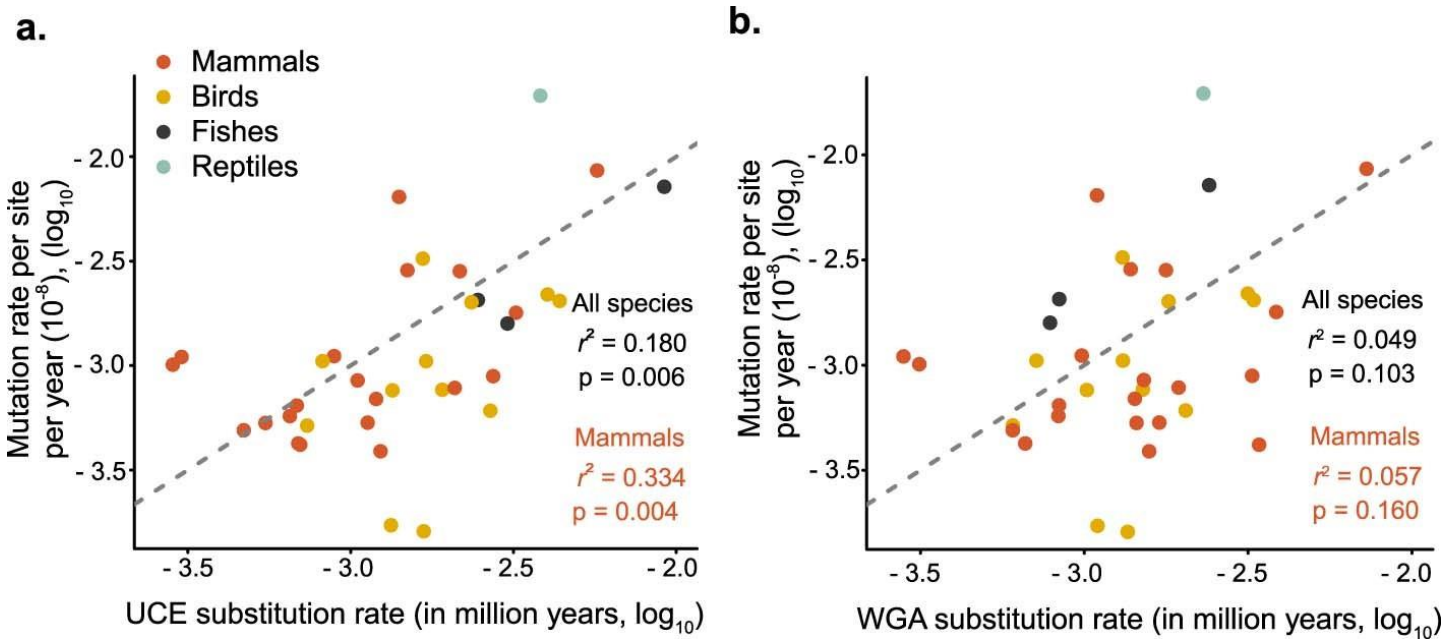

a
b
P = 0.0015
***
P = 0.085
NS
Mutation rate per site per year (10^{-8}) μ_{yearly}
Mutation rate per site per year (10^{-8}) $\mu_{yearly\_modelled}$
Yes
No
Domestication status
Mammals
Birds
Fishes
Reptiles

