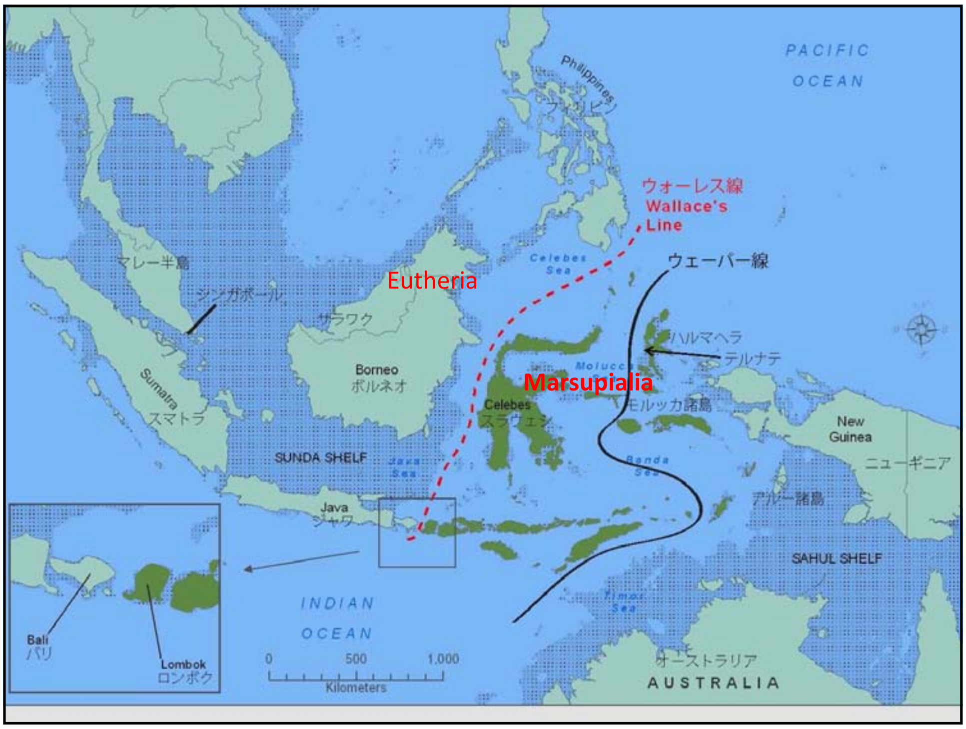
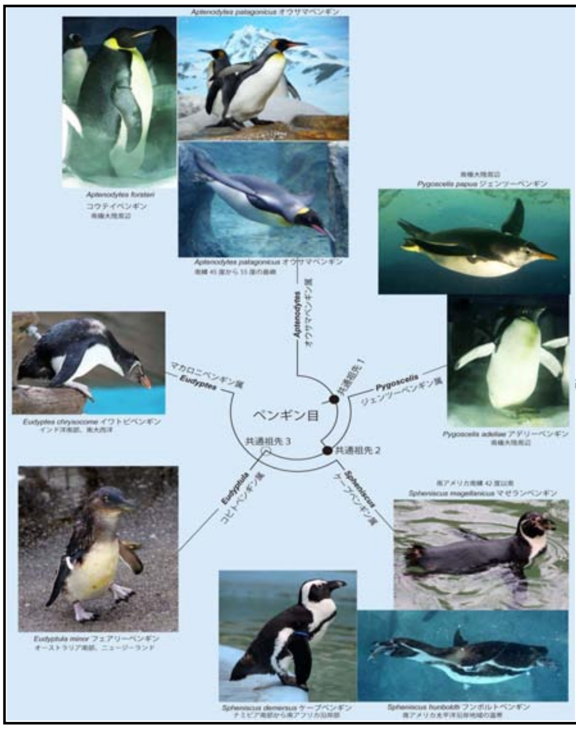
生物地理学Biogeography

- 環境が同じでも、違った生物が見られることがある。Similar species are not necessarily found in similar environments.
- ホッキョクグマはなぜ南極にいないか？Why polar bears are not found in Antarctica.
- 進化は祖先→子孫の系列（時間）に沿って起るとともに、地理的枠組みのなかで（空間）起こる。Evolution proceeds in the framework of time and space.

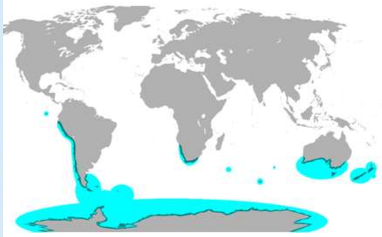


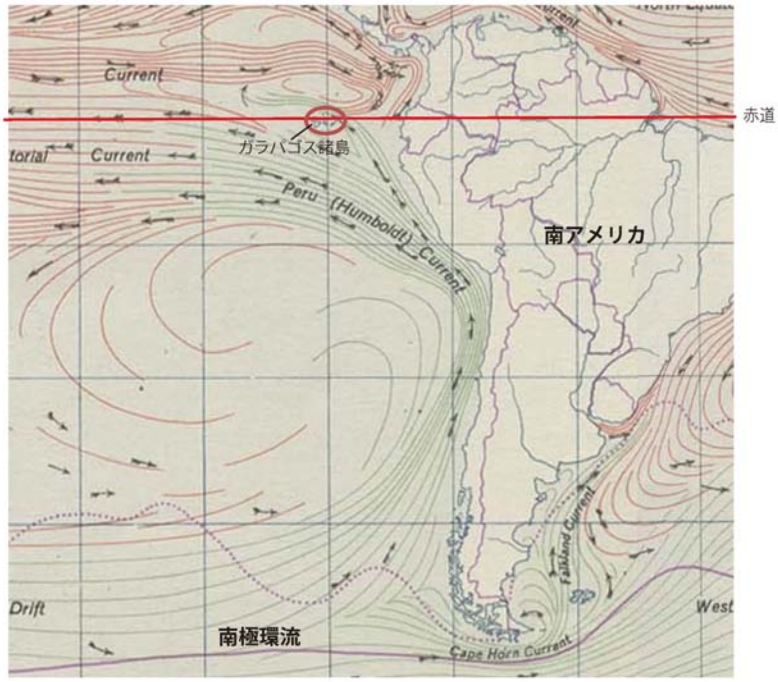
コバタン*Cacatua sulphurea*. 現在ロンボク島では絶滅したとされるが、ウォーレスはロンボク島がこの種の分布の西端であり、これよりも西のバリ、ジャワ、ボルネオには分布しないことを明らかにした。この境界線はウォーレス線と呼ばれる.
In spite of similar environment of Bali and Lombok, Lombok is the west end of the distribution of parrots.



