

Supplementary Information

Early penguin fossils, plus mitochondrial genomes, give a firm calibration point for avian evolution

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Description of the oldest fossil penguins, genus *Waimanu*

Age determination

The Waipara Greensand yields microfossils (foraminifera, radiolaria and calcareous nannofossils)^{1,2,3} (Jenkins 1971; Strong 1984; Hollis and Strong 2003) indicating a wholly Paleocene age, clearly younger than the K/T boundary⁴ (Vajda et al. 2001). The Greensand lies within the local (New Zealand) Teurian stage. The top of the Waipara Greensand marks the Teurian - Waipawan local stage boundary, which is correlated internationally with the Paleocene - Eocene boundary⁵ (Cooper 2004).

The stratigraphically lowest stem-penguin, CM zfa 35 (fossil record number M34/f453, holotype of *Waimanu manneringi*), provides a well-preserved calcareous nannofossil assemblage. The sample includes two key age-diagnostic taxa, *Chiasmolithus bidens* and *Hornibrookina teuriensis*. Based on the latest correlations of New Zealand sequences to the international timescale⁵ (Cooper 2004: Fig 11.1, 11.4, 11.10), these nannofossils indicate that the age is high in the lower Teurian local stage. Of note, the top of the range of *Hornibrookina teuriensis* is lower Selandian, no younger than about 60.5Ma. The overlap of *Chiasmolithus bidens* and *Hornibrookina teuriensis* indicates an age of about 60.5-61.6Ma.

Matrix from the holotype of *W. tuatahi*, OU 12651 (fossil record number M34/f138), produced Paleocene dinoflagellates including *Palaeocystodinium golzowense* and *Deflandrea foveolata* (G.J. Wilson, personal communication); the former indicates local Teurian Stage, Paleocene, while the latter indicates the *Deflandrea foveolata* zone, roughly Selandian or early Late Paleocene⁵, 58-60 Ma (Cooper 2004: Fig 11.5). Such an age is consistent with known origin from the middle to upper Waipara Greensand. The other specimens of *W. tuatahi*, CM zfa 34 (M34/f454) and CM zfa 33 (M34/f455), produced no age-diagnostic fossils; based on superposition and known age of overlying strata, they are from the upper Waipara Greensand and no younger than Late Paleocene. There is no reason to propose that they are significantly different in age from the holotype of *W. tuatahi* (OU 12651, M34/f138).

Mitochondrial genomes and phylogenetic analysis

Mitochondrial Genomes: Material and Methods

DNA was extracted from muscle or liver using High Pure™ PCR Template Purification Preparation Kit (Roche). In order to avoid amplifying nuclear copies, mitochondrial DNA was amplified first as two main fragments from 8-12.3Kb, using the Expand™ Long template PCR kit (Roche). This could leave small gaps that were covered by fragments > 3.5Kb that had extensive overlap with the longest fragments. The long-range PCR fragments were used as template for short-range PCR reamplifications (1~2kb). We used the Fasta search in the GCG program (Wisconsin Package, version 10.0) to search our primer database for appropriate targets for primer walking. Where possible, primers from Kocher⁶, Cooper⁷ or Sorensen⁸ were used. Otherwise, new primers were designed using Oligo®4.03 (National BioSciences, Inc.). Sequencing

reactions were done according to standard protocols and run on a 377 ABI Applied BioSystems DNA sequencer. Some rechecking was done on an ABI 3730. Sequences were checked and assembled using Sequencher™ 4.1 (Gene Codes Corp).

Mitochondrial Genomes: Selection of taxa

In addition to the three mt genomes reported here, 15 other neognath taxa are included in the analyses: chicken (*Gallus gallus*; GenBank accession number X52392), quail (*Coturnix japonica*, AP003195), redhead duck (*Aythya americana*; AF090337), greater white-fronted goose (*Anser albifrons*, AF363031), magpie goose (*Anseranas semipalmata*; AY309455), rook (*Corvus frugilegus*; Y18522), village indigobird (*Vidua chalybeata*; AF090341), gray-headed broadbill (*Smithornis sharpei*; AF090340), rifleman (N Z wren, *Acanthisitta chloris*; AY325307), buzzard (*Buteo buteo*, AF380305), peregrine falcon (*Falco peregrinus*; AF090338), ruddy turnstone (*Arenaria interpres*, AY074885), blackish oystercatcher (*Haematopus ater*, AY074886), Oriental white stork (*Ciconia boyciana*; AB026193), and little blue penguin (*Eudyptula minor*, AF362763). In addition, seven paleognaths (five ratites and two tinamou) were included. They are, Great spotted kiwi (*Apteryx haastii*, AF338708); emu (*Dromaius novaehollandiae*, AF338711); double-wattled cassowary (*Casuarius casuarius*, AF338713); ostrich (*Struthio camelus*, Y12025); greater rhea (*Rhea americana*; AF338713); great tinamou (*Tinamus major*, AF338707); and elegant crested-tinamou (*Eudromia elegans*, AF338710). This gives a total of 25 avian mt genomes.

