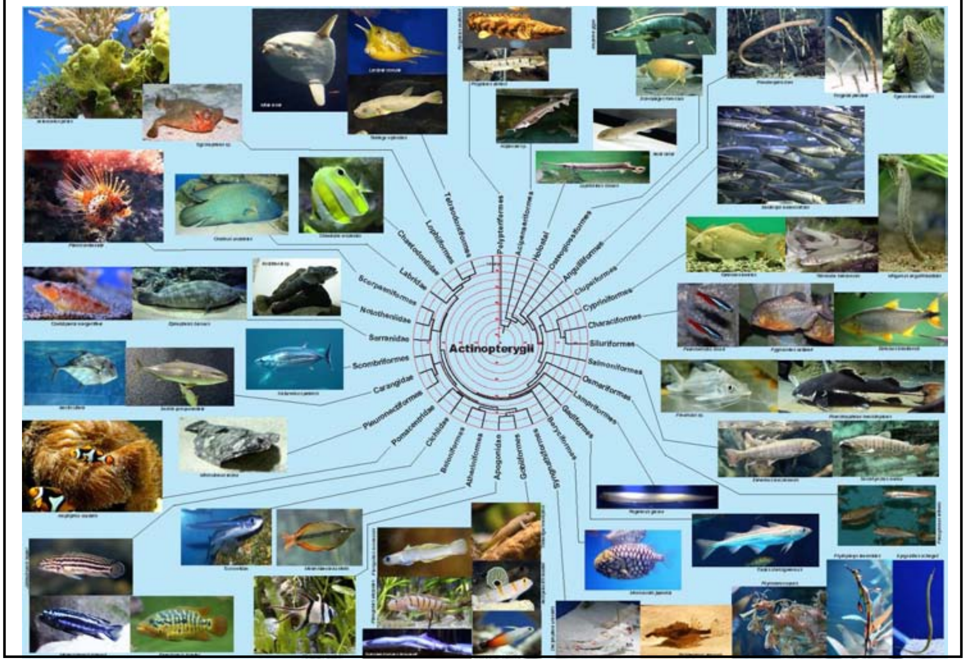
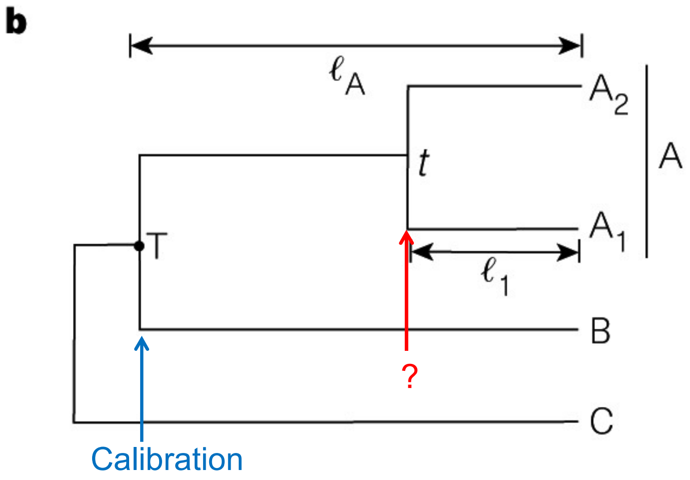
How to estimate the branching dates



Molecular clock

$$t = (\ell_1 / \ell_A) \times T$$



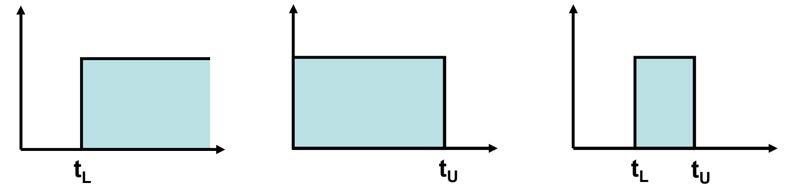
Bayesian Method for Estimating Branching Dates

- Modeling rate variation among different lineages
- Calibration based on fossil evidence

Thorne-Kishino – multidivtime

Ziheng Yang – MCMCtree

Hard Bound



minimum (younger) limit

($t > t_L$)

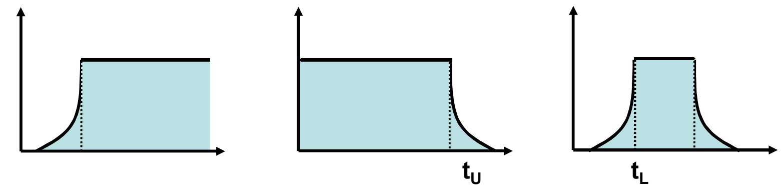
maximum (older) limit

($t < t_U$)

Minimum and maximum limit

($t_L < t < t_U$)

Soft Bound



minimum (younger) limit

($t > t_L$)

maximum (older) limit

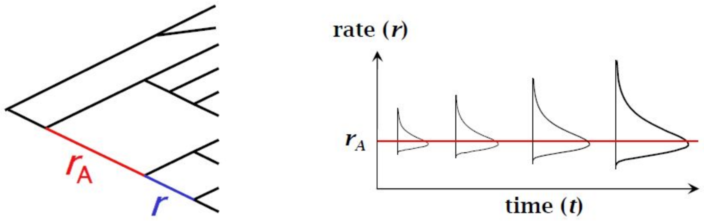
($t < t_U$)

minimum and maximum limit

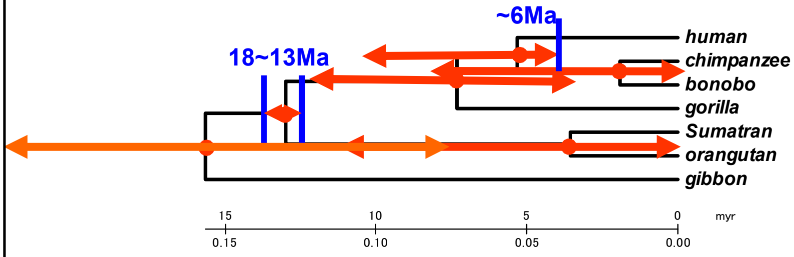
($t_L < t < t_U$)

Prior model of rate drift (geometric Brownian motion)

The rate r of a branch (node) is a random variable centred around the ancestral rate r_A. The variance σ^2 determines how variable the rates are on the tree.