ペンギンはなぜ北極にいないか

Why penguins are not distributed in the Arctic





ハシブトウミガラス *Uria lomvia*
（Alaska）
（チドリ目）

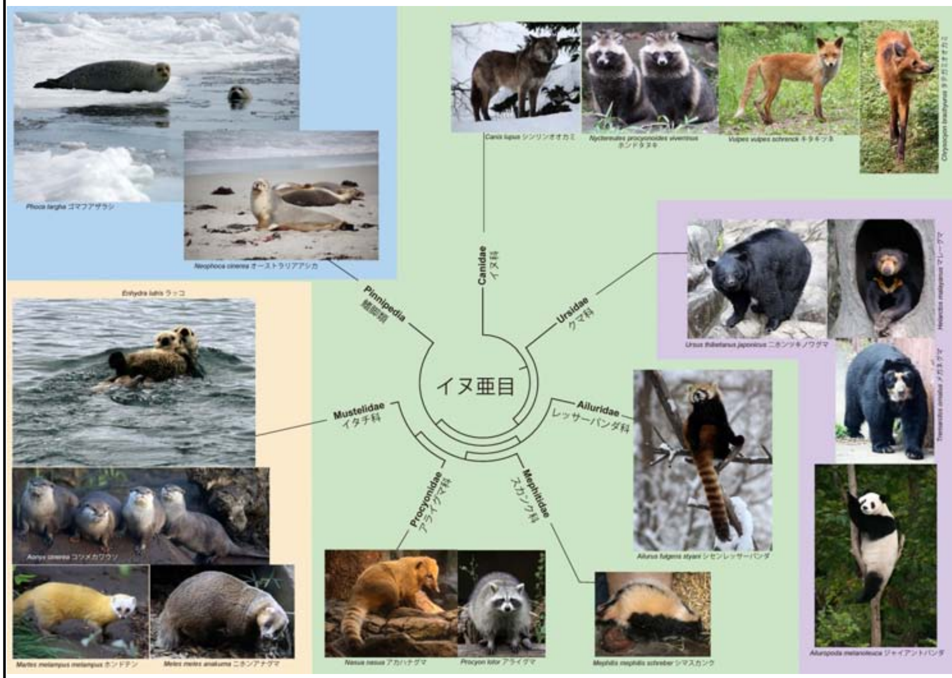
コウテイペンギン
Aptenodytes forsteri
（ペンギン目）

ハシブトウミガラス*Uria lomvia*（Alaska）

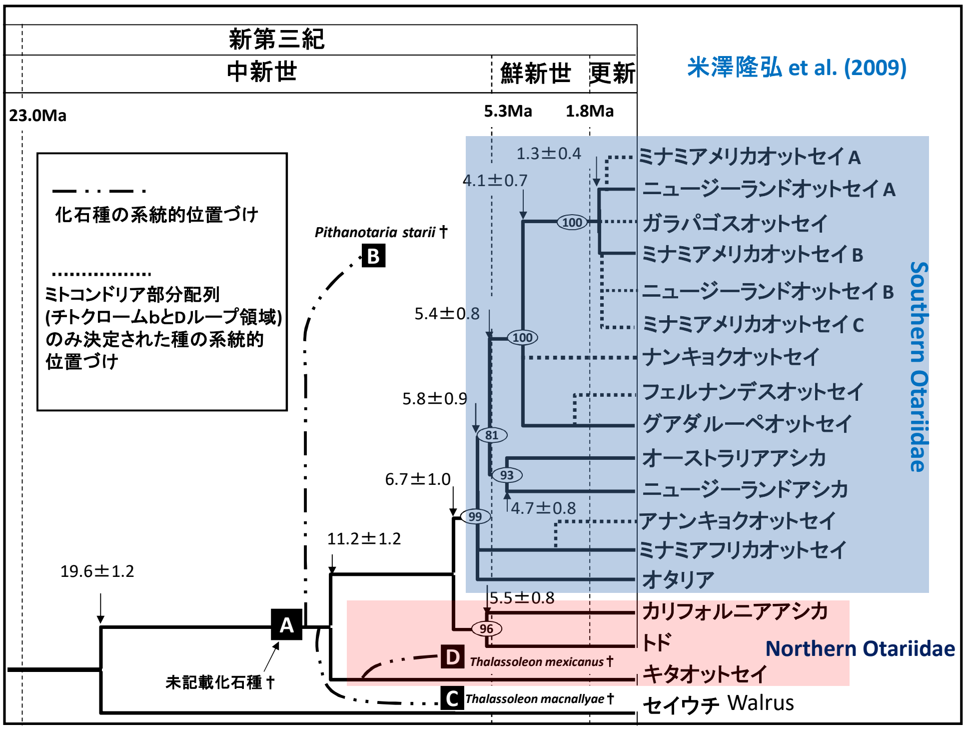
ハシブトウミガラス（厚嘴海鴉）*Uria lomvia*

オオウミガラス
Pinguinus impennis

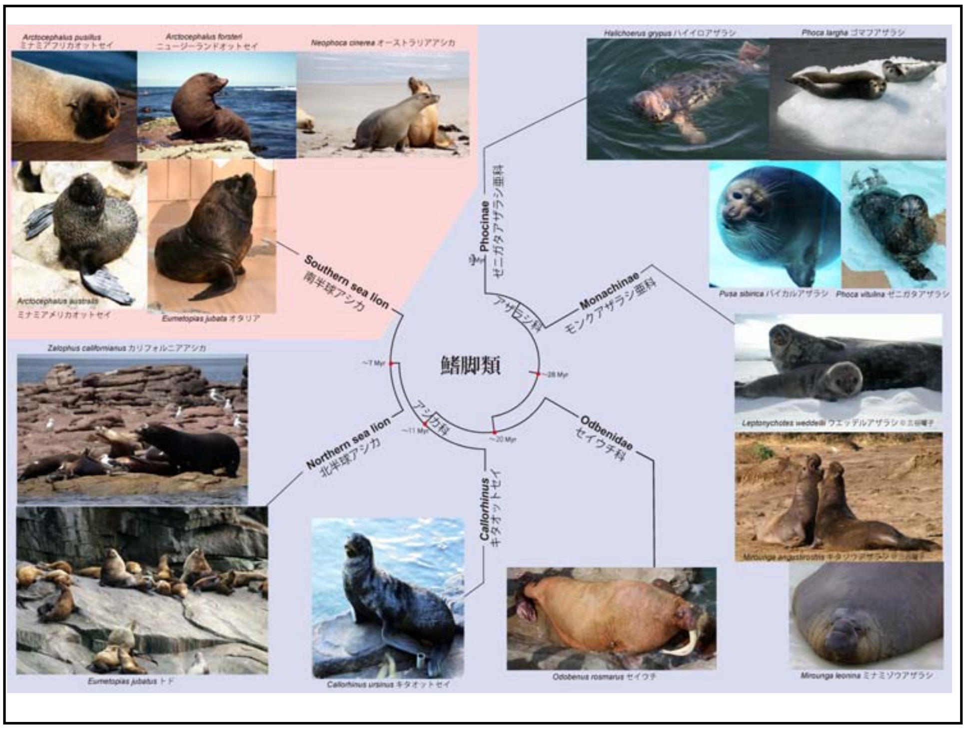
Gould (1862–1873)（玉川大学教育博物館所蔵)



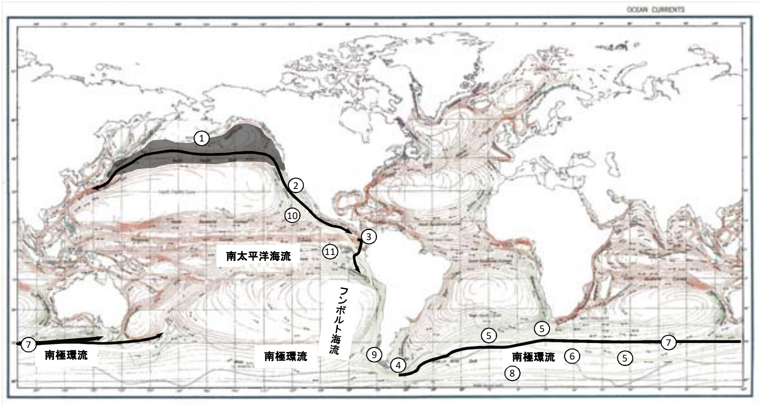
Evolutionary history of Otariidae
アシカ科



新第三紀
中新世
鮮新世
更新
23.0Ma
5.3Ma
1.8Ma
米澤隆弘 et al. (2009)
化石種の系統的位置づけ
ミトコンドリア部分配列
(チトクロームbとDループ領域)
のみ決定された種の系統的
位置づけ
Pithanotaria starii †
B
A
未記載化石種 †
D
Thalassoleon mexicanus †
C
Thalassoleon macnallyae †
19.6±1.2
11.2±1.2
6.7±1.0
5.8±0.9
5.4±0.8
4.1±0.7
1.3±0.4
4.7±0.8
5.5±0.8
100
100
81
93
99
96
ミナミアメリカオットセイ A
ニュージーランドオットセイ A
ガラパゴスオットセイ
ミナミアメリカオットセイ B
ニュージーランドオットセイ B
ミナミアメリカオットセイ C
ナンキョクオットセイ
フェルナンデスオットセイ
グアダルーペオットセイ
オーストラリアアシカ
ニュージーランドアシカ
アナンキョクオットセイ
ミナミアフリカオットセイ
オタリア
Southern Otariidae
カリフォルニアアシカ
トド
キタオットセイ
Northern Otariidae
セイウチ Walrus