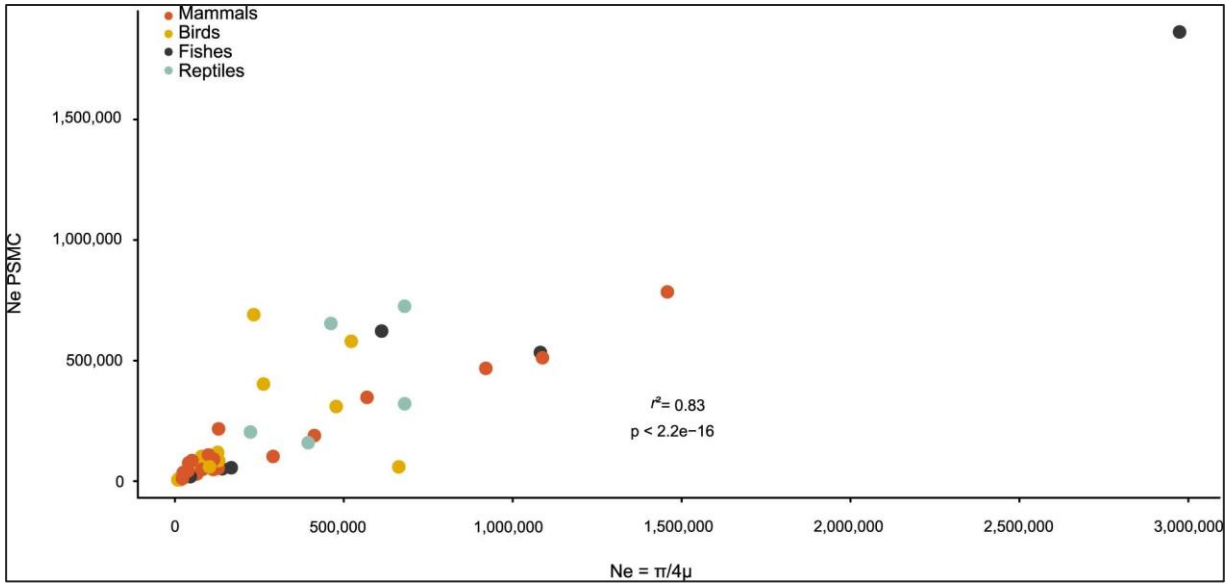

a
b
Mutation rate per site per generation (10^{-8})
All species
r^2 = 0.150
P = 0.002
Generation time
All species
r^2 = 0.184
P = 0.0006
Age at sexual maturity

