

Electronic Supplementary Material

Postcopulatory sexual selection influences baculum evolution in primates and carnivores

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These supplementary materials provide information additional to that contained in the main paper on: trait data, ancestral state reconstructions using additional data and the variable rates model, and other analyses.

Notes on Trait Data

a) Baculum data

When more than one data point was available, the mean baculum length was used.

b) Body mass data

All body masses are those of adult males, aside from species in which no body size dimorphism exists.

c) Intromission data

'Long' intromission was defined as that which continued for longer than 180 seconds and 'short' intromission was defined as that which continued for less than 180 seconds (following Dixson [1]).

d) Mating system data

Primates for which more than one mating system was cited in the literature were coded as such. If the polymorphism included polygamy, the species was removed from the dataset before analyses were run as this effectively meant it fell on both sides of the binary grouping variable ('polygamy' versus 'other').

e) Breeding seasonality data

Primates were classed as 'seasonal breeders' if over 67% of births occurred over a peak three-month period [2].

Mammalian Ancestral State Reconstructions

Species within the orders Pholidota and Xenarthra have been consistently excluded from literature describing the mammalian orders in which the baculum is present, suggesting that a baculum is not present in these orders. However, since it was not possible to find a source explicitly stating that this was the case, these orders were excluded from our main reconstruction of the evolution of the baculum across mammals. Similarly, species within the orders Afrosoricida and Eulipotyphla have been consistently defined as orders in which a baculum is present and it has not been possible to find any indication that this is not the case for all species within the order [3,4]. However, since no source has directly stated that all species within these orders have a baculum, they too were excluded from our main reconstruction of bacular evolution.

This approach, although cautious, may not be as accurate as if these orders were to be included. For this reason, we re-ran exactly the same multistate analysis across the mammalian phylogeny, this time including Pholidota, Xenarthra, Afrosoricida and Eulipotyphla. The results of this analysis (table S1) produce a more specific time frame for the first evolution of the baculum, suggesting an initial appearance after node 2, but before node 4 (see figure S1). Another notable change in this version of the analysis is that the baculum is indicated to be absent at node 5, rather than present as in the original analysis. This is understandable given the addition of an entire order in which a baculum is absent to this clade.

Table S1. Probability of baculum presence or absence at the root and seven nodes of the mammalian phylogeny.

	Baculum Absent		Baculum Present	
	Mean Probability	Standard Error	Mean Probability	Standard Error
Root	1.00	0.0000	0.00	0.0000
Node 1	1.00	0.0001	0.00	0.0001
Node 2	0.92	0.0005	0.08	0.0005
Node 3	1.00	0.0000	0.00	0.0000
Node 4	0.00	0.0000	1.00	0.0000
Node 5	0.89	0.0005	0.11	0.0005
Node 6	0.01	0.0000	0.99	0.0000
Node A	0.03	0.0000	0.97	0.0000

