

MOLECULAR CLOCK, ZOOONOMIA PAPER



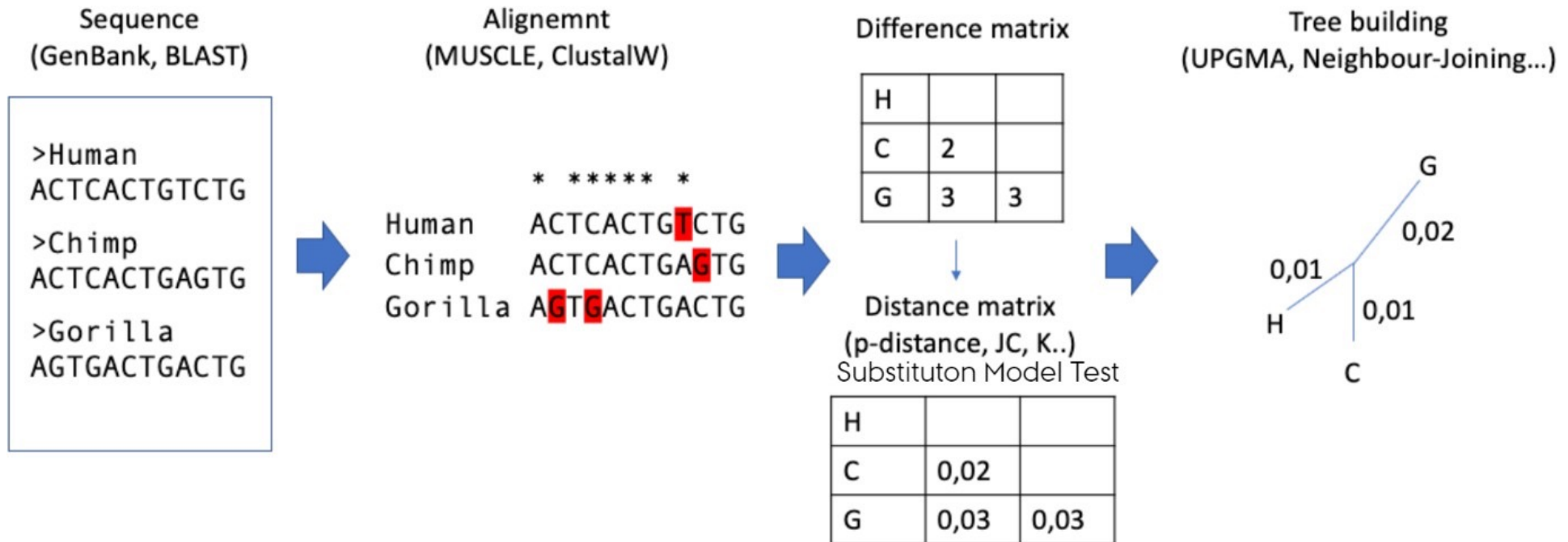
AARHUS
UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

EVOLUTIONARY THINKING 2023
WEEK 37

JANEK SENDROWSKI
PHD STUDENT



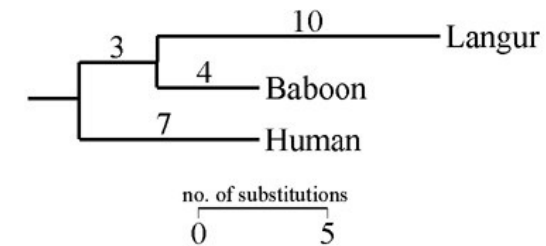
BRIEF RECAP



Distance based phylogeny tree building

MOLECULAR CLOCK

- sequence evolution rate constant across time or among lineages
- discrepancy between molecular divergence dates and fossil-based estimates
 - why?
- substitution rate heterozygosity
 - also why? And how to circumvent this?