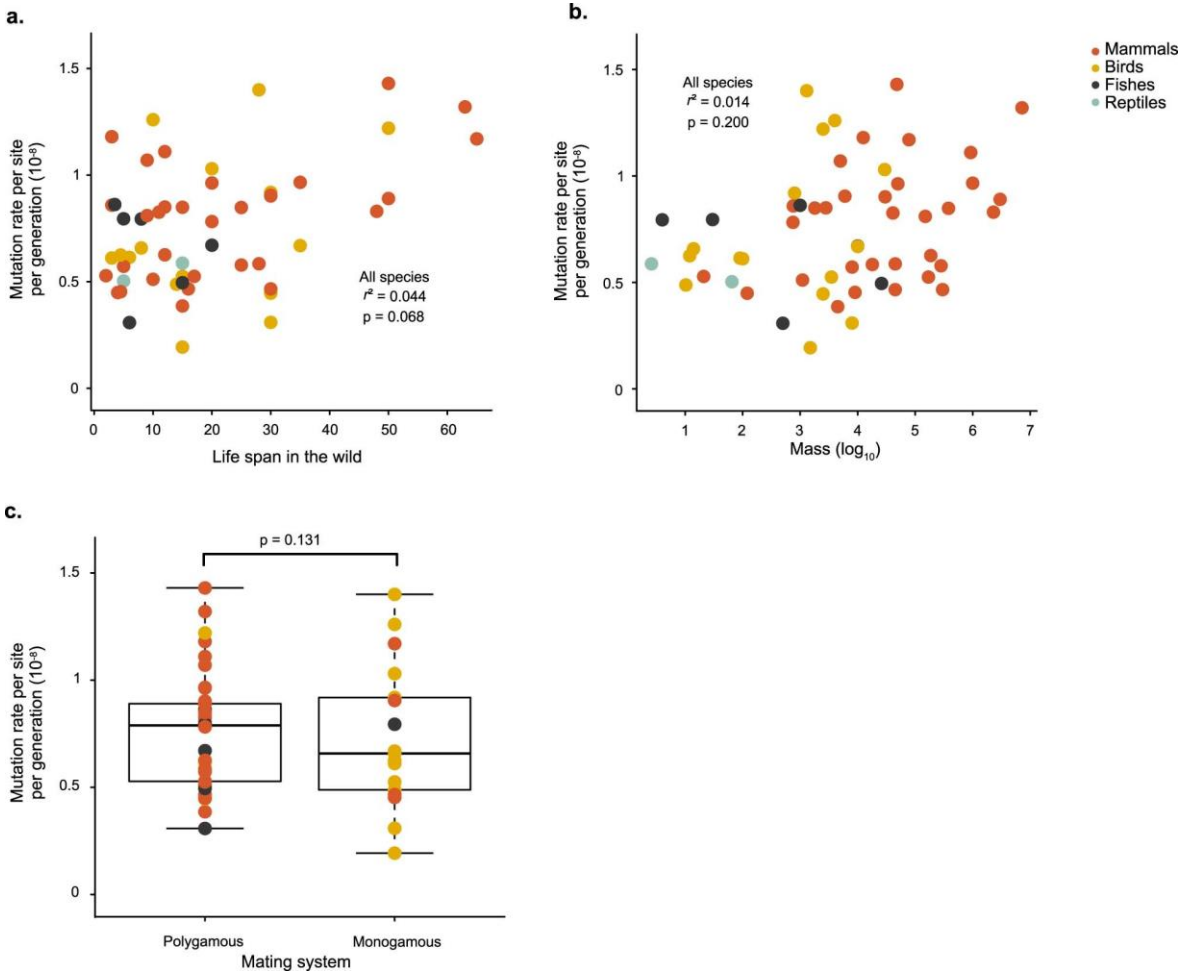

c
d
All species
P = 0.013
Mammals
P = 0.011
Birds
P = 0.720
NS
**
**
Mutation rate per site per generation (10^{-8})
Few
Many
Few
Many
Few
Many
Number of offspring per generation
Mutation rate per site per generation (10^{-8}) ($\log_{10}$)
All species
r^2 = 0.081
P = 0.020
Harmonic mean N_e ($\log_{10}$)
Mammals
Birds
Fishes
Reptiles