Within the Neoaves, an owl and a parrot were omitted. In the current dataset both are isolated taxa in the Neoavian portion of the tree⁹ and their positions are still a little unstable – though none come within the seabird/shore bird group that is the focus of this study. The owl and parrot can group together weakly, or the owl comes close to the passerines, and the parrot towards the falconiforms group. We are in the process of sequencing a barn owl (*Tyto*), an African parrot (lovebird, *Agapornis*) and a forest falcon (*Micrastur*) (www.awcmee.massey.ac.nz/mt_genomes). Based on previous experience of improved taxon sampling^{9,10}, we expect that these new sequences will help stabilize the position of both the owls and parrots. Once again, parrots and owls are not the focus here, rather it is the time of origin of modern seabird and shore bird lineages and whether they predate the decline of hesperornids, ichthyornids and pterosaurs.

Six reptiles were used as outgroups: American alligator (*Alligator mississippiensis*; Y13113), eastern painted turtle (*Chrysemys picta*; AF069423), green turtle (*Chelonia mydas*; AB012104), blue-tailed mole skink (*Eumeces egregius*; AB016606), common iguana (*Iguana iguana*; AJ278511) and spectacled caiman (*Caiman crocodylus*; AJ404872).

Mitochondrial Genomes: Phylogenetic analysis

In previous work^{11,12,13} we found that RY-coding of nucleotide data both increases the proportion of changes on internal branches of the tree (treeness) and decreases the differences in nucleotide composition

(Relative Compositional Variability, RCV). Consequently this is our preferred method of analysis of animal mitochondrial data, and the tree reported here (Figure S2) has the third codon positions recoded as R & Y. The full data set is available from www.awcmee.massey.ac.nz/downloads.

Dating estimates were made on the tree shown in Figure Suppl_3 using the program packages PAML and Multidivtime. However, because of limitations of the dating program, third codon positions (3rd cdp) could not be analyzed as transversions (RY-coded). Two variants of the 25 bird + 6 reptile protein-coding + RNA dataset were therefore analyzed: one without 3rd cdp (8582 nucleotides [nt]) and one with 3rd cdp coded as nt data (11709 nt). The T3: (Thornian Time Traveler version <http://abacus.gene.ucl.ac.uk/>; see also Yang & Yoder¹⁴) of the Multidivtime program package¹⁵ was used to estimate divergence times. Multidivtime uses Markov chain Monte Carlo (MCMC) procedures for Bayesian estimation of evolutionary divergence times and rates. The program baseml in the PAML version 3.14beta package¹⁶ (<http://abacus.gene.ucl.ac.uk/software/paml.html>) was used to estimate base frequencies, the ratio of within to between group substitution rates (κ) and the relative substitution rate of each category (r values) under the F84 plus discrete gamma model ($\text{ncatG} = 8$). These values were used in the Multidivtime program `est_branches` to estimate branch-lengths for the specified tree (ingroup only) and to produce a variance-covariance matrix for the branch-length estimates. The multidivtime program was then used to estimate divergence times (plus standard deviations and 95% confidence intervals) for each node in the tree (without assuming a molecular clock).

We estimated both the prior (no data) and posterior distribution of divergence times, analyzed the dataset both with and without third codon positions and constrained the three calibration points to different extents. We also ran the same analysis five times (Fig Suppl_2) with different random seed numbers to check that the results were similar, therefore indicating convergence of the MCMC. Table S1 summarizes our estimates of avian divergence times.

Three calibration points were used (indicated in bold in table S1): 1. The divergence between magpie goose and (duck, goose): lower bound set at 66 MY in all analyses, upper bound set at 66 MY in FIXED analyses and unconstrained in VARIABLE analyses; 2. The divergence between penguin and stork: lower bound set at 62 MY in all analyses, upper bound set at 62 MY in FIXED analyses and unconstrained in VARIABLE analyses; 3. The divergence between emu and cassowary: when used the lower bound was set at 30 million years (MY) and upper bound at 35 MY. Note that the in the 'variable' analyses the calibration point is used in the mathematical sense as a bound, not as a point estimate. The numbers in the first (lefthand) column of the table are those shown in Figure 3. The parameters used in the analyses were as for Figure 3, except that `rt_rate` was 0.010582 and `rtrate_sd` was 0.005291 when 3rd cdp were included. 95% confidence intervals were calculated but are not shown. SD: standard deviation.

A priori estimates for multidivtime parameters were as follows: 84 MY for the mean of the prior distribution for the time separating the ingroup root and the present (rt_tm) and 42 MY for the standard deviation of rttm (rttmsd); 0.001687 for the mean of the prior distribution for the rate at the ingroup root node (rtrate) and 0.000844 for the standard deviation of rtrate (rtratesd); 0.01 for both the mean of the prior distribution for Brownian motion constant 'nu' (brown_mean) and the standard deviation of brown_mean (brown_sd); 500 MY for the length of time between the root and the present (big_time). The Markov chain was sampled 10,000 times (num_samps), the number of cycles between samples (samp_freq) was 100 and the number of cycles before the first sample of the Markov chain (burnin) was 100,000. The results of other dating analyses (approximation of prior distributions of divergence times; with 3rd cdp, coded as nt data; without an upper bound on the penguin/stork and magpie goose/(duck + goose) calibration points) are summarized in Table S1.