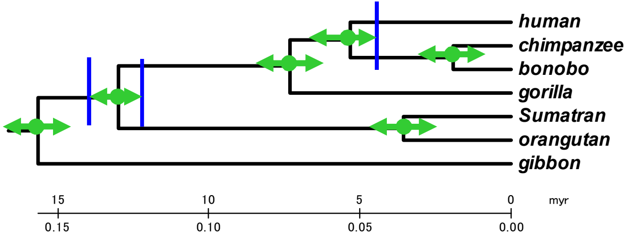


Prior distribution of the branching dates

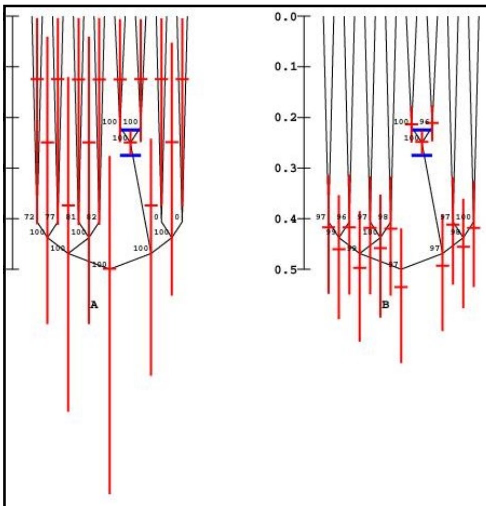


The prior distribution of the divergence times were given based on the prior distribution of "root (mean) substitution rate parameter", "rate drift parameter" and "fossil constraint"

Posterior distribution of the branching dates



By estimating the likelihood function from the data, the posterior distribution of the divergence times is obtained.

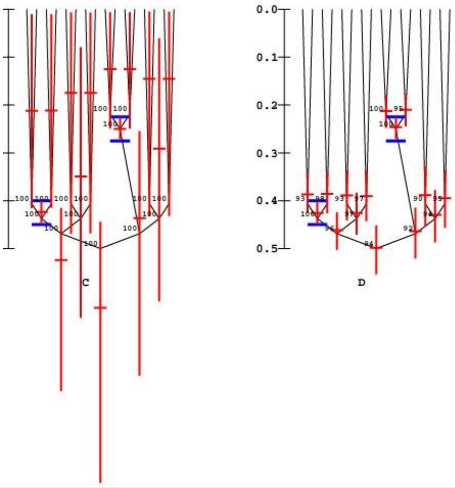


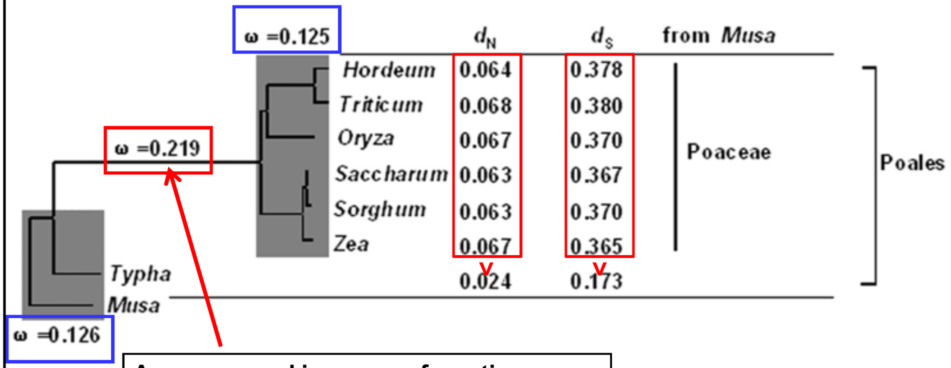
Prior distribution Posterior distribution

Only one constraint

Addition of a constraint on the 2nd nodes based on some fossil evidence

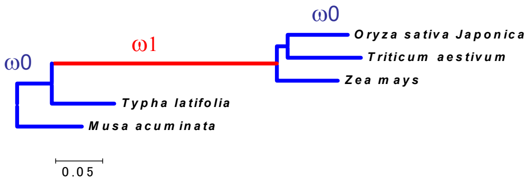
Prior distribution Posterior distribution





	d_N	d_S
Hordeum	0.064	0.378
Triticum	0.068	0.380
Oryza	0.067	0.370
Saccharum	0.063	0.367
Sorghum	0.063	0.370
Zea	0.067	0.365
	0.024	0.173

A pronounced increase of ω ratio occurred in the common ancestral branch of Poaceae, followed by reversion in the terminal branches.



Is the high evolutionary rate of grasses correlated with the high ω ratio or with the adaptive evolution? Is the rate high in grasses living today, or low similarly as the ω ratio reverted to the low level typical of the basal lineages?

To answer this question, we must explicitly take account of the time-scale of evolution.