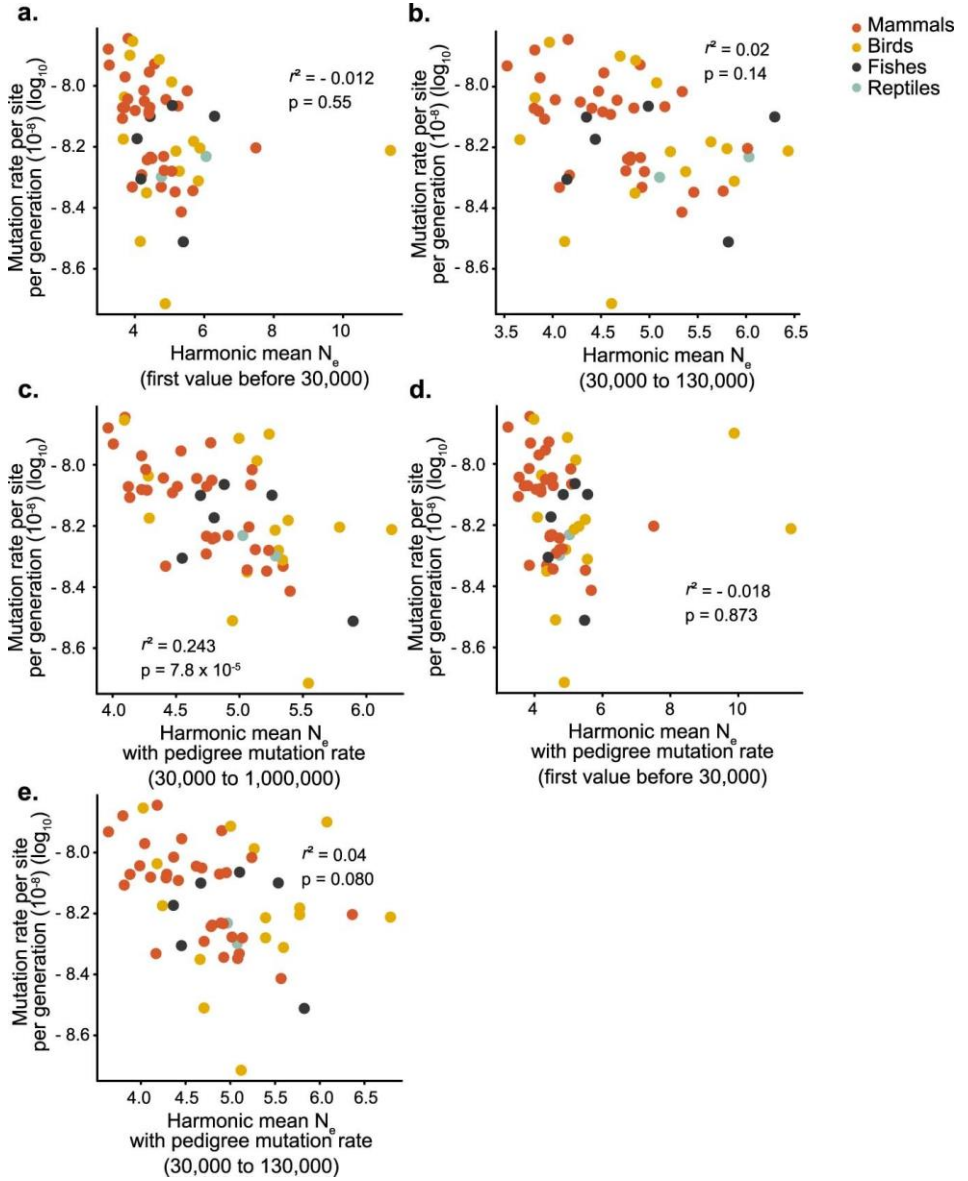

Actinopterygii
Carnivora
Perissodactyla/Suina/Tylopoda
Cetartiodactyla
Rodentia
Primates
Marsupials/Hyracoidea
Reptiles
Galliformes/Anseriformes
Passeriformes
Charadriiformes/Phoenicopteriformes
Sphenisciformes/Pelecaniformes
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
Male bias (α)


Actinopterygii
Carnivora
Laurasiatheria
Eutheria
Rodentia
Primates
Mammalia
Lepidosauria
Aves
Neoaves
8 Fishes
19 Trios
36 Mammals
76 Trios
6 Reptiles
18 Trios
18 Birds
48 Trios
400 300 200 100 0
Time (My)
0 1 2 3 4 5
Pedigree-based mutation rate per site per generation (x 10-8)


a.
Mammals
Birds
Fishes
Reptiles
Mutation rate per site per year (10^{-8}), ($\log_{10}$)
- 2.0
- 2.5
- 3.0
- 3.5
All species
r^2 = 0.180
p = 0.006
Mammals
r^2 = 0.334
p = 0.004
- 3.5
- 3.0
- 2.5
- 2.0
UCE substitution rate (in million years, $\log_{10}$)
b.
Mutation rate per site per year (10^{-8}), ($\log_{10}$)
- 2.0
- 2.5
- 3.0
- 3.5
All species
r^2 = 0.049
p = 0.103
Mammals
r^2 = 0.057
p = 0.160
- 3.5
- 3.0
- 2.5
- 2.0
WGA substitution rate (in million years, $\log_{10}$)


Mammals
Birds
Fishes
Reptiles
Ne PSMC
1,500,000
1,000,000
500,000
0
r^2= 0.83
p < 2.2e−16
0
500,000
1,000,000
1,500,000
2,000,000
2,500,000
3,000,000
Ne = π/4μ


a.
Mutation rate per site per generation (10^{-8})
Life span in the wild
All species
r^2 = 0.044
p = 0.068
b.
All species
r^2 = 0.014
p = 0.200
Mass ($\log_{10}$)
Mammals
Birds
Fishes
Reptiles
c.
p = 0.131
Polygamous
Monogamous
Mating system


a.
r^2 = - 0.012
p = 0.55
Harmonic mean N_e
(first value before 30,000)
b.
r^2 = 0.02
p = 0.14
Harmonic mean N_e
(30,000 to 130,000)
c.
r^2 = 0.243
p = 7.8 x 10^{-5}
Harmonic mean N_e
with pedigree mutation rate
(30,000 to 1,000,000)
d.
r^2 = - 0.018
p = 0.873
Harmonic mean N_e
with pedigree mutation rate
(first value before 30,000)
e.
r^2 = 0.04
p = 0.080
Harmonic mean N_e
with pedigree mutation rate
(30,000 to 130,000)
Mutation rate per site per generation (10^{-8}) ($\log_{10}$)
Mammals
Birds
Fishes
Reptiles