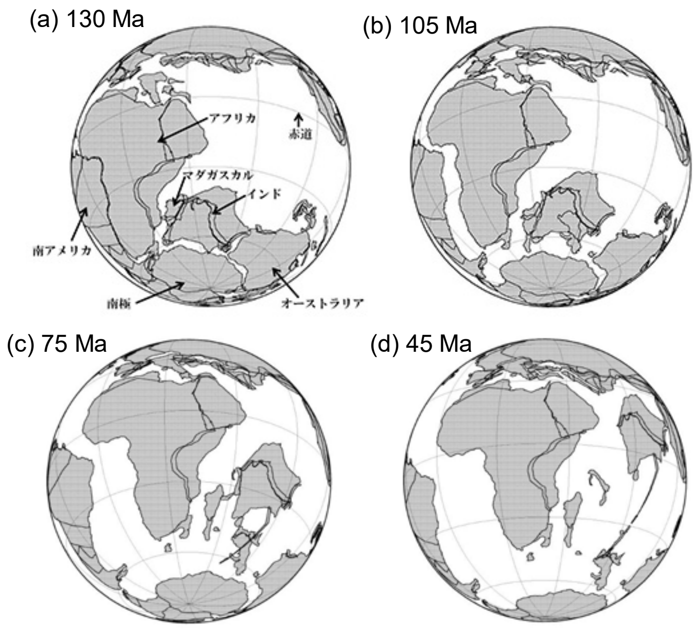


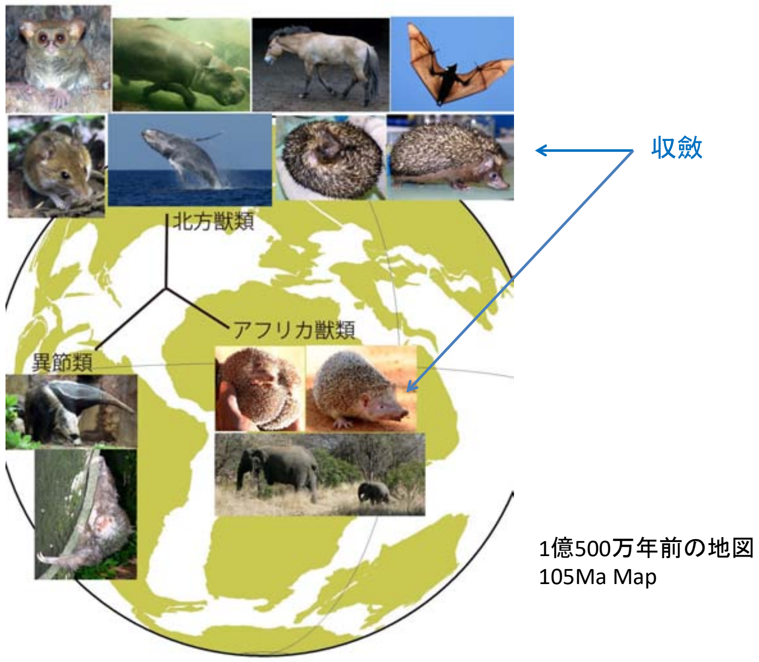
Arctocephalus pusillus ミナミアフリカオットセイ
Arctocephalus forsteri ニュージーランドオットセイ
Neophoca cinerea オーストラリアアシカ
Arctocephalus australis ミナミアメリカオットセイ
Eumetopias jubata オタリア
Southern sea lion
南半球アシカ
Zalophus californianus カリフォルニアアシカ
Eumetopias jubatus トド
Northern sea lion
北半球アシカ
Callorhinus ursinus キタオットセイ
Callorhinus
キタオットセイ
鰭脚類
アシカ科
アザラシ科
Phocinae
ゼニガタアザラシ亜科
Monachinae
モンクアザラシ亜科
Odobenidae
セイウチ科
Odobenus rosmarus セイウチ
Halichoerus grypus ハイイロアザラシ
Phoca largha ゴマフアザラシ
Pusa sibirica バイカルアザラシ
Phoca vitulina ゼニガタアザラシ
Leptonychotes weddellii ウエッデルアザラシ
Mirounga angustirostris キタゾウアザラシ
Mirounga leonina ミナミゾウアザラシ



米澤隆弘 et al. (2009)

Breakup of Gondwana





CellPress
Yonezawa et al., 2017, Current Biology 27, 68–77
January 9, 2017 © 2017 Elsevier Ltd.
http://dx.doi.org/10.1016/j.cub.2016.10.029
Current Biology
Report

Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites

Takahiro Yonezawa,[1,2,3,22] Takahiro Segawa,[4,5,22] Hiroshi Mori,[6,22] Paula F. Campos,[7,8] Yuichi Hongoh,[9] Hideki Endo,[10] Ayumi Akiyoshi,[5] Naoki Kohno,[11,12] Shin Nishida,[13] Jiaqi Wu,[1,14] Haofei Jin,[1] Jun Adachi,[2,3] Hirohisa Kishino,[14] Ken Kurokawa,[6] Yoshifumi Nogi,[5] Hideyuki Tanabe,[3] Harutaka Mukoyama,[15] Kunio Yoshida,[10] Armand Rasoamiaramanana,[16] Satoshi Yamagishi,[17] Yoshihiro Hayashi,[11,17] Akira Yoshida,[18,19] Hiroko Koike,[20] Fumihito Akishinonomiya,[10,17,21] Eske Willerslev,[7,*] and Masami Hasegawa[1,2,3,23,*]

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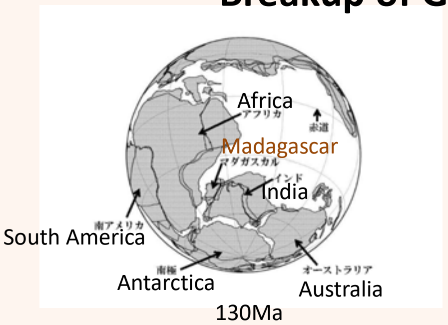
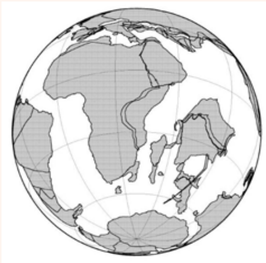
Breakup of Gondwana