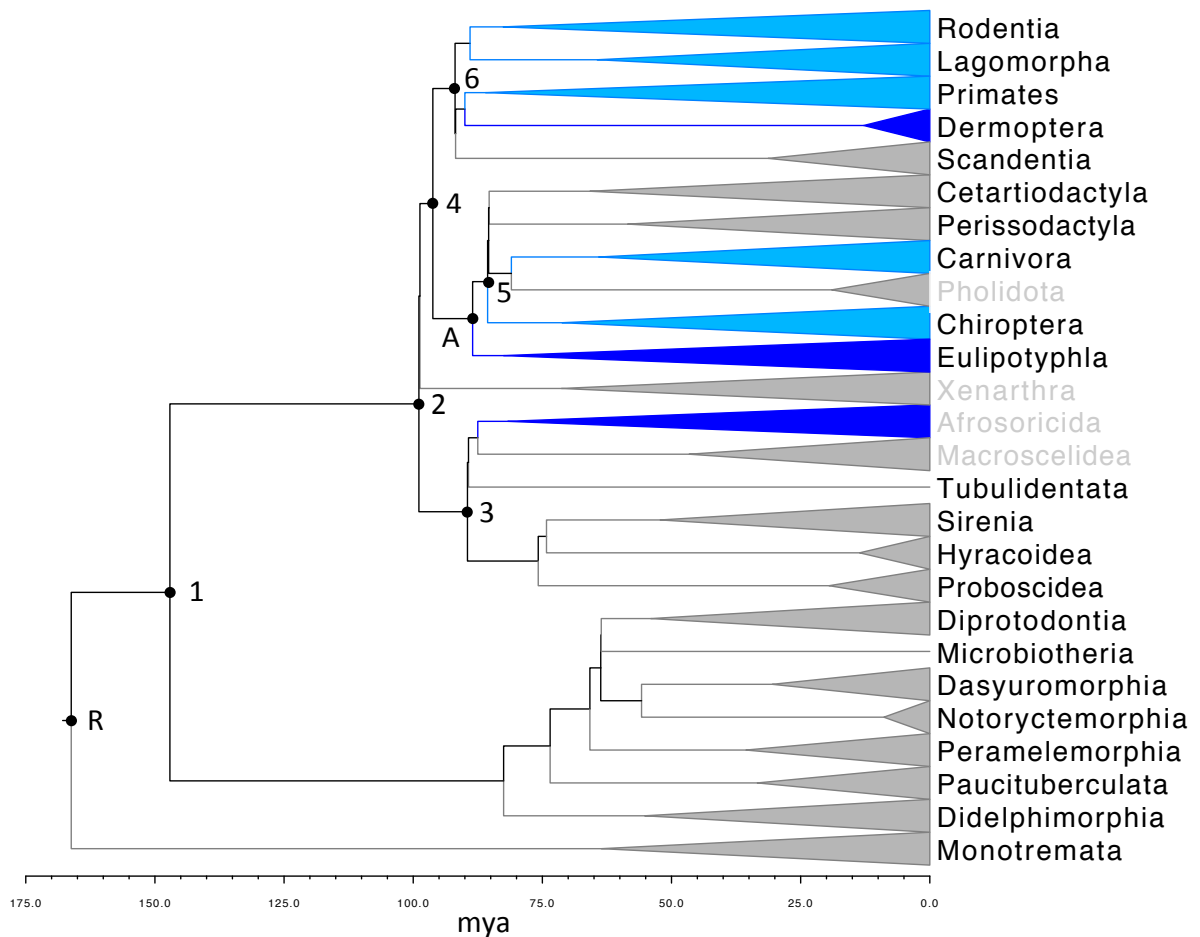


Figure S1. Mammal phylogeny [5] with the ancestral nodes (R = root, nodes 1-6) used for reconstruction (table 1, table S1). Node A is only relevant when the orders Eulipotyphla and Pholidota are included in the analyses (table S1). Orders are colour coded: grey = no species with bacula, blue = all species have bacula, light blue = mixed, some species with bacula. Taxa names are grey if they were excluded from the main analyses (table 1), but are included in the broader analysis (table S1).

Ancestral State Reconstructions: variable rates model

A single time-calibrated phylogenetic tree is required to use the variable rates model. Tree Annotator, a programme available in the BEAST software package [6], was used to create a single maximum clade credibility (MCC) tree from the block of 10,000 trees used in the variable rates analyses [7].