Table S1. Summary of avian divergence time estimates.

Divergences	Posterior approximation								Prior approximation							
	Without 3rd cdp				With 3rd cdp				Without 3rd cdp				With 3rd cdp			
	FIXED		VARIABLE		FIXED		VARIABLE		FIXED		VARIABLE		FIXED		VARIABLE	
	Age	SD	Age	SD	Age	SD	Age	SD	Age	SD	Age	SD	Age	SD	Age	SD
emu/cassowary	33.1	1.3	33.2	1.3	33.0	1.4	33.3	1.3	32.4	1.4	32.4	1.4	32.4	1.4	32.5	1.4
kiwi/emu+cassowary	56.7	4.0	59.3	4.8	56.7	3.2	59.1	3.8	56.2	21.9	63.2	27.9	56.5	22.2	62.4	26.8
greater rhea/kiwi+emu+cassowary	63.7	4.5	67.2	5.7	65.7	3.9	69.4	4.8	80.3	29.2	93.9	37.2	80.7	29.6	93.4	36.2
ostrich/greater rhea+kiwi+emu+cassowary	70.1	4.8	74.5	6.2	71.9	4.2	76.3	5.4	103.8	33.2	124.7	42.1	104.7	33.7	124.0	41.2
tinamou/crested-tinamou	42.6	4.9	45.3	5.7	44.1	4.2	46.7	4.8	64.3	42.5	76.4	51.1	64.7	42.4	77.4	51.4
Struthioniformes (ratites)/Tinamiformes (tinamous)	75.2	5.0	80.3	6.6	80.2	4.6	85.6	6.0	128.0	35.3	154.9	43.9	128.9	36.1	155.0	44.1
chicken/quail	29.9	3.5	32.9	4.5	29.9	2.7	33.7	3.8	51.5	34.0	68.7	45.6	52.0	34.0	70.0	45.9
duck/goose	29.6	3.2	32.7	4.4	25.2	2.2	28.9	3.4	33.1	19.1	53.6	36.2	33.3	19.0	53.9	36.2
magpie goose/duck+goose	66.0	0.0	72.5	5.0	66.0	0.0	74.2	5.1	66.0	0.0	107.2	32.9	66.0	0.0	107.1	33.1
Galliformes/Anseriformes	77.1	2.5	84.1	5.7	75.5	2.0	83.6	5.4	102.4	28.1	138.8	38.8	102.8	28.5	139.3	38.9
penguin/stork	62.0	0.0	66.7	4.1	62.0	0.0	65.9	3.6	62.0	0.0	77.6	15.6	62.0	0.0	77.6	15.6
loon/penguin+stork	67.1	2.1	72.5	4.7	65.1	1.3	69.7	4.0	74.4	12.7	93.0	21.8	75.0	12.9	93.1	21.9
albatross/petrel	58.7	3.2	63.4	5.0	56.1	2.2	60.0	4.0	43.9	27.4	54.0	35.0	44.1	27.6	54.1	35.2
Procellariiformes/loon+penguin+stork	71.1	2.3	76.8	5.0	67.2	1.5	72.0	4.1	87.3	18.3	108.7	26.6	88.1	18.4	108.7	27.1
oystercatcher/turnstone	69.1	3.0	74.8	5.3	61.9	2.5	66.5	4.4	49.8	31.9	62.6	40.0	50.4	32.0	61.9	40.0
Charadriiformes/Procellariiformes+loon+penguin	73.6	2.5	79.6	5.2	71.3	1.8	76.8	4.5	100.1	22.7	124.1	30.6	100.8	22.5	124.5	31.5
falcon/buzzard	65.1	3.7	70.5	5.6	66.5	2.7	71.6	4.8	56.5	36.1	69.6	44.6	56.8	36.0	68.4	45.3
Falconiformes/Charadriiformes+Procellariiformes+penguin+stork	77.2	2.9	83.6	5.6	74.7	2.1	80.6	4.8	112.8	26.2	139.8	34.4	113.6	26.1	140.1	35.2
indigobird/rook	30.1	3.7	32.7	4.5	34.2	3.1	37.0	3.9	42.3	32.0	51.5	39.9	42.2	32.2	52.0	40.5
rifleman/broadbill	59.0	4.0	63.9	5.7	62.3	3.2	67.4	5.0	42.1	31.9	51.4	40.0	42.5	31.9	51.7	40.0
indigobird+rook (oscines)/broadbill (suboscine)+rifleman	67.4	3.5	73.0	5.6	71.1	2.7	76.9	5.1	83.8	36.0	103.5	45.8	84.4	36.3	104.4	45.9
Passeriformes/other Neoaves	79.6	3.0	86.2	5.7	80.1	2.4	86.8	5.2	125.4	29.6	155.3	37.7	126.1	29.5	155.8	38.5
Gallianeres/Neoaves	89.8	3.5	97.4	6.6	91.0	2.9	99.1	6.2	138.0	32.6	171.0	40.9	138.9	32.7	171.6	41.7
Palaeognathae/Neognathae	98.4	5.1	106.1	7.8	102.5	4.7	110.6	7.3	151.7	36.1	185.4	44.3	152.9	36.5	185.9	44.7