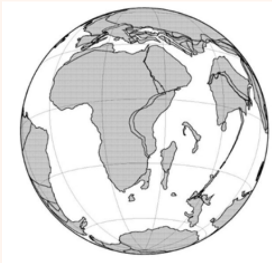


130Ma

105Ma



75Ma

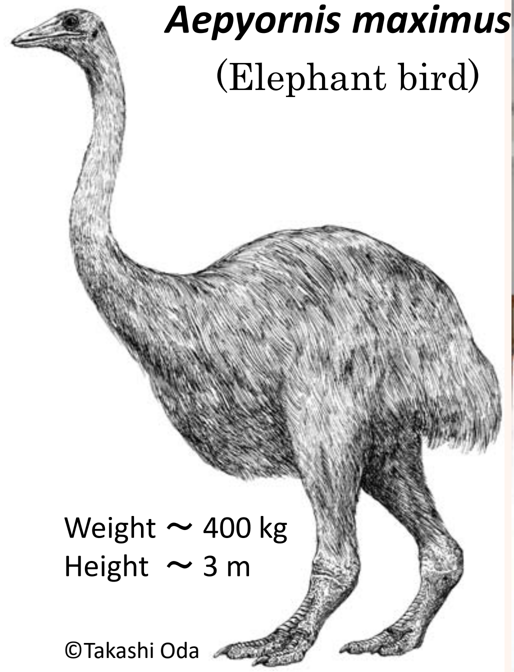


45Ma

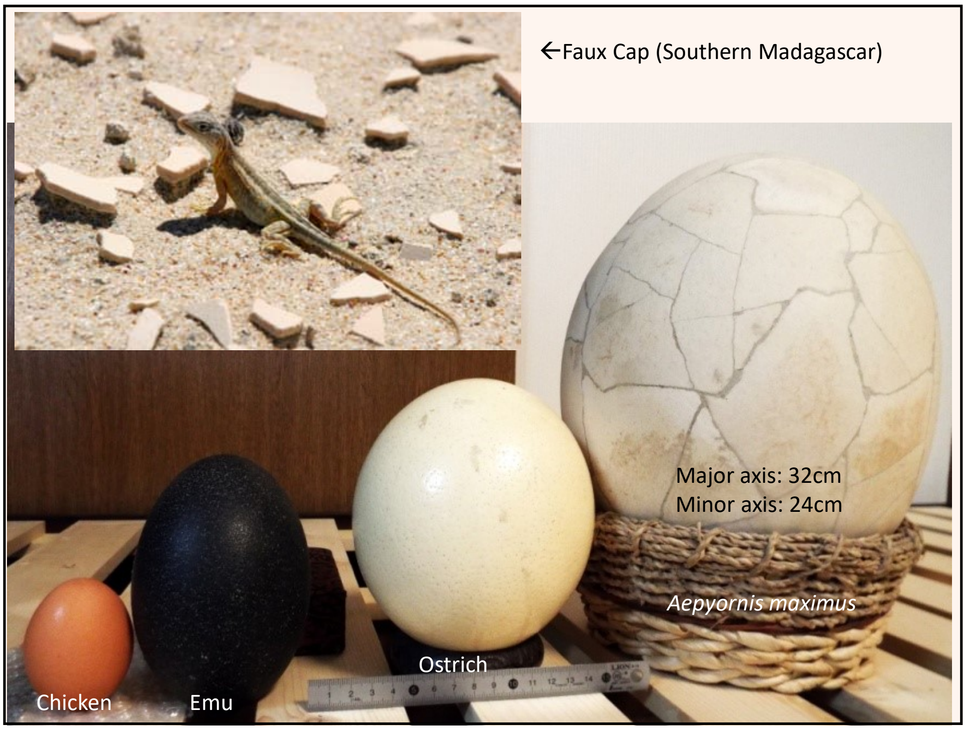
http://www.odsn.de/odsn/services/paleomap/paleomap.html

Aepyornis maximus

(Elephant bird)



Weight ～ 400 kg
Height ～ 3 m



2596 B.E. Crowley / Quaternary Science Reviews 29 (2010) 2591–2603

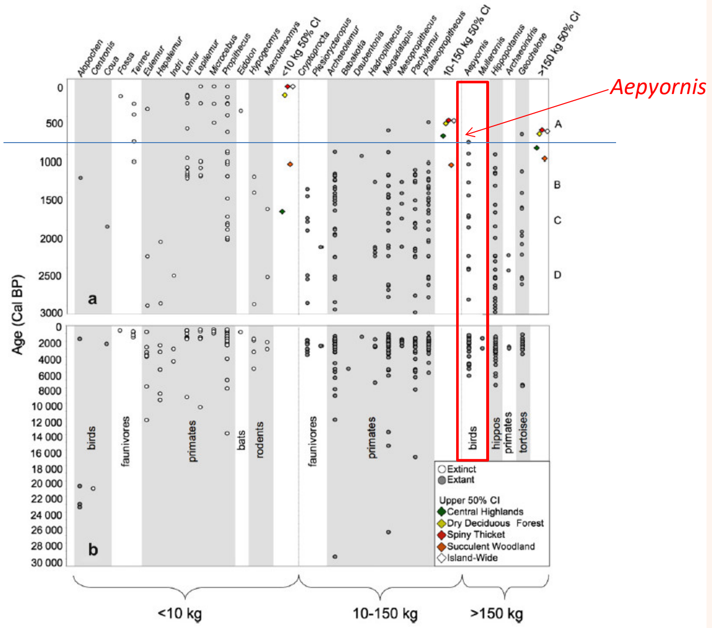
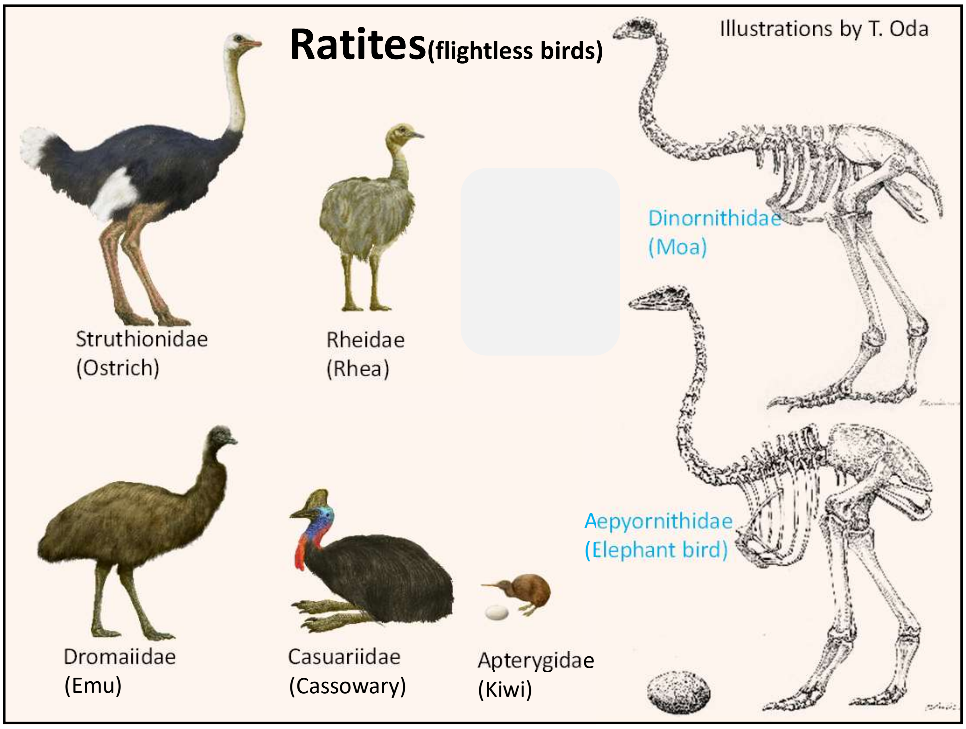
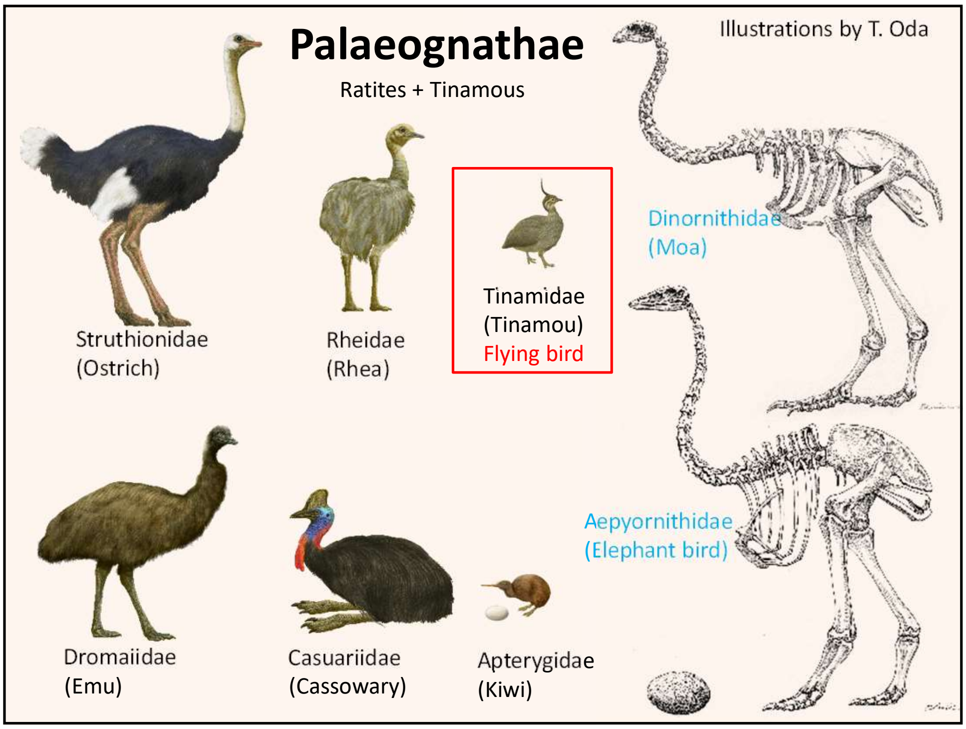