Time estimation with a relaxed molecular clock, allowing variable rates among lineages

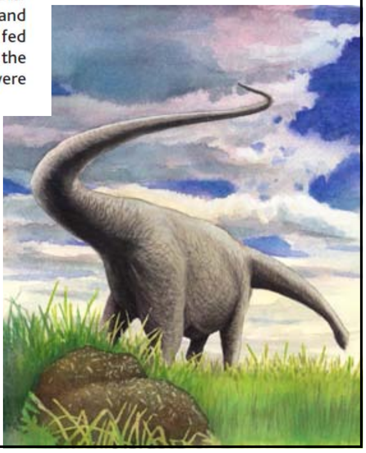
To obtain reliable time estimates, it is important to use reliable time constraints based on fossil evidence. The poor quality of the fossil record for early grasses, however, has prevented us from addressing this issue. Recent findings of grass phytoliths in Cretaceous dinosaur coprolites provided evidence that the major group of core Poaceae had already diversified before 65 Ma.

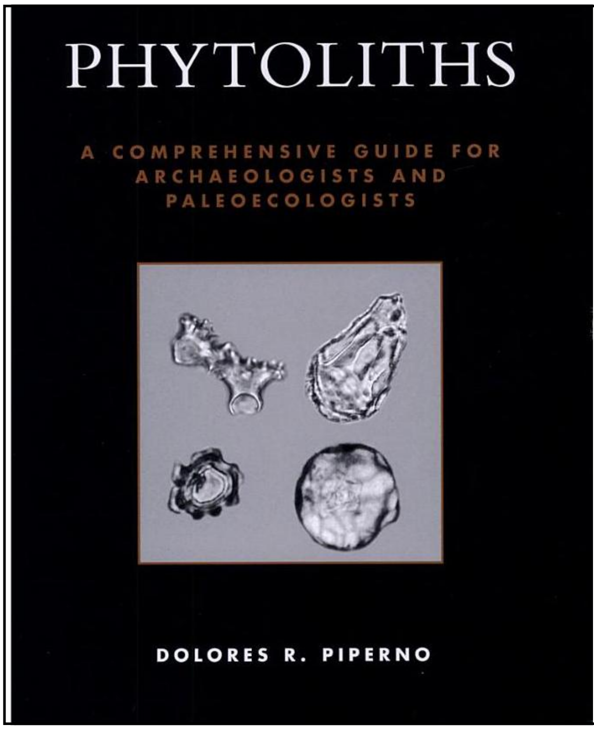
Dinosaur Coprolites and the Early Evolution of Grasses and Grazers

Vandana Prasad,[1] Caroline A. E. Strömberg,[2*]
Habib Alimohammadian,[3] Ashok Sahni[3]

SCIENCE VOL 310 18 NOVEMBER 2005

Silicified plant tissues (phytoliths) preserved in Late Cretaceous coprolites from India show that at least five taxa from extant grass (Poaceae) subclades were present on the Indian subcontinent during the latest Cretaceous. This taxonomic diversity suggests that crown-group Poaceae had diversified and spread in Gondwana before India became geographically isolated. Other phytoliths extracted from the coprolites (from dicotyledons, conifers, and palms) suggest that the suspected dung producers (titanosaur sauropods) fed indiscriminately on a wide range of plants. These data also make plausible the hypothesis that gondwanatherian mammals with hypsodont cheek teeth were grazers.