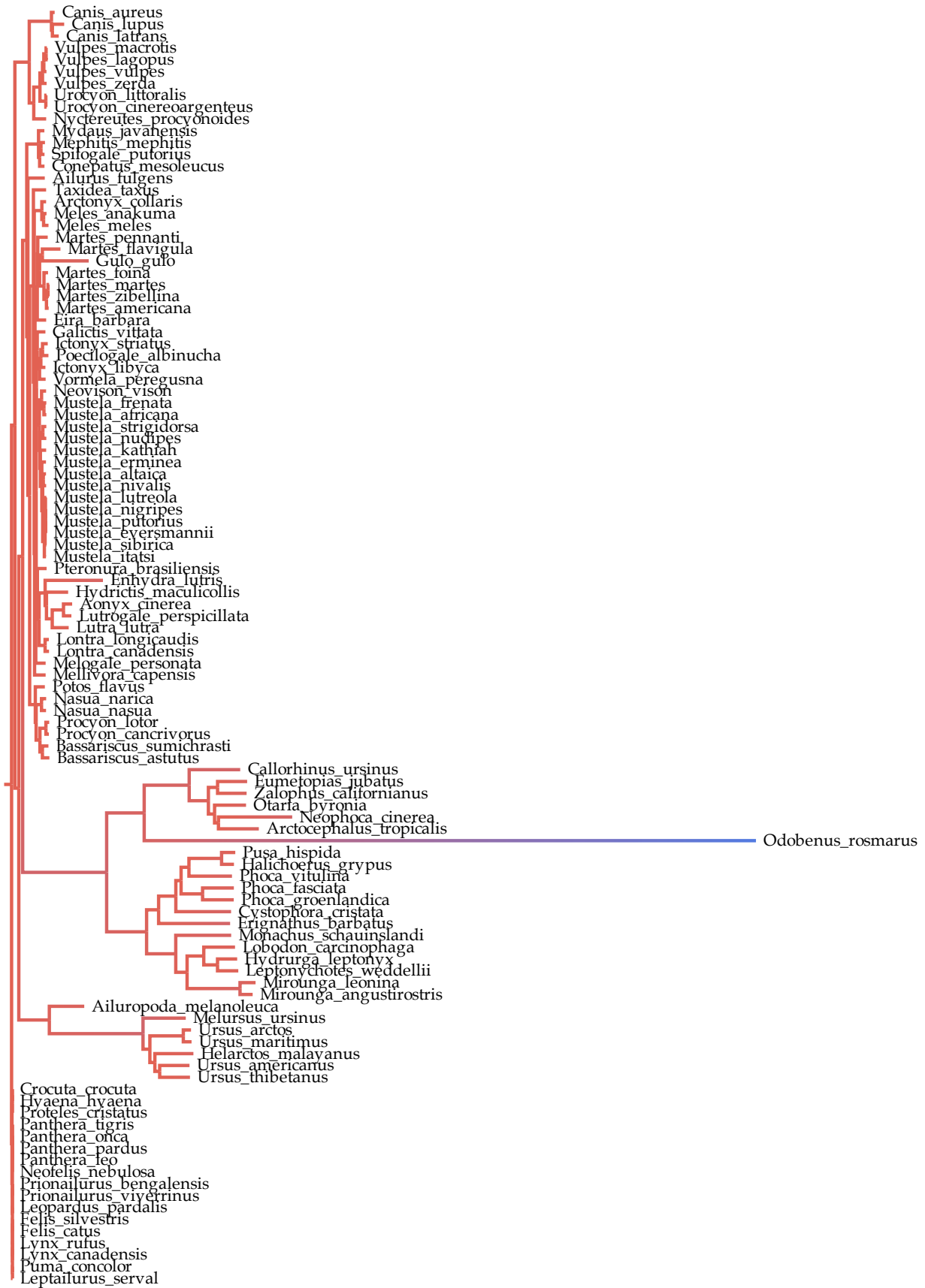


Figure S2. A carnivore phylogeny [7] scaled to reflect the rate of bacular evolution [8]. Darker red branches indicate lower rates of evolution; blue branches indicate particularly high rates of evolution.



Figure S3. A primate phylogeny [7] scaled to reflect the rate of testes evolution [8]. Darker red branches indicate lower rates of evolution; blue branches indicate particularly high rates of evolution.



Figure S4. A carnivore phylogeny [7] scaled to reflect the rate of testes evolution [8]. Darker red branches indicate lower rates of evolution; blue branches indicate particularly high rates of evolution.

Continuous Regression

Table S2. Phylogenetic regression between baculum length and testes mass in primates and carnivores.

Model	Primates			Carnivores		
	Log likelihood	p-value	R ²	Log likelihood	p-value	R ²
Baculum length and testes mass	-192.08	p=0.14	0.03	-173.99	p=0.23	0.37

These analyses suggest that testes mass (a proxy for postcopulatory selection pressure) is not a significant predictor of baculum length in primates or carnivores.

Correlated Evolution

It was not possible to test for correlated evolution between baculum presence and intromission duration in carnivores. Since the Hyaenidae family are the only carnivores in which a baculum is completely absent, the sample was not large enough to produce meaningful results. For this reason, carnivores are only included in analyses examining baculum length.

Hypothesis Testing

Species were divided into groups by creating binary variables and regressing baculum length onto these (following Organ *et al.* [9]). Adult male body mass was included as a predictor variable in order to account for its effect on baculum length.

Unfortunately it was not possible to gather enough data on carnivore mating systems or seasonality to allow meaningful replications of the tests conducted with primates.

References

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Data Sources

Mammals

Baculum Present: Afrosoricida [1,2], Dermoptera [3], Eulipotyphla [1,2].

Baculum Absent: Artiodactyla [3], Cetacea [1,3], Dasyuromorphia [3], Didelphimorphia [3], Diprodontia [3], Hyracoidea [4], Lagomorpha [3] (except *Ochotonia princeps* [5]), Macroscelidea [6,7], Microbiotheria [3], Monotremata [8], Notoryctemorphia [3], Paucituberculata [3], Paramelomorphia [3], Perissodactyla [3], Pholidota [1,2], Proboscoidea [3], Scandentia [3], Sirenia [3] and Tubulidentata [9], Xenarthra [1,2].

Baculum Present & Absent: Carnivora, Chiroptera [10], Primates and Rodentia (all [11], aside from *Hydromys chrysogaster* [12], *Uromys caudimaculatus* [12] and *Notomys alexis* [13]). See individual sections for Primates and Carnivora.

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Primates

- Baculum Presence: 0 = Absent
 1 = Present
- Intromission Duration: 0 = Short (<180 seconds)
 1 = Long (>180 seconds)
- Mating System: 0 = Monogamy
 1 = Polygyny
 2 = Polyandry
 3 = Polygamy
- Breeding Seasonality: 0 = <33% births occur within peak 3 months
 1 = >33% but <67% births occur within peak 3 months
 2 = >67% births occur within peak 3 months

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Intromission Duration: 0 = Short (<180 seconds)
 1 = Long (>180 seconds)

Carnivore Data References

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