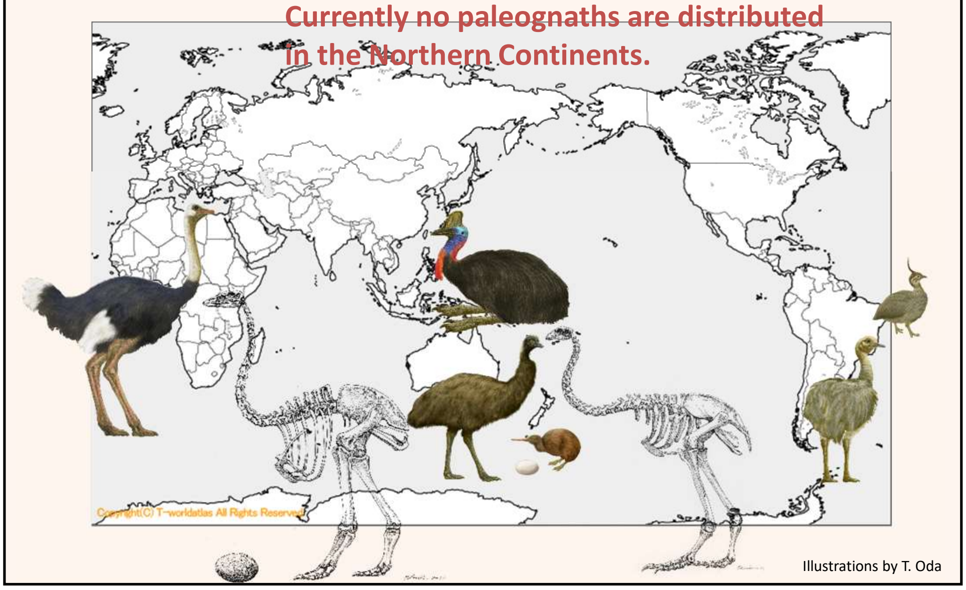
Fig. 3. Scatterplots showing the subset of ^{14}C dates for subfossil endemic genera from 0 to 3000 BP and 50% confidence intervals for each body mass group (a), and all radiocarbon dates (b). White and grey circles identify extant and extinct taxa, respectively. Due to calibration constraints, dates >22 000 years are presented in uncalibrated conventional ^{14}C years before present (^{14}C BP). An eggshell from *Aepyornis* sp. deemed too old to carbon date (Clarke et al., 2006) was not included. Letters correspond to European contact (A), the peak in Late Holocene aridity (B), first large human settlements (C), and initial human colonization (D).


Ratites(flightless birds)
Illustrations by T. Oda
Struthionidae
(Ostrich)
Rheidae
(Rhea)
Dinornithidae
(Moa)
Aepyornithidae
(Elephant bird)
Dromaiidae
(Emu)
Casuariidae
(Cassowary)
Apterygidae
(Kiwi)


Palaeognathae
Ratites + Tinamous
Illustrations by T. Oda
Struthionidae
(Ostrich)
Rheidae
(Rhea)
Tinamidae
(Tinamou)
Flying bird
Dinornithidae
(Moa)
Aepyornithidae
(Elephant bird)
Dromaiidae
(Emu)
Casuariidae
(Cassowary)
Apterygidae
(Kiwi)

Palaeognathae originated in Gondwana?
All living and recently extinct paleognaths are distributed in Gondwana-derived landmasses in the Southern Hemisphere.

Currently no paleognaths are distributed in the Northern Continents.



Illustrations by T. Oda

Mito-genome analyses

Cooper et al. (2001) *Nature* 409:704-707

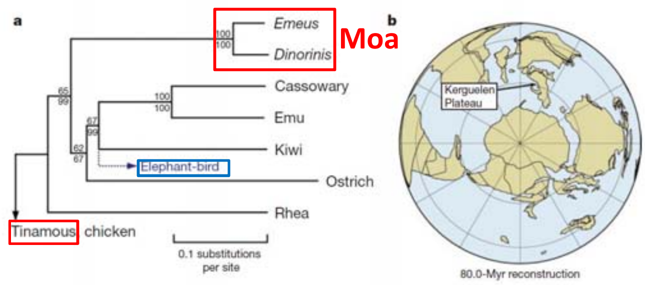
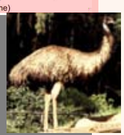


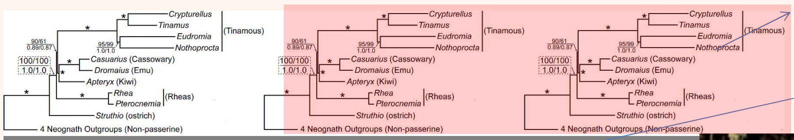
Figure 2 Ratite phylogeography. **a**, Unconstrained maximum-likelihood tree of ratite taxa, rooted with two tinamou and the chicken, using 10,767 bp of mtDNA protein coding sequence. Bootstrap values from 1,000 replications are given above the lines, with nearest-neighbour values[4] underneath. The maximum-likelihood position of the elephant-bird calculated with the short dataset is indicated, but the data prevent an accurate estimate of branch length. Alternative phylogenetic hypotheses for ratites (New Zealand ratites as monophyletic outgroup[1,8] or ostrich as outgroup[2,6]) both fit the data significantly worse than Fig. 2a ($P < 0.001$). **b**, Tectonic reconstruction of Gondwana at 80 Myr BP. The ostrich (and elephant-bird) are proposed to have crossed the Kerguelen Plateau (indicated) to Indo-Madagascar[24,25] and eventually Eurasia. Reconstruction map from www.odsn.de/odsn/services/paleomap/paleomap.html.

Tinamous were assumed to be sister to ratites.
Only 1kb could be analyzed probably because of humid and high temperature of Madagascar.

Phylogenetic analyses of a 20-gene, 24-kb nuclear DNA dataset strongly supporting ratite polyphyly

Tinamous (flying birds) are placed within ratites. The common ancestor of ratites could fly, and have lost the flying ability convergently?



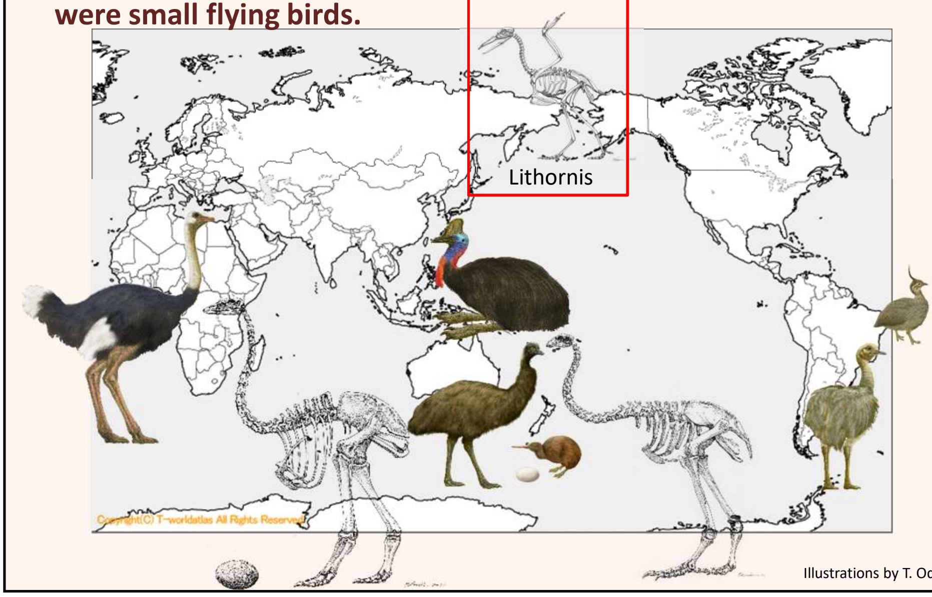


Flying bird?