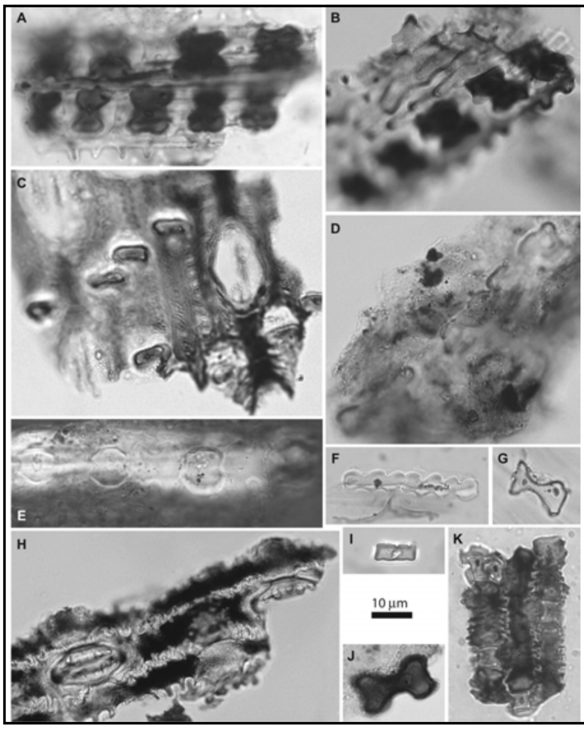
PHYTOLITHS

A COMPREHENSIVE GUIDE FOR
ARCHAEOLOGISTS AND
PALEOECOLOGISTS

DOLORES R. PIPERNO

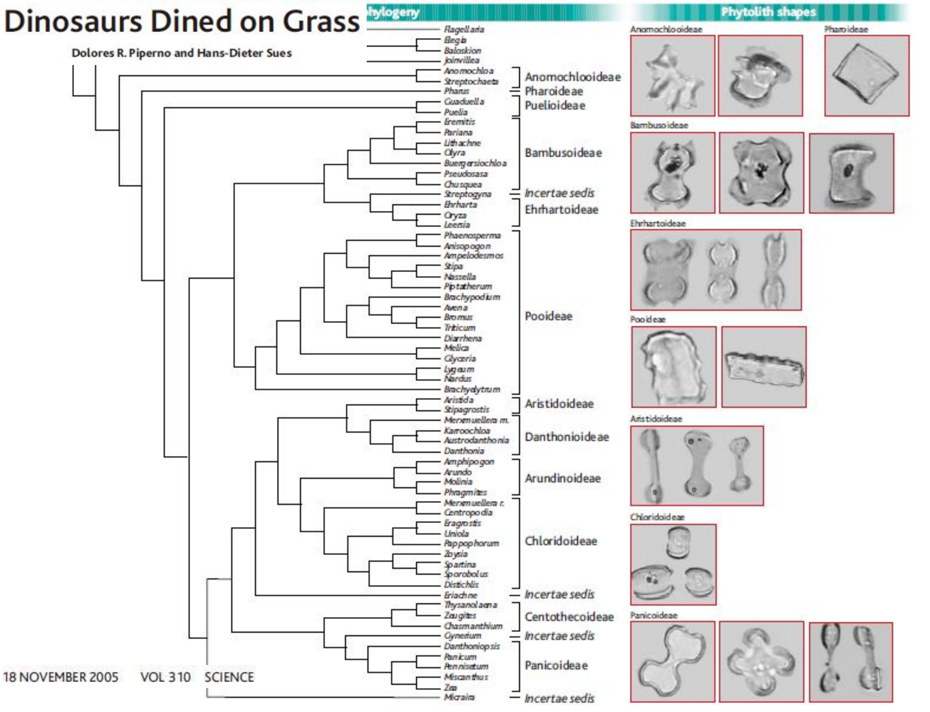
Phytoliths (Plant opal):
Silica bodies, that precipitate in plant tissues, are especially abundant in the grass family Poaceae. This is regarded as a defense against herbivores. Since shapes of phytoliths differ among different lineages of grasses, we can evaluate the ancient diversity of grasses by analyzing phytoliths found in fossils.

Alta Mira Press
Oxford, UK (2006)



Fossil phytolith in dinosaurs coprolites

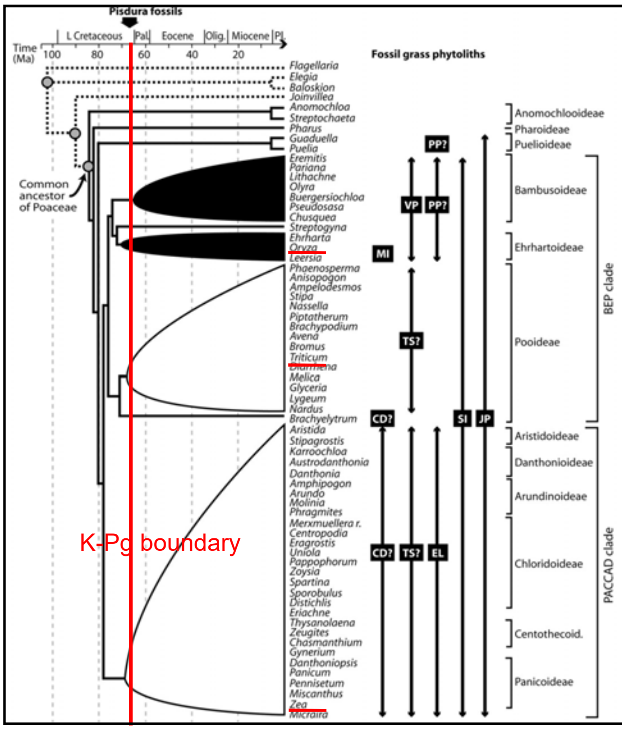
Prasad et al. (2005) Science



Dinosaurs Dined on Grass

Dolores R. Piperno and Hans-Dieter Sues

18 NOVEMBER 2005 VOL 310 SCIENCE



The major divergence among core Poaceae (e.g., *Zea/Oryza* separation) preceded the K/Pg boundary (65 Ma).

Prasad et al. (2005) Science

Bayesian methods for time estimation with a relaxed clock

	Multidivtime (Jeff Thorne)	MCMCtree (Ziheng Yang)
Calibrations	Hard bounds	Soft bounds
Prior on rates	Auto-correlated rates	Auto-correlated rates + Independent rates

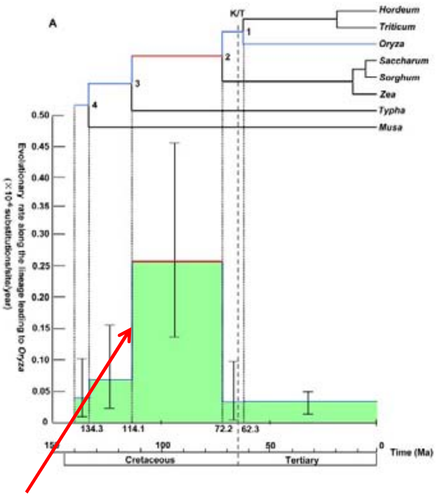
・Since the bounds provided by fossil evidence are not always correct, soft bounds in calibrating a clock is preferable to hard bounds. By using the soft bounds, the probability that the true divergence time is outside the bounds is small but not zero.
・In the Jeff Thorne's "Multidivtime", rates are assumed to be correlated between neighboring branches, but it might be interesting to check whether this assumption holds by using both the auto-correlated and the independent rates models implemented in "MCMCtree" by Ziheng Yang.

Table S3. Posterior estimates of divergence times by MCMCTREE in PAML (Yang, 2007). 95% highest posterior density (HPD) is shown in parentheses. Rate refers to the rate of the branch preceding the node. Node numbers refer to those in Fig. 2. The >65 Ma constraint is given to the *Zea/Oryza* separation.