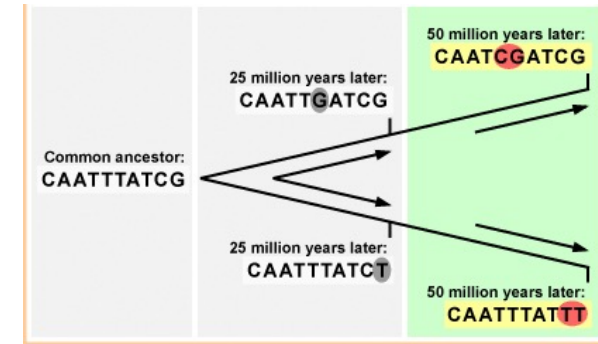
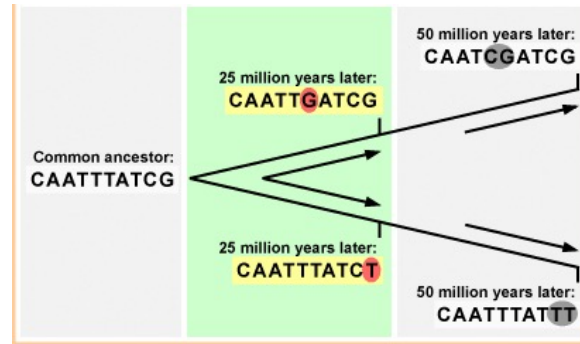
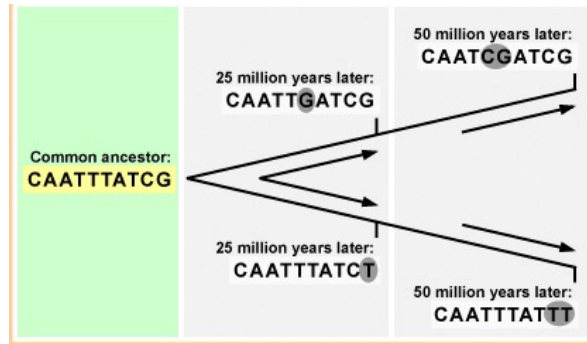
Amino acid substitutions in lysozyme C
in some primates

Data from C-B Stewart & A.C. Wilson 1987, Sequence convergence and functional adaptation of stomach lysozymes from foregut fermenters. Cold Spring Harb. Symp. Quant. Biol. 52: 891-899



MOLECULAR CLOCK

12:15-12:25



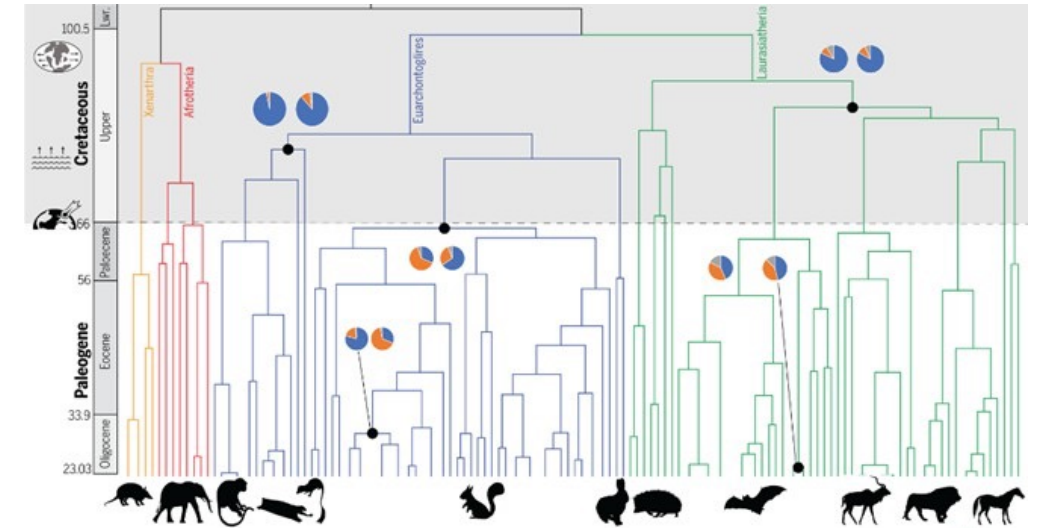
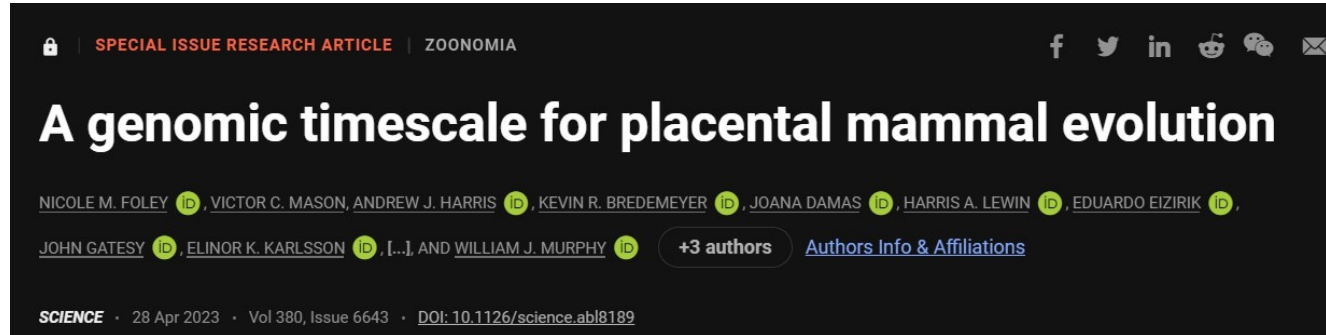
But!