Harshman J. et.al. PNAS 2008;105:13462-13467

PNAS

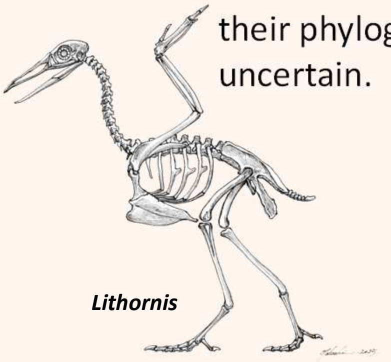
Extant and recently extinct paleognaths are distributed in Gondwana-derived landmasses, but early paleognaths, such as Lithornis (Paleocene—Eocene), were in Laurasia, and they were small flying birds.



Illustrations by T. Oda

Origin of Palaeognathae

- Extant and recently extinct paleognaths are distributed in Gondwana-derived landmasses.
- Early paleognaths, such as *Lithornis* which was small and could fly, were in Laurasia, but their phylogenetic positions have been uncertain.



Lithornis

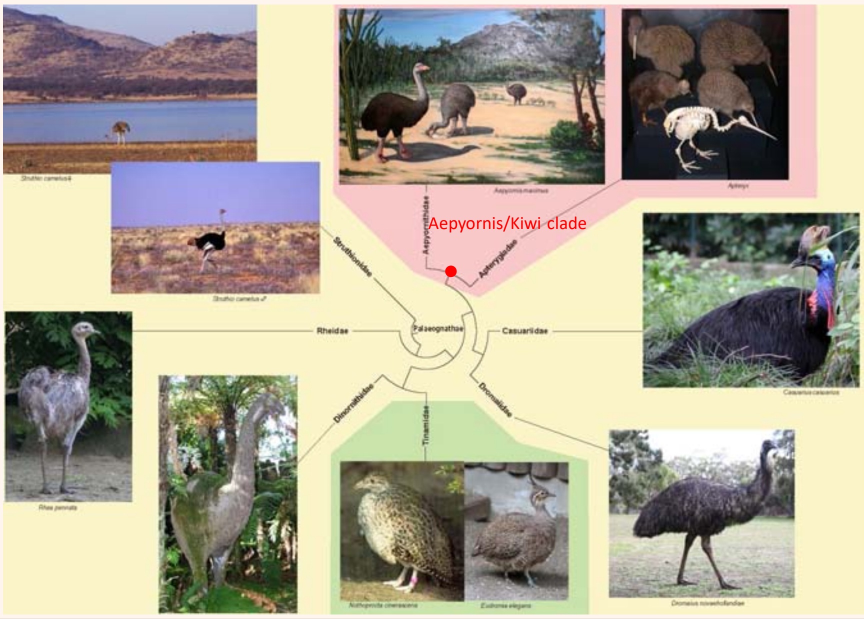
At a first glance, they look similar to tinamous, but since the position of tinamous was revised, the position of *Lithornis* must be reconsidered.

Illustration by T. Oda

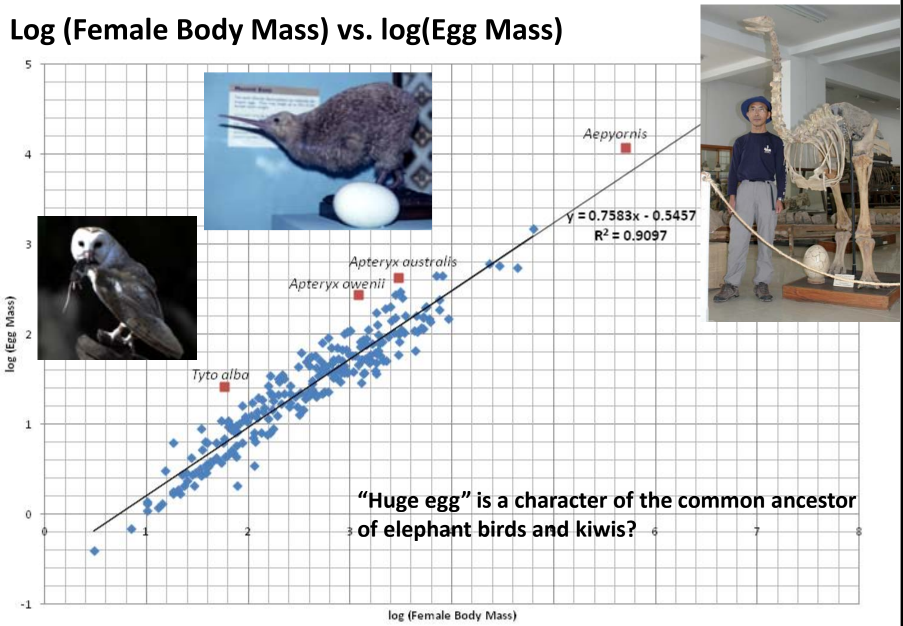
Aim of our project

- Clarify the origin of Aepyornithidae (Elephant birds) in Madagascar by ancient DNA analyses.
- Compared to Neognathae which is comprised of 10,000 species, Palaeognathae consists of less than 100 species, most of which are tinamous. In order to clarify the evolution of Palaeognathae, a robust time-tree (phylogenetic tree with time scale) is prerequisite, and dense taxon sampling is important, but the sampling must inevitably be sparse in the analyses of Palaeognathae. Therefore, inclusion of recently extinct species, such as elephant birds and moas, are important.

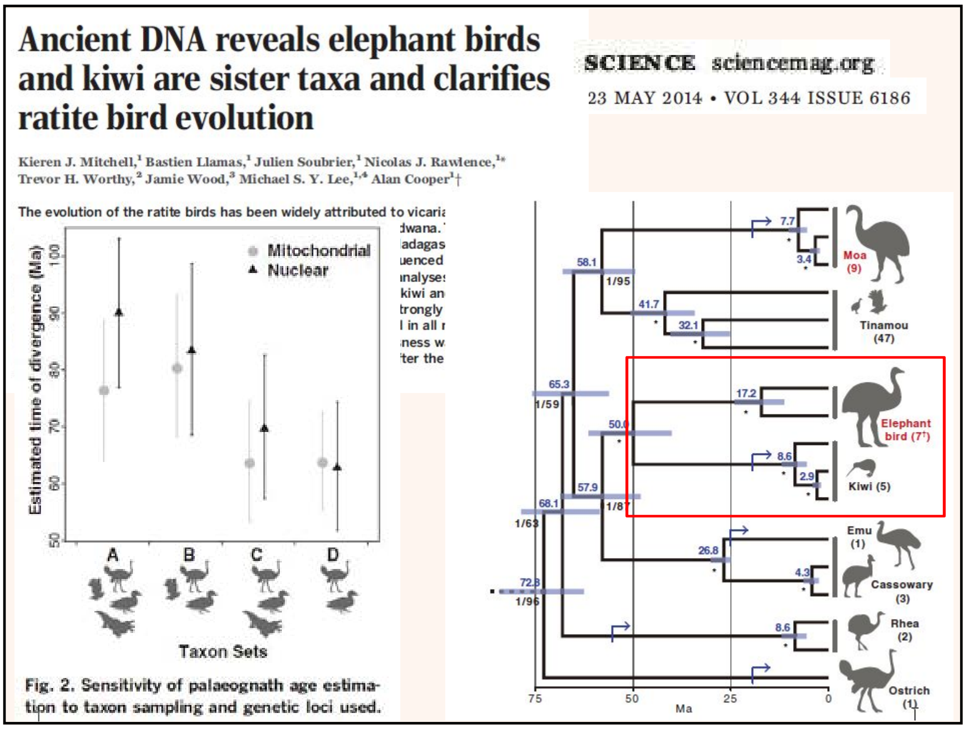
Mitogenome phylogeny of Palaeognathae with our data from *Aepyornis maximus* and *Mullerornis* sp.



Log (Female Body Mass) vs. log(Egg Mass)



"Huge egg" is a character of the common ancestor of elephant birds and kiwis?