Node	Independent-rates model		Correlated-rates model	
	Time (Ma)	Rate	Time (Ma)	Rate
1 (*Musa*)	115.18 (67.47-137.89)	0.059 (0.017-0.168)	88.15 (47.14-129.47)	0.109 (0.056-0.240)
2 (*Typha*)	98.30 (59.70-122.54)	0.085 (0.032-0.236)	78.38 (42.99-119.04)	0.131 (0.061-0.318)
3 (*Zea*/ *Oryza*)	**67.76** (47.84-84.90)	**0.291** (0.149-0.714)	**45.84** (19.66-71.66)	**0.278** (0.143-0.961)
4 (*Oryza*/ *Triticum*)	54.44 (34.22-71.48)	0.038 (0.011-0.115)	36.51 (15.51-61.98)	0.053 (0.017-0.146)

The independent-rates model gives time estimates more in accord with the fossil evidence than the correlated-rates model, suggesting that the elevation of the rate in grasses was abrupt.

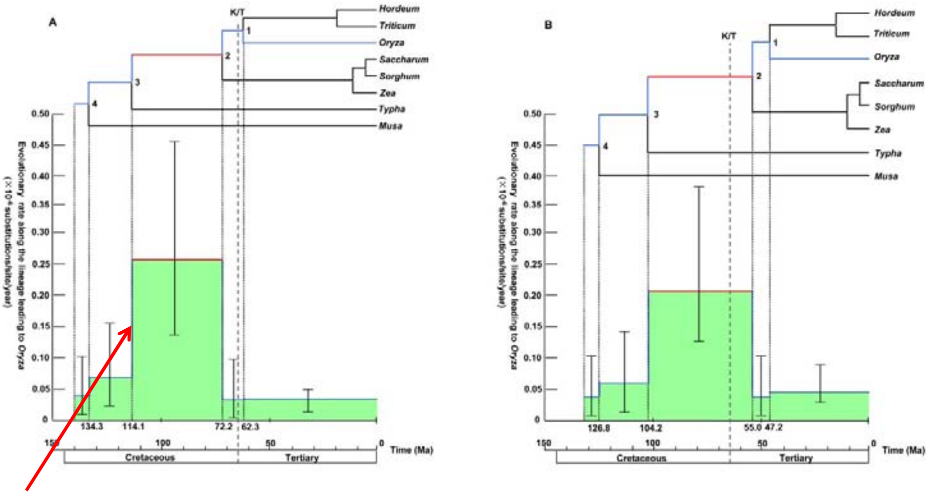
>65 Ma constraint to *Zea*/*Oryza* separation



Rate change along the lineage from the root to *Oryza*.

>65 Ma constraint to *Zea*/*Oryza* separation

No constraint to *Zea*/*Oryza* separation

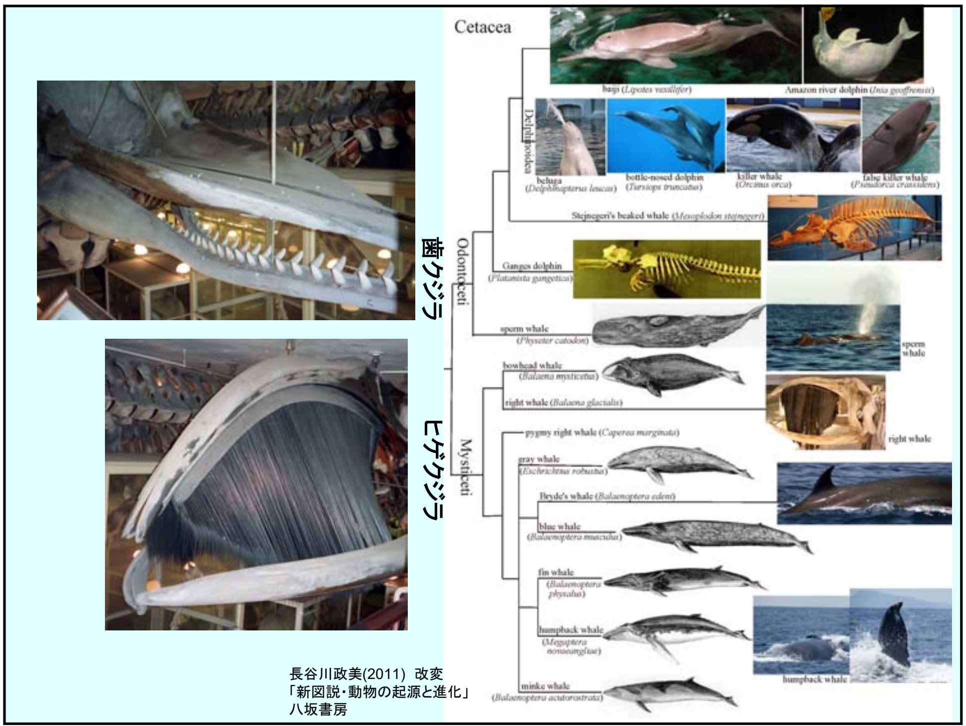


Rate change along the lineage from the root to *Oryza*.

Conclusion

1. Elevation of the evolutionary rate and adaptive evolution in chloroplast genomes were observed in the common ancestral branch of grasses after they diverged from *Typha*.