[Molecular clock mirages \(Ayala 1999\)](#) - nice summary on Wikipedia:

- Changing generation times (If the rate of new mutations depends at least partly on the number of generations rather than the number of years)
- Population size (Genetic drift is stronger in small populations, and so more mutations are effectively neutral)
- Species-specific differences (due to differing metabolism, ecology, evolutionary history, ...)
- Change in function of the protein studied (can be avoided in closely related species by utilizing non-coding DNA sequences or emphasizing silent mutations)
- Changes in the intensity of natural selection.



ZOONOMIA PAPER



- A look into estimating divergence times based on multiple clock models
- Simple idea: look at how differently recombining chromosomes evolve
- Let's see how that went!



GROUP DISCUSSIONS

Group 1

Last Name	First Name	Username	Org Defined ID
Bondia Portoles	Pablo Javier	au777573	777573
Cerniauskaite	Migle	au777576	777576
Hegedus	Mark	au777578	777578
Svenningsen	Laurids	au632957	632957

Group 4

Last Name	First Name	Username	Org Defined ID
Christensen	Svend Bechmann Vang	au706411	706411
Danger	Stinna Weisberg	au643227	643227
Olesen	Johan	au700629	700629

Group 7

Last Name	First Name	Username	Org Defined ID
Hansen	Lærke Brandt	au681665	681665
Manginas	Ilias	au777554	777554
Svendsen	Cecilie	au682949	682949
Vilstrøm	Victoria Hagelskjær	au638823	638823

Group 2

Last Name	First Name	Username	Org Defined ID
Andersen	Line Witt	au668392	668392
Dyhr	Sebastian Steenstrup	au676699	676699
Stankeviciute	Martyna	au777575	777575
Zhang	Ruiqi	au779759	779759

Group 5

Last Name	First Name	Username	Org Defined ID
Cavallo	Giovanni Vincenzo	au777577	777577
Gergely	Péter	au777945	777945
Ramírez	Marina	au777574	777574
Wang	Chunni	au779762	779762

Group 8

Last Name	First Name	Username	Org Defined ID
Cooper	Helena Charlotte Carlsen	au640170	640170
Jerideh	Aban Radwan	au603885	603885

Group 3

Last Name	First Name	Username	Org Defined ID
Lück	Kjeld Janke	au691027	691027
Matthiesen	Olivia Scharf	au696268	696268
Mehlig	Antonia Christine	au777579	777579
Singh	Aakriti	au779761	779761

Group 6

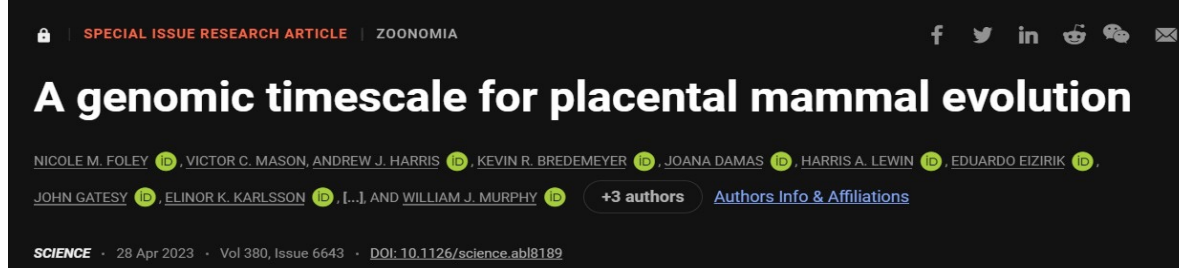
Last Name	First Name	Username	Org Defined ID
Lopez Errasti	Unai	au777552	777552
Lütken	Gorm Hjorth	au681865	681865
Núñez Martínez	Diego	au777550	777550
Rico	Grace Adalía	au779763	779763

Group 9

Last Name	First Name	Username	Org Defined ID
Birkmose	Sidsel	au683834	683834
Daskalaki	Eftychia	au777555	777555
Jensen	Elise Ledet	au702432	702432
Nielsen	Rasmine Andersson	au483502	483502