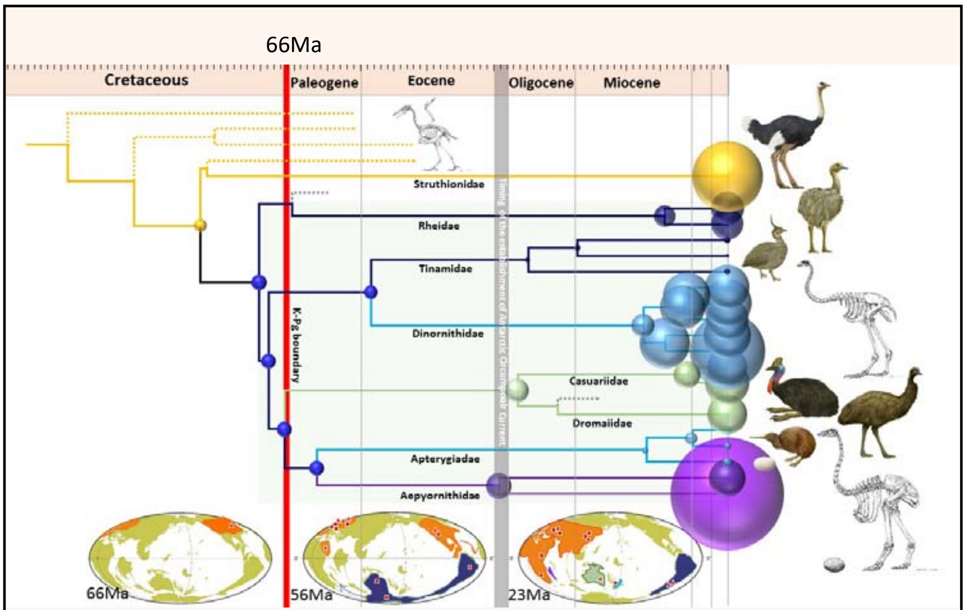
A new direction of our project

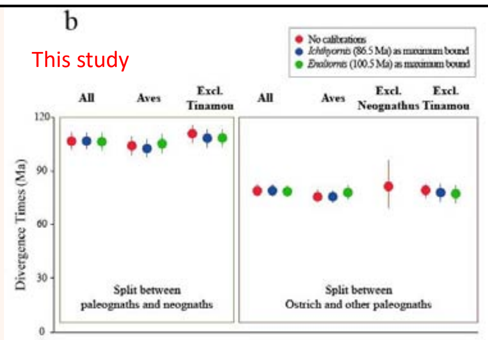
- Mitchell et al. established the branching order in Palaeognathae by mito-genome analyses, but the confidence intervals of the estimated branching times are huge, and the estimates depend very much on taxon sampling and assumed calibration.
- In order to obtain more precise estimates, nuclear DNA analyses are needed, and we carried out nuclear DNA analyses of two species of elephant birds; *Aepyornis maximus & Mullerornis* sp.

	mtgenome	Haddrath and Baker (2012)	Harshman et al. (2008)	Smith et al. (2013)	Baker et al. (2014)	Total
genes	37	10	20	40	594	701
length	15985 bp	9888 bp	26775 bp	25113 bp	795492 bp	873253 bp
	(11364 bp)	(9888 bp)	(6360 bp)	(0 bp)	(795492 bp)	(823104 bp)
species	39	34	27	12	11	44

Molecular phylogenetic analyses were carried out by using alignments of **873,263 bp**

Our additional data:
Aepyornis: **89,023 bp**
Mullerornis: **49,480 bp**





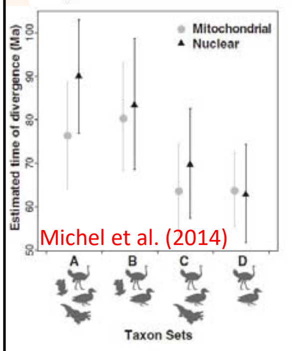
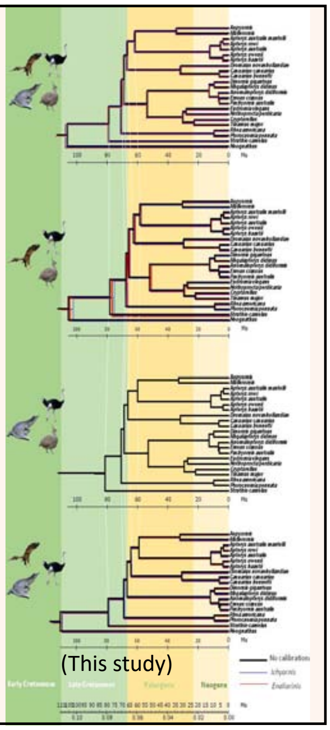
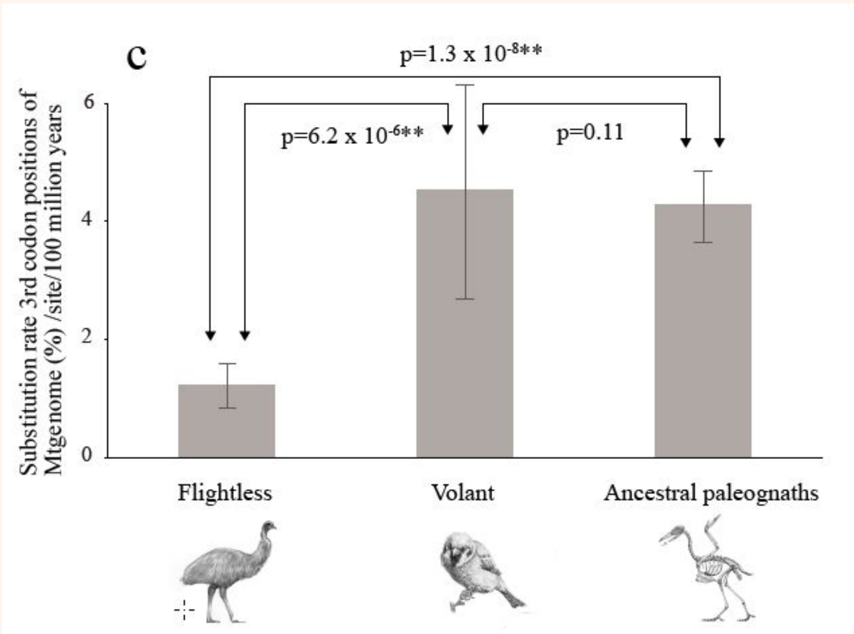


Fig. 2. Sensitivity of palaeognath age estimation to taxon sampling and genetic loci used.

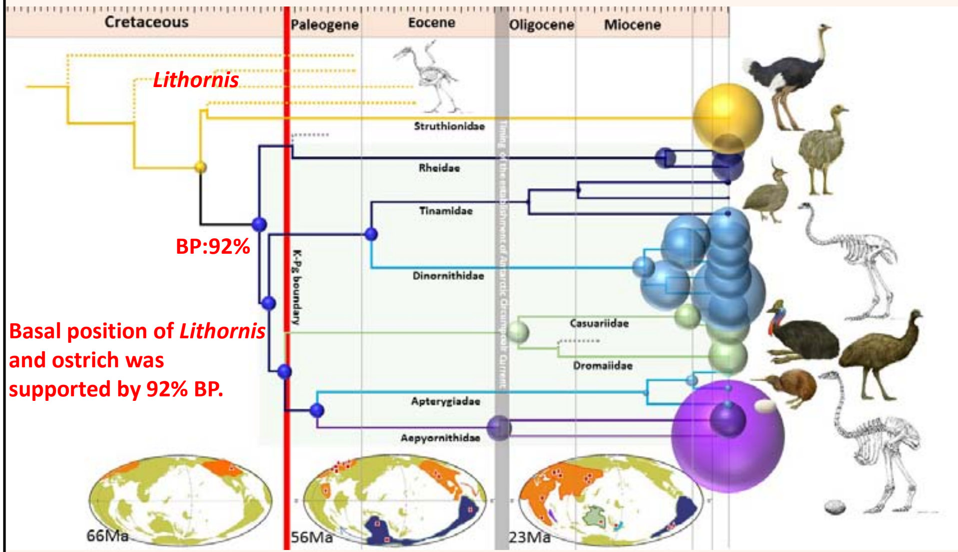
Our time-tree based on very long alignments of **873,263 bp** provided robust divergence time estimates. The estimates were little influenced by taxon sampling, models, or fossil calibrations .