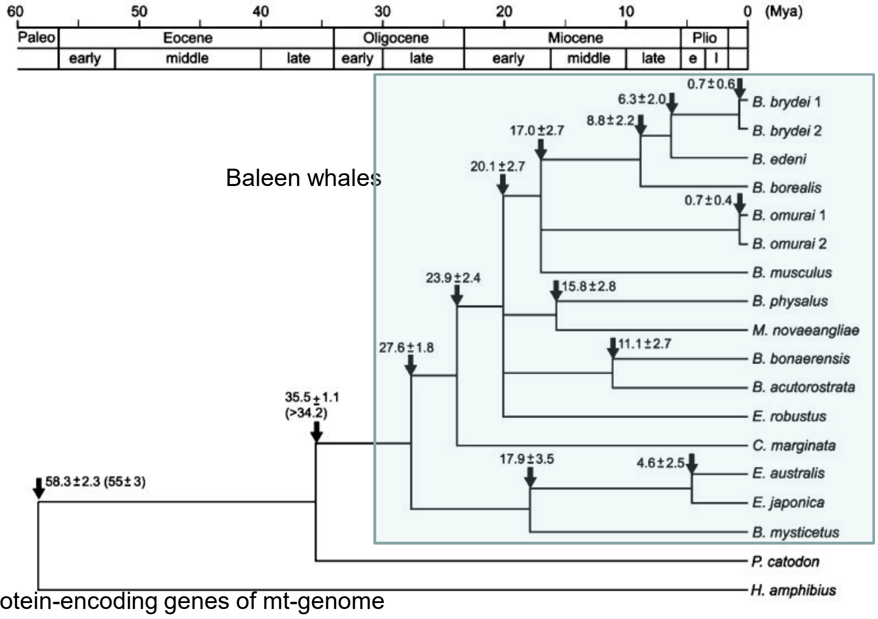
2. Our finding highlights the need for paying attention to rates of internal branches rather than averaging along a whole lineage in addressing the rate heterogeneity problem.



長谷川政美(2011) 改変
「新図説・動物の起源と進化」
八坂書房

Divergence time estimates within Mysticeti (baleen whales) by Sasaki et al. (2006)

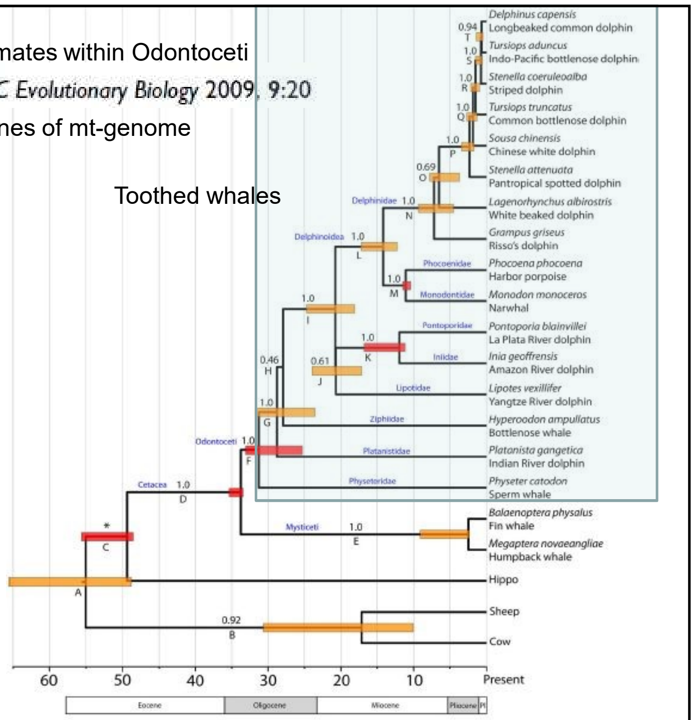
T. Sasaki et al. / Molecular Phylogenetics and Evolution 41 (2006) 40–52



Protein-encoding genes of mt-genome

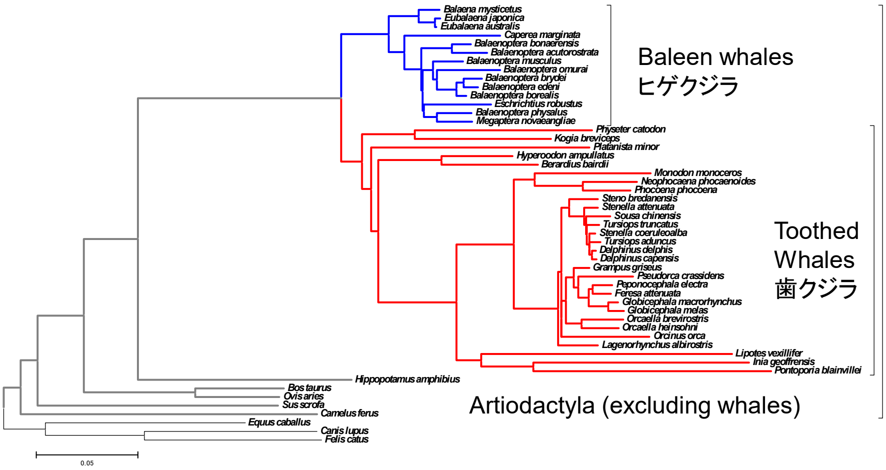
Divergence time estimates within Odontoceti
by Xiong (2009) *BMC Evolutionary Biology* 2009, 9:20

Protein-encoding genes of mt-genome



Toothed whales

The evolutionary rate of mtDNA is high in cetaceans; particularly high in toothed whales but not very much in baleen whales.