Table S2. Character matrix of 148 morphological character for *Waimanu*, "*Palaeedyptes*", and *Platydyptes*.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	
<i>Waimanu</i>	?	?	?	?	0	?	?	?	?	?	?	0	0	?	?	?	?	?	?	?	?	?	?	?	?	1
" <i>Palaeedyptes</i> "	1	0	0	1	?	?	?	?	?	?	?	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?
<i>Platydyptes</i>	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	
<i>Waimanu</i>	?	?	?	?	?	?	1	?	1	?	?	1	0	?	0	1	1	0	?	?	?	?	?	?	?	?
" <i>Palaeedyptes</i> "	?	?	?	?	?	?	?	?	1	0	0	1	0	?	0	?	1	0	0	0	0	0	0	?	?	?
<i>Platydyptes</i>	?	?	?	?	?	?	?	?	?	?	?	?	?	?	0	?	1	0	0	0	?	?	?	?	?	?
	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	
<i>Waimanu</i>	?	?	?	0	?	?	0	1	1	?	?	0	0	0	0	0	0	0	?	?	?	?	?	?	?	0
" <i>Palaeedyptes</i> "	?	?	?	?	?	?	0	?	1	0	0	0	0	0	0	0	0	0	?	1	0	1	?	?	0	
<i>Platydyptes</i>	?	?	0	?	?	?	0	?	1	0	0	0	0	0	0	0	0	1	1	1	0	1	?	?	0	
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
<i>Waimanu</i>	0	0	0	1	0	1	0	1	0	0	0	?	?	?	?	0	1	0	1	1	0	0	0	0	1	1
" <i>Palaeedyptes</i> "	0	0	0	1	0	1	0	?	?	0	0	?	?	?	?	0	1	0	1	1	0	0	0	0	1	1
<i>Platydyptes</i>	0	0	0	1	0	1	0	?	?	0	0	?	?	?	?	0	?	0	1	1	0	0	0	0	1	1
	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	
<i>Waimanu</i>	0	0	0	0	0	0	0	1	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
" <i>Palaeedyptes</i> "	0	0	0	0	0	0	1	1	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
<i>Platydyptes</i>	0	0	0	0	0	0	1	1	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148			
<i>Waimanu</i>	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
" <i>Palaeedyptes</i> "	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
<i>Platydyptes</i>	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?