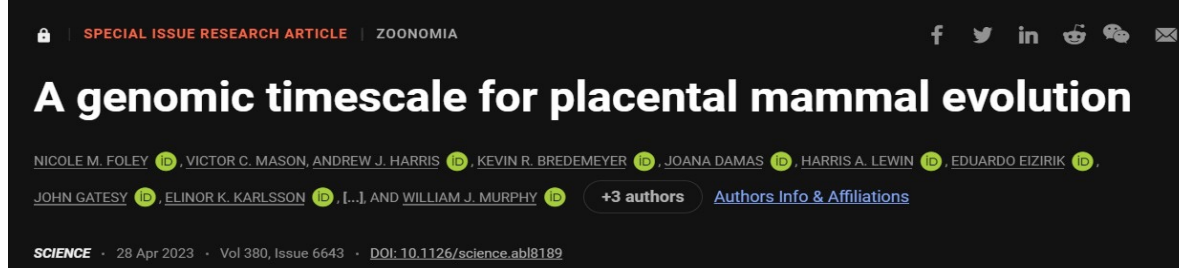
ZOONOMIA PAPER



BREAK



ZOONOMIA PAPER

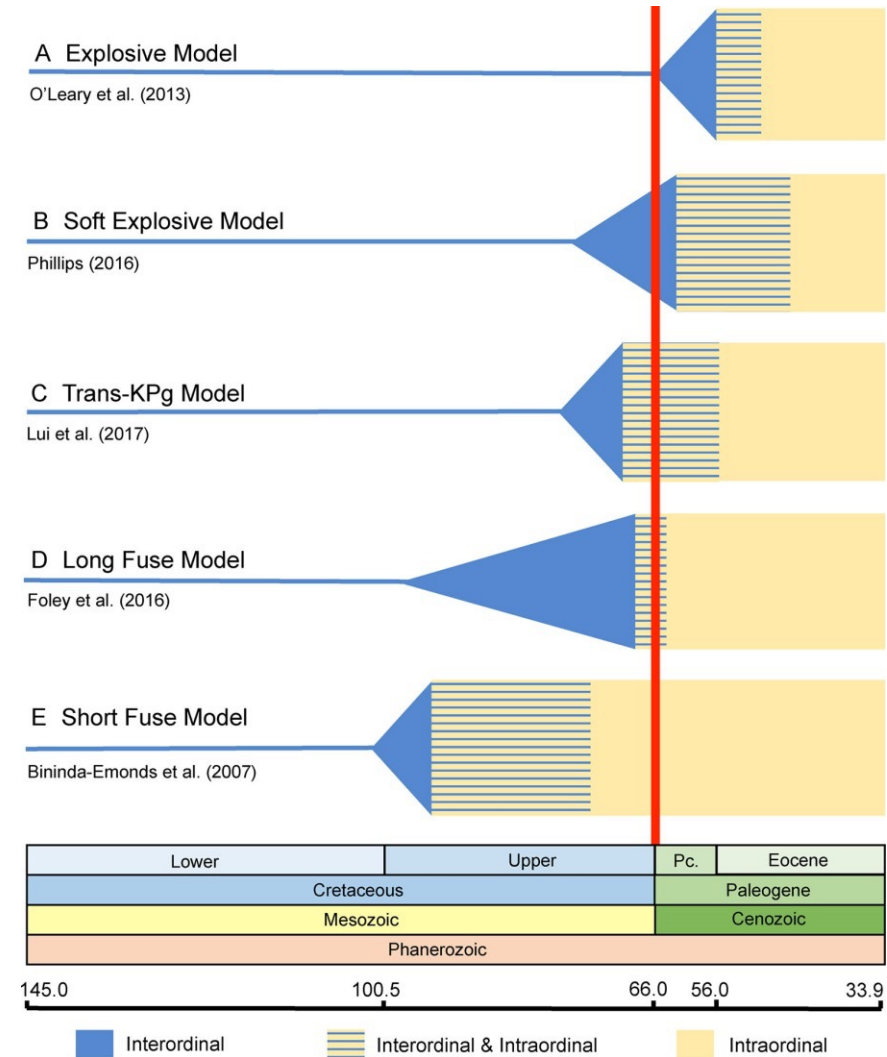


EUTHERIAN DIVERSIFICATION

Very brief discussion on the models

Use your intuition from the Zoonomia paper:
does the long fuse model make sense?

What arguments supporting the other
models can you think of?





AARHUS
UNIVERSITY