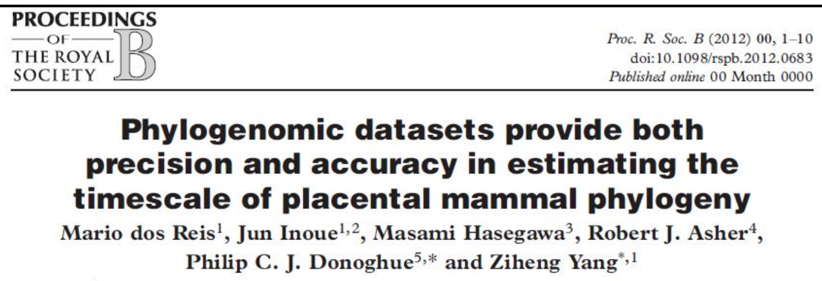


Baleen whales
ヒゲクジラ

Toothed
Whales
歯クジラ

偶蹄鯨類

Artiodactyla (excluding whales)



PROCEEDINGS OF THE ROYAL SOCIETY B

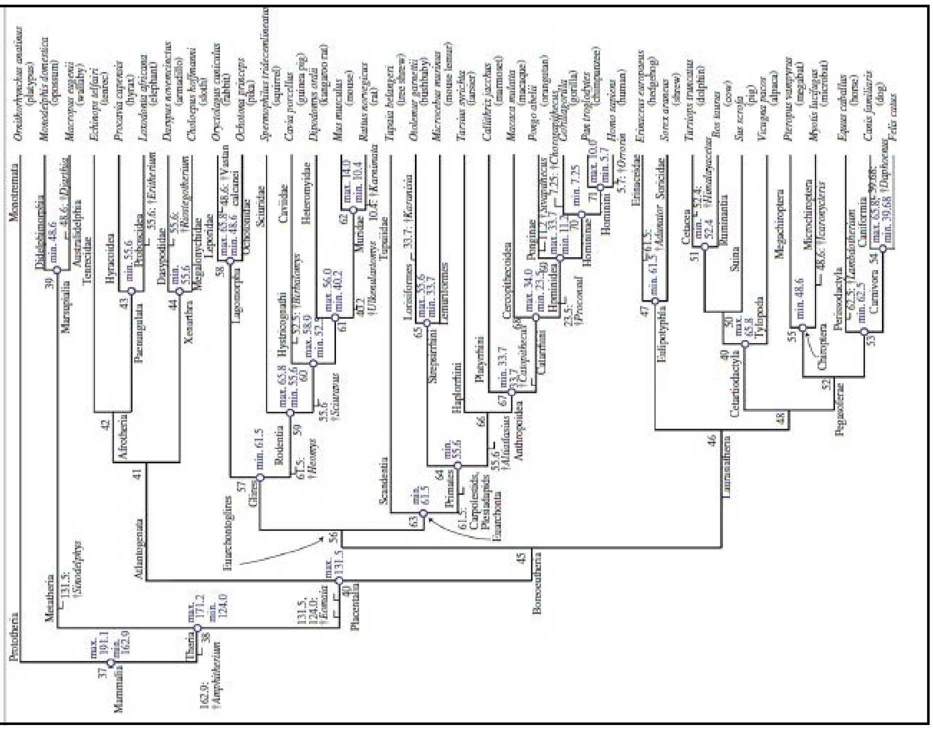
Proc. R. Soc. B (2012) 00, 1–10
doi:10.1098/rspb.2012.0683

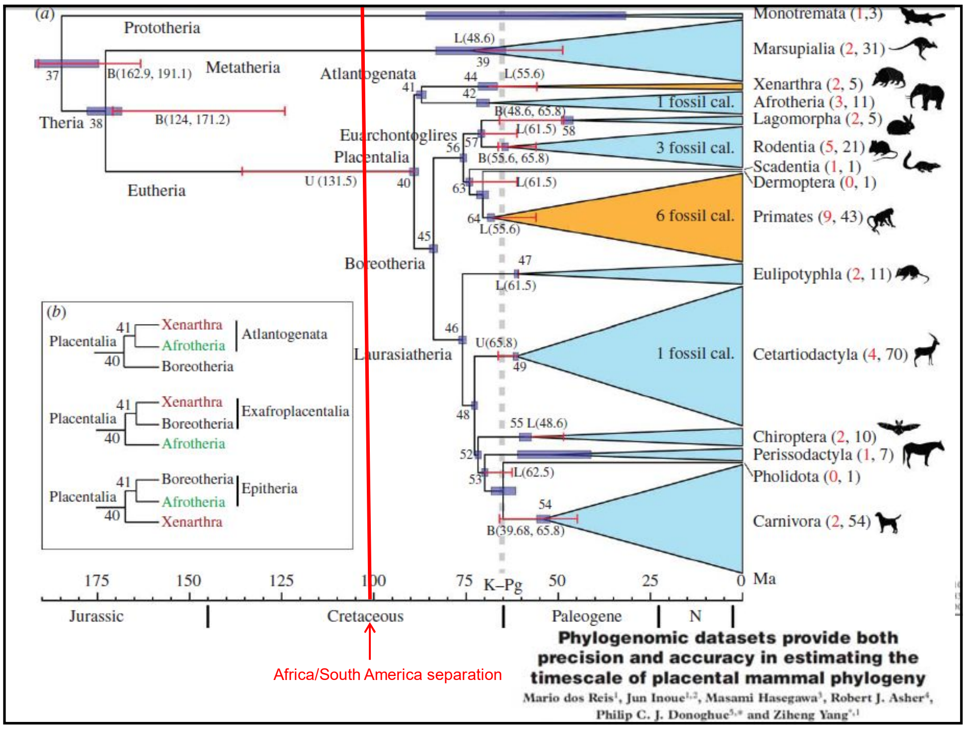
Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny

Mario dos Reis[1], Jun Inoue[1,2], Masami Hasegawa[3], Robert J. Asher[4], Philip C. J. Donoghue[5,*] and Ziheng Yang[*,1]

Analysis of 2 stages

- 14,632 nuclear gene (20.6x10^6 bp) from 36 mammalian species (33 eutherians + 2 marsupials + 1 monotreme)
- The posterior probability of the divergence times obtained in the 1st stage was used to construct the time prior for mt-genome analysis of 274 mammal species.