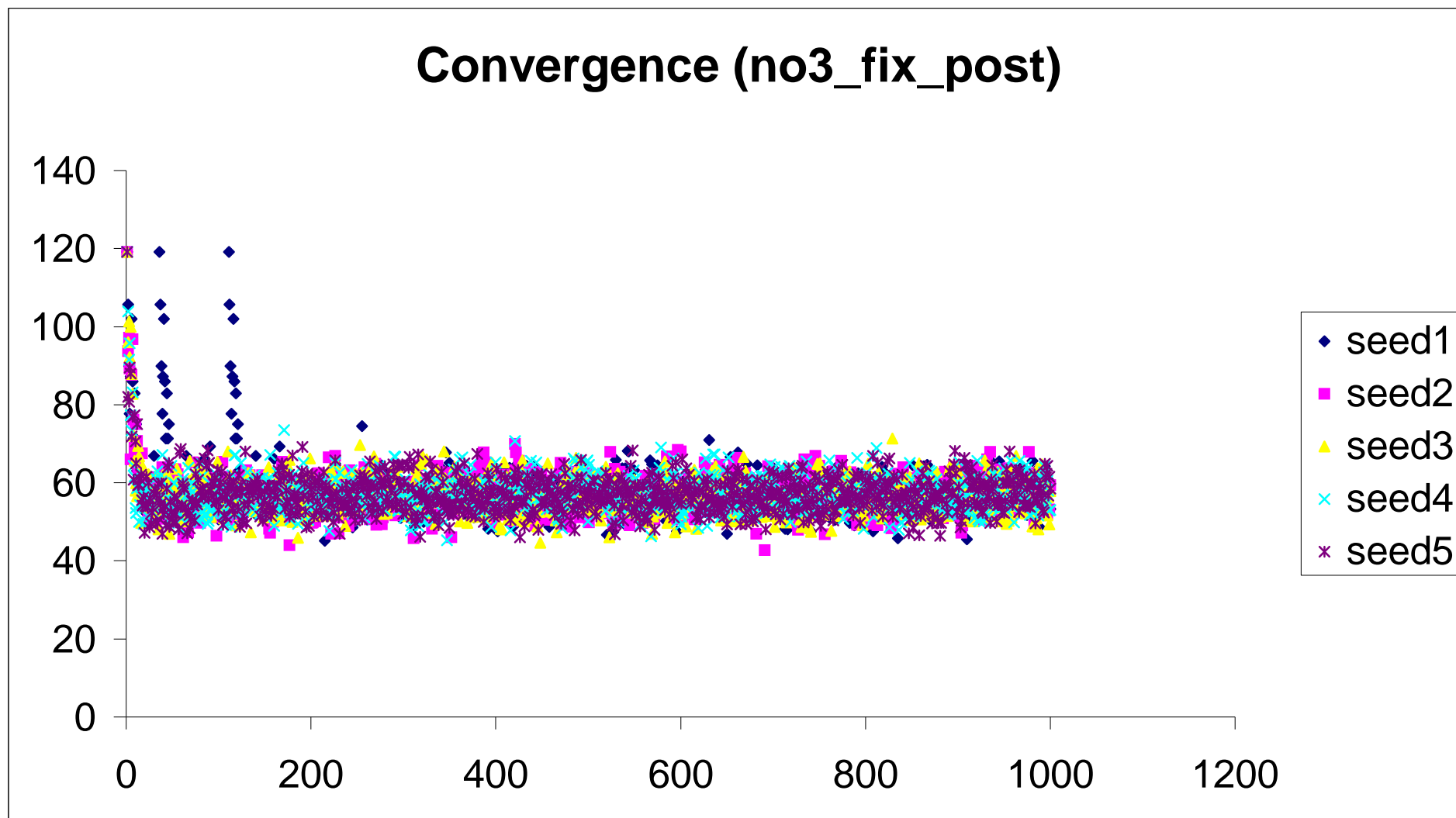


Figure S1. Output from five MCMC runs to show that the runs both had converged and to similar values. Every 1000th step of each chain is plotted

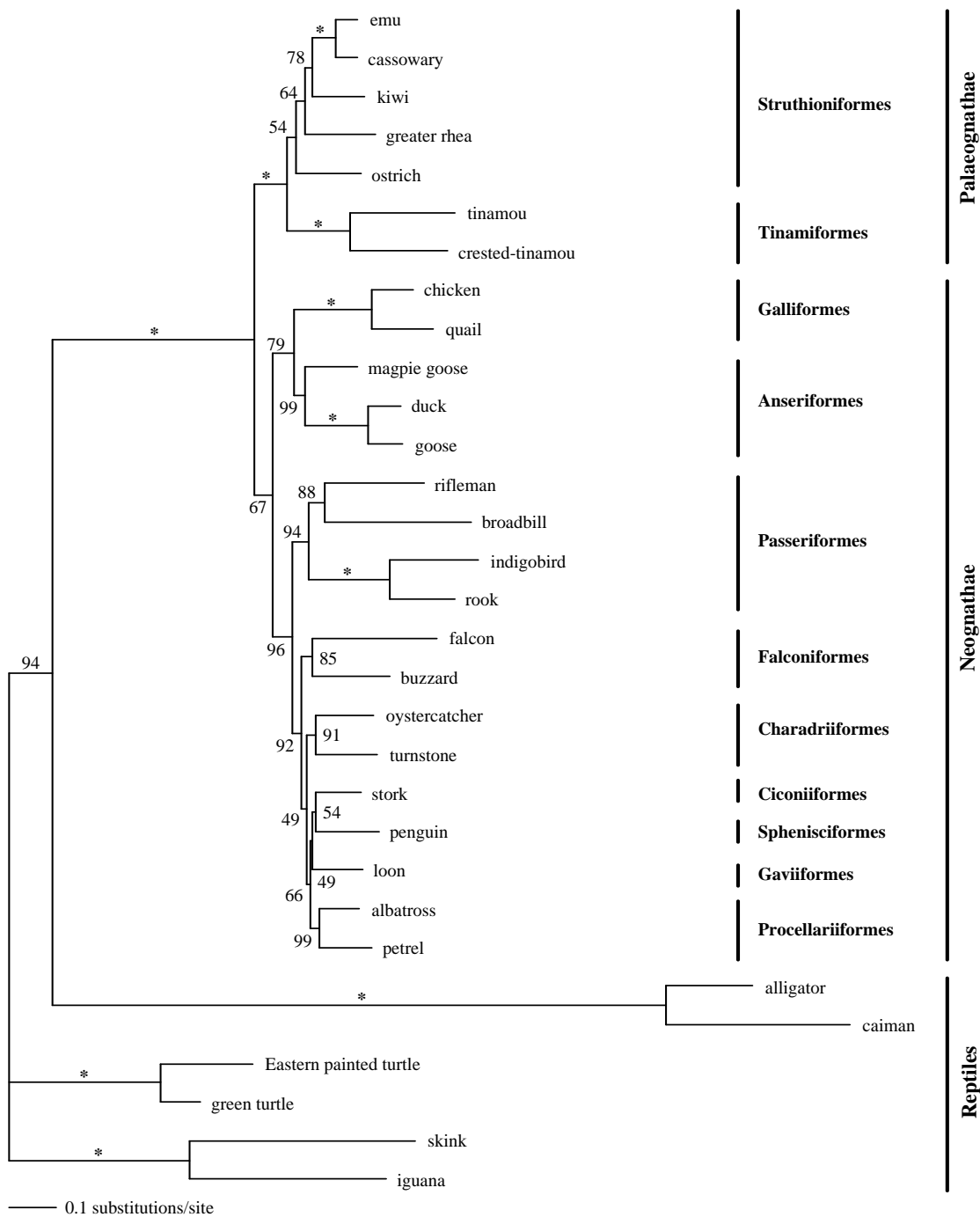


Figure S2. Maximum likelihood tree for 25 birds and six reptiles. The dataset is the 12 protein-coding genes from the mitochondrial heavy strand plus 22 RNAs (two ribosomal RNAs and 20 transfer RNAs - tRNA-Phe and tRNA-Glu were excluded due to missing data). Gaps, ambiguous sites around gaps, and stop codons were removed, giving a dataset of 11709 nt. First and second codon positions (cdp) and RNAs were analyzed as nucleotide (nt) data, third cdp were analyzed as transversion (RY) data. The analysis used the likelihood settings from the best-fit (GTR+I+G) model selected by the Akaike Information Criterion (AIC) in Modeltest Version 3.06. The tree has a $-\ln$ likelihood value of 107275.44 and is to scale. Numbers represent bootstrap values (1000 independent bootstrap replicates); 100% bootstrap support is indicated by *.

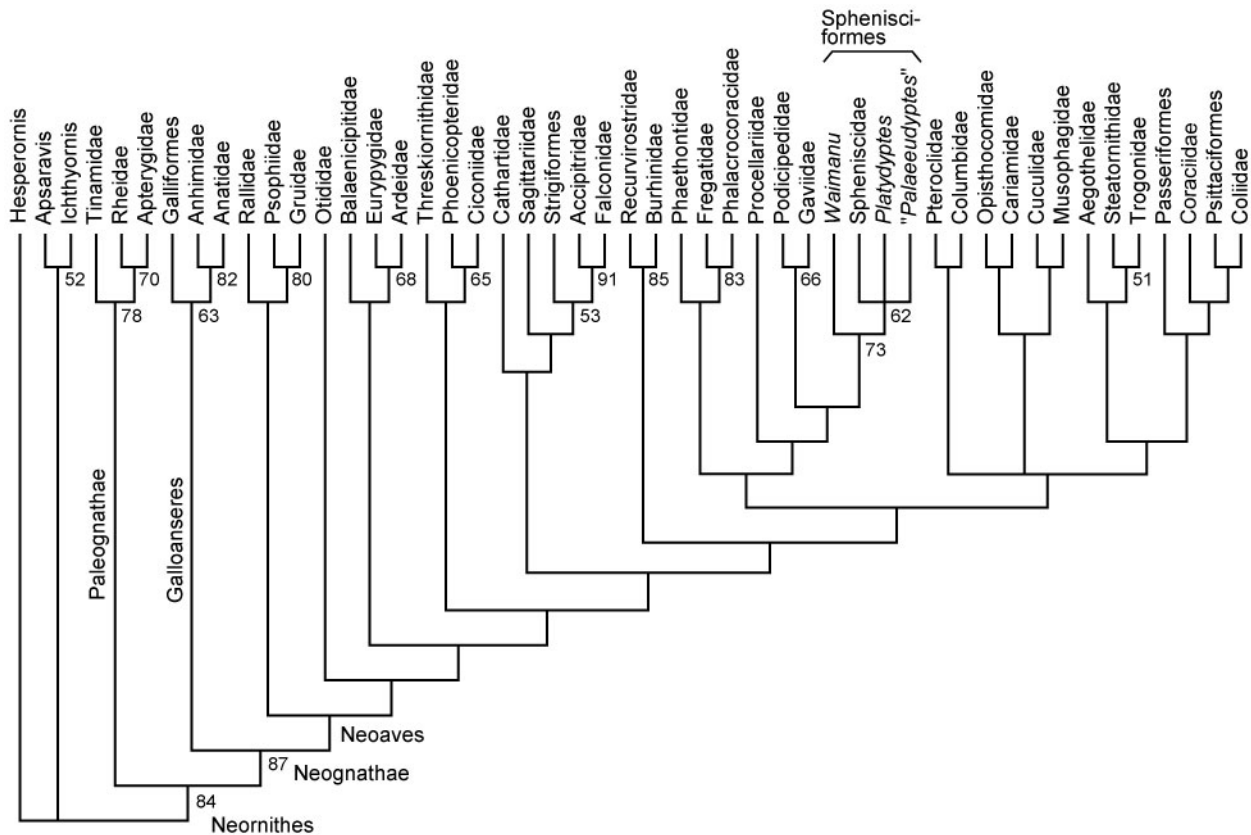


Figure S3. Phylogenetic position of *Waimanu* within Sphenisciformes in the strict consensus cladogram of 6 most parsimonious trees resulting from the analysis of morphological data (Length = 822, CI = 0.3228, RI = 0.4871, RC = 0.1573). Bootstrap support values more than 50% are indicated below and to the right of corresponding nodes. *Waimanu* and the penguins are not close to the Charadriiformes (represented here by Burhinidae and Recurvirostridae), nor to the Pelecaniformes (such as Fregatidae, Phalacrocoracidae and the Phaethontidae)

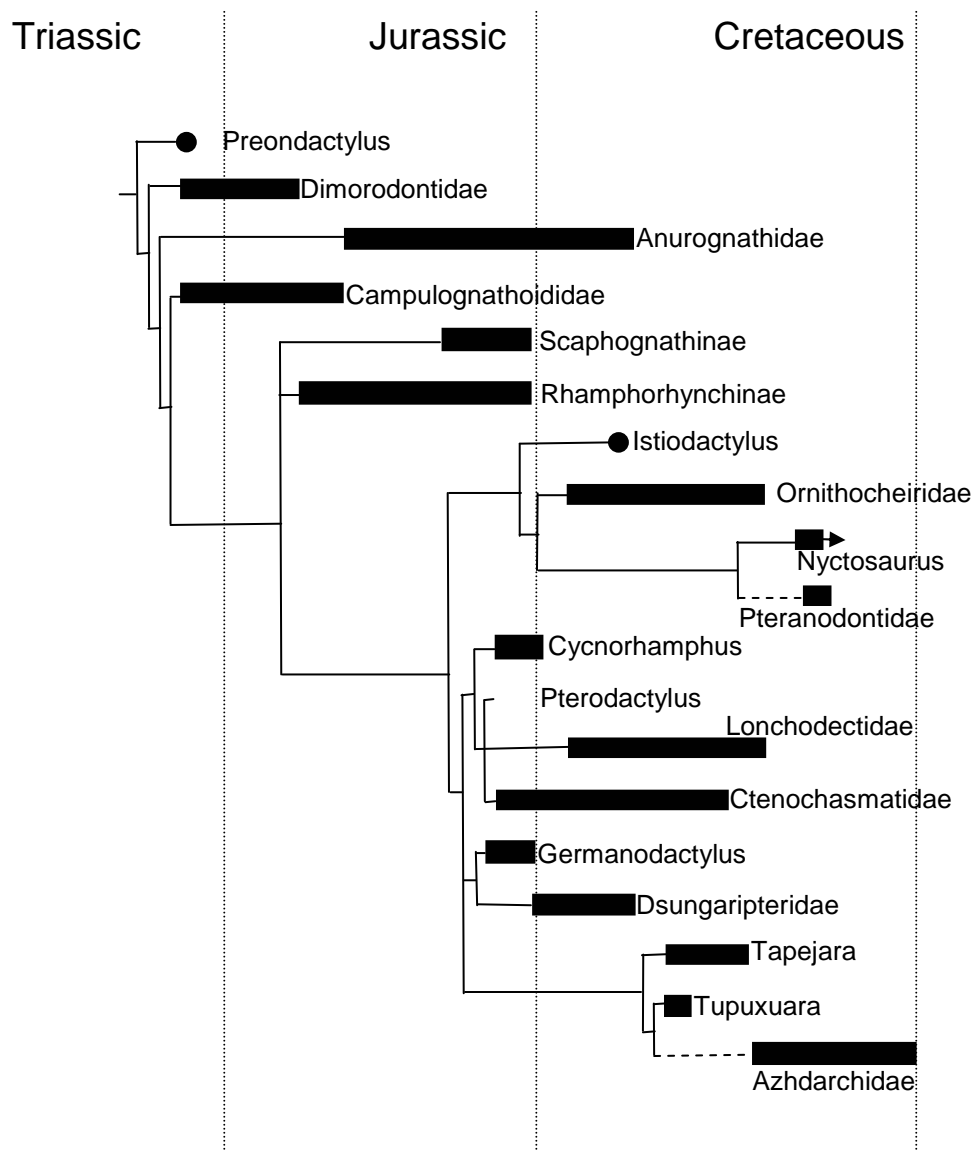
Table S3, Data and references for pterosaur (figure 3) - Data

			Age Ma	span, m				
Eudimorphodon ranzii	Italy	p60	220	10	1	p60	Ramphorhynch	<i>eudimorpodont</i>
Eudimorphodon cf. ranzii	Austria	B_M24	210	20	0.75	B_M7	Ramphorhynch	<i>eudimorpodont</i>
Peteinosaurus zambellii	Tethys	p60	220	10	0.6	p62	Ramphorhynch	<i>dimorpodont</i>
Preondactylus (Padian)	Italy	p64	225	5	1.5	p64	Ramphorhynch	<i>ramphorhynch</i>
Preondactylus buffarini		p64	225	5	0.45	p65	Ramphorhynch	<i>ramphorhynch</i>
<u>Austriadactylus cristatus</u>	<u>Austria</u>	<u>B_M27</u>	<u>210</u>	<u>20</u>	<u>1.2</u>	<u>D_VWHR02</u>	<u>Ramphorhynch</u>	<u>?eudimorpodont?</u>
	England							
Dimorphodon macronyx	Lias	p70	205	25	1.4	p70	Ramphorhynch	<i>dimorpodont</i>
Ramphinion jenkinsi	Arizona	p74	200	30	1.5	p78		<i>undetermined</i>
Dorygnathus banthensis	Germany	p74	196	34	1	p74	Ramphorhynch	<i>ramphorhynch</i>
Campylognathoides liasicus	Germany	p74	194	36	1	p76	Ramphorhynch	<i>ramphorhynch</i>
Campylognathoides zitteli	Germany	p74	195	35	1.75	p76	Ramphorhynch	<i>ramphorhynch</i>
Parapsicephalus purdoni	England	p74	190	40	1	p78	Ramphorhynch	<i>ramphorhynch</i>
agnurognathid	Mongolia	U96_297	175	55	0.4	U96_298	Ramphorhynch	<i>anurognathidae</i>
Huizacal pterosaur	Mexico	U96_298	172	58	1.4	U96-298	Ramphorhynch	<i>campylognathoid?</i>
Ramphocephalus bucklandii	England	p81	165	65	1.05	p80	Ramphorhynch	<i>ramphorhynch</i>
Ramphocephalus depressirostris	England	p81	164	66	1	U96	Ramphorhynch	<i>ramphorhynch</i>
Ramphocephalus	England	U96_293	163	67	2	U96_295	Ramphorhynch	<i>ramphorhynch</i>
Ramphorhynchus	England	U96_295	160	70	1.1	U96_296	Ramphorhynch	<i>ramphorhynch</i>
Angustinaripterus longicephalus	China	p86	165	65	2	UBLML	Ramphorhynch	<i>ramphorhynch</i>
<u>Herbstosaurus pigmaeus</u>	<u>Argentina</u>	<u>p81</u>	<u>160</u>	<u>70</u>	<u>1.5</u>	<u>U96_299</u>	<u>Pterodactyloidea</u>	<u>dsungaripteridae</u>
Ramphorhynchus longicaudus	Solnhofen	p86	152	78	0.4	p84	Ramphorhynch	<i>ramphorhynch</i>
Ramphorhynchus longiceps	W Europe	p86	155	75	1.75	p84	Ramphorhynch	<i>ramphorhynch</i>
Pterodactylus longicollum	W Europe	p86	151	79	1.45	p88	Pterodactyloidea	<i>pterodactylidae</i>
Pterodactylus grandis	W Europe	p86	149	81	2.5	p88	Pterodactyloidea	<i>pterodactylidae</i>
Pterodactyloidea indet	Switzerland	M_H99	151	79	3.5	M_H99	Pterodactyloidea	<i>indeterm</i>
Scaphognathus crassirostris	Solnhofen	p90	151	79	0.9	p93	Ramphorhynch	<i>scaphogn</i>
Anurognathus ammoni	Solnhofen	p90	148	82	0.5	p93	Ramphorhynch	<i>anurognathidae</i>
Germanodactylus cristatus	Solnhofen	p95	149	81	0.98	p95	Pterodactyloidea	<i>germanodactylidae</i>
Germanodactylus ramphastinus	Solnhofen	p95	145	85	1.08	p95	Pterodactyloidea	<i>germanodactylidae</i>

Gallodactylus suevicus	Solnhofen	p95	151	79	1.35	p97	Pterodactyloidea	<i>gallodactylidae</i>	
Ctenochasma roemeri	Fr/Germ	p98	150	80	1.2	p98	Pterodactyloidea	<i>ctenochasmatidae</i>	
Gnathosaurus subulatus	Solnhofen	p98	150	80	1.7	p100	Pterodactyloidea	<i>ctenochasmatidae</i>	
Huanhepterus quingyangensis	China	p98	150	80	2.5	p105	Pterodactyloidea	<i>ctenochasmatidae</i>	
Gen et sp indet	north France	KB01	148	82	2.5	KB01	Pterodactyloidea	<i>pterodactylidae</i>	
Dermodactylus montanus	Colorado	p102	144	86	1	p105	Pterodactyloidea	<i>undetermined</i>	
Comodactylus ostromi	Colorado	p102	145	85	2.5	p105	Ramphorhynch	<i>undetermined</i>	
Harpactognathus gentryii	Wyoming	B_M46	153	77	2.5	B_M51	Ramphorhynch	<i>scaphogn</i>	
Batrachognathus volans	Kazakhstan	p102	150	80	0.75	U&B423	Ramphorhynch	<i>anurognathidae</i>	
<u>Sordes pilosus</u>	Kazakhstan	B_M51	155	75	0.7	B_M51	Ramphorhynch	<i>scaphogn</i>	
Ornithocheirus sp	France	p117	133	97	3.7	p117	Pterodactyloidea	<i>ornithocheiridae</i>	
Criorhynchus simus	England	p110	130	100	5	p111	Pterodactyloidea	<i>criorhynchidae</i>	& other spp
Ornithodesmus latidens	Isle of Wight	p114	120	110	5	p115	Pterodactyloidea	<i>ornithodesmidae</i>	
Dsungaripterus weii	China	p118	140	90	3.25	p119	Pterodactyloidea	<i>dsungaripteridae</i>	Dsungaripterus parvus
Phobetor parvus	China	p118	140	90	1.5	p119	Pterodactyloidea	<i>dsungaripteridae</i>	
Toxaster caste	France	Buff04	133	97	7	Buff04	Pterodactyloidea	<i>ornithocheiridae</i>