Aepyornis: **89,023 bp**
Mullerornis: **49,480bp**





A phylogenetic analysis including *Lithornis* was carried out based on the morphological data excluding characters which show contradiction with the tree for the species from which molecular data are available.

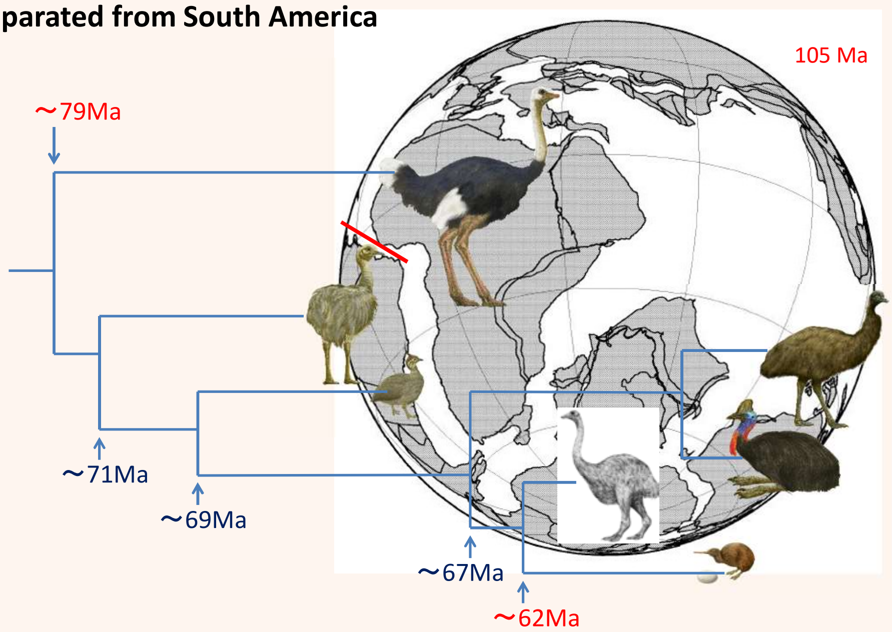


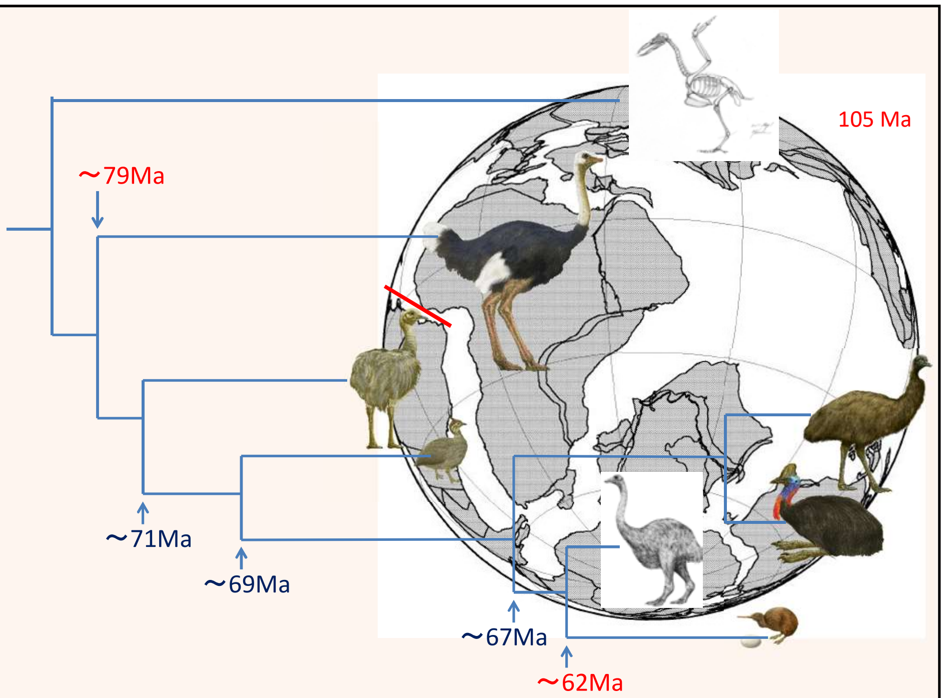
Elephant birds and Kiwis separated about 62Ma, later than K-Pg.

Two alternative hypotheses of Palaeognathae evolution

- Vicariance hypothesis — Phylogenetic separation accompanying the breakup of Gondwana
- Overseas dispersal hypothesis — Chance dispersal crossing the sea is important in the evolution of Palaeognathae

Configuration of the continents 105 Ma when Africa separated from South America





A new scenario of Palaeognathae evolution

① The common ancestors of Palaeognathae were small flying birds, like *Lithornis*, and were distributed in Eurasia and North America.

② Ostriches evolved in Eurasia, and some of them migrated to Africa after the land connection in Miocene.

25,000 years old ostrich from China

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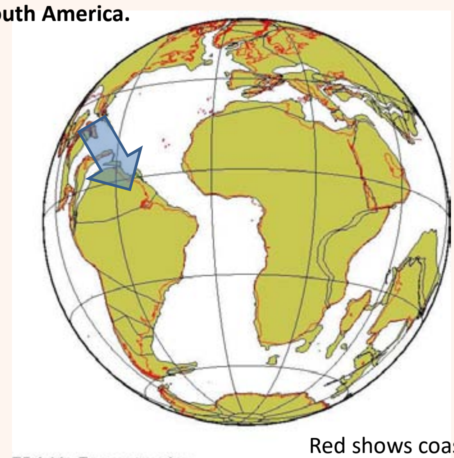
③ Another group of early paleognaths (flying birds) crossed Panama strait from North America to South America.



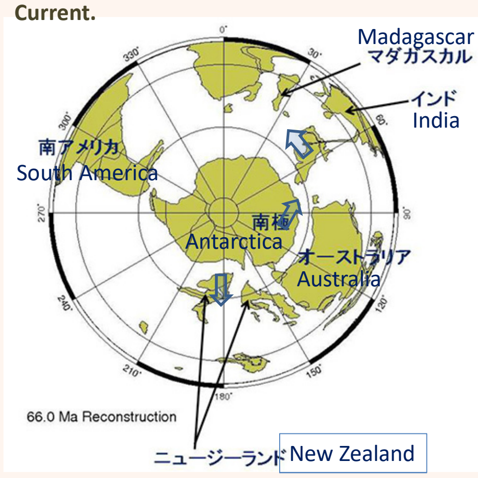
75.0 Ma Reconstruction

Red shows coast line.

http://www.odsn.de/odsn/services/paleomap/paleomap.html

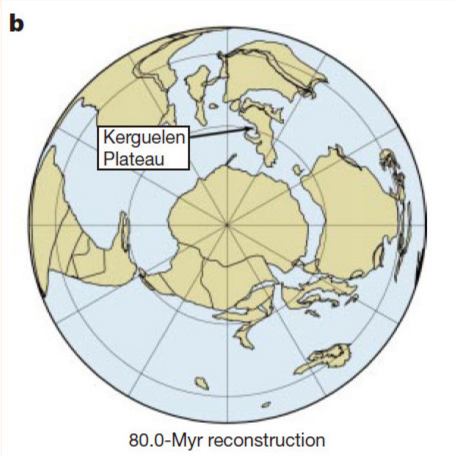
④At that time, South America was connected to Antarctica and Australia, and the ancestral paleognaths migrated to Antarctica and Australia. In South America, rheas and tinamous evolved, and in Australia emus and cassowaries evolved.

⑤**Ancestors of elephant birds and kiwis migrated from Antarctica to Madagascar and New Zealand, respectively, crossing the seas. Such migrations ended 34 Ma when Antarctica became totally glaciated after the establishment of the Antarctic Circumpolar Current.**



Gondwana of 66 Ma

http://www.odsn.de/odsn/services/paleomap/paleomap.html



Gondwana of 80 Ma, when Kerguelen Plateau connected Antactica with Madagascar (via India), but our analysis suggests much later time for the migration of the ancestor of the elephant birds.