Africa/South America separation

Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny

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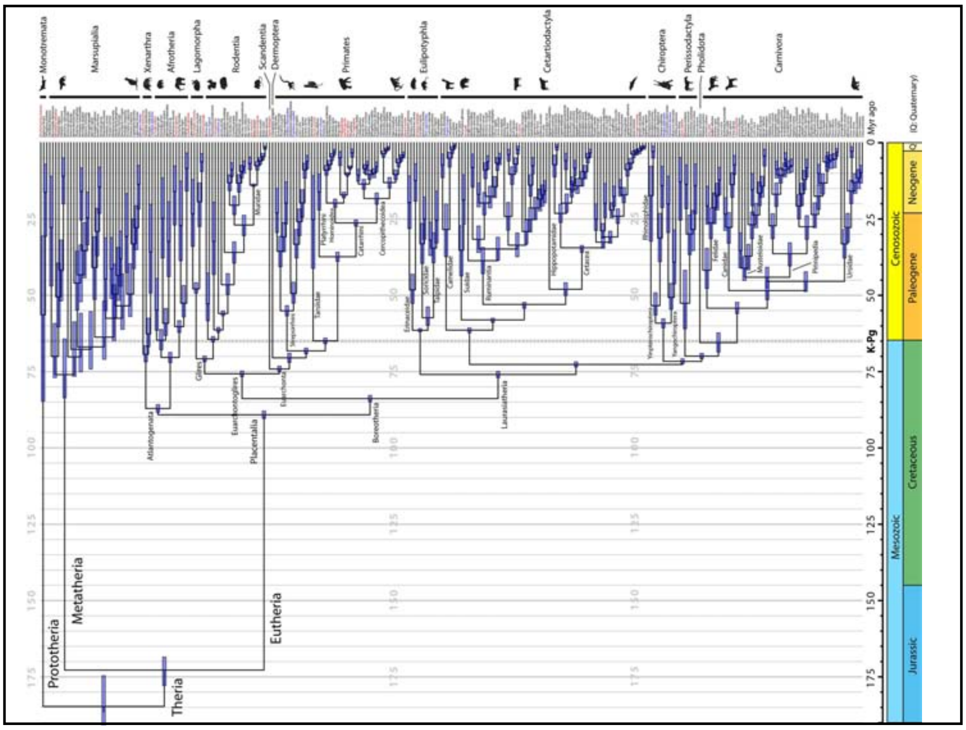

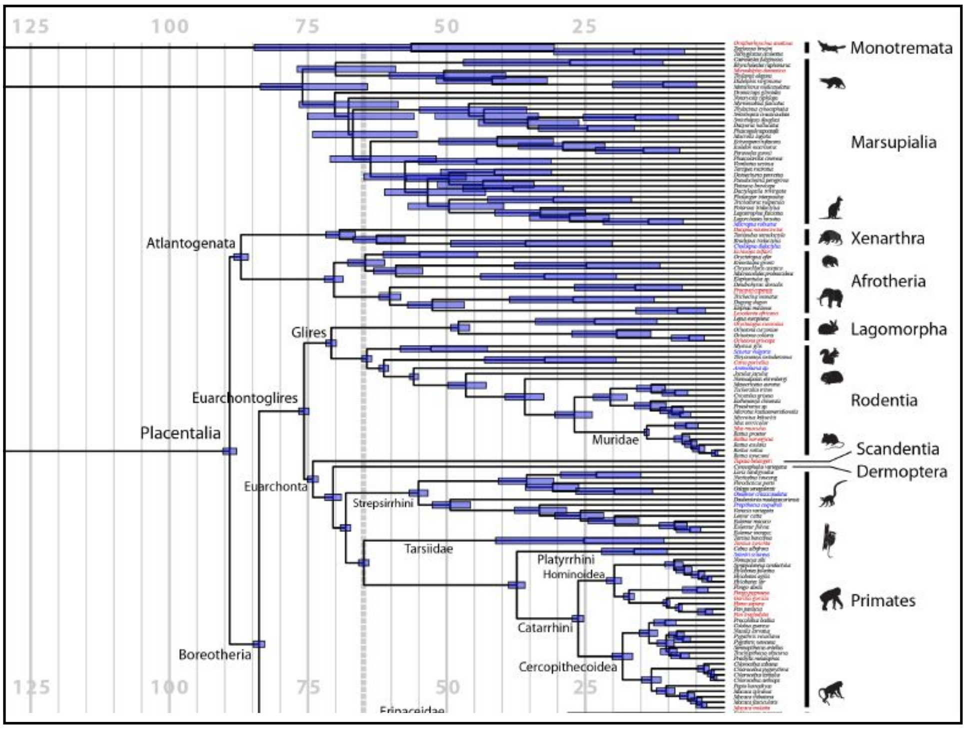
125
100
75
50
25
Monotremata
Marsupialia
Atlantogenata
Xenarthra
Afrotheria
Glires
Lagomorpha
Euarchontoglires
Rodentia
Placentalia
Muridae
Scandentia
Dermoptera
Euarchonta
Strepsirrhini
Tarsiidae
Platyrrhini
Hominoidea
Primates
Catarrhini
Boreotheria
Cercopithecoidea
125
100
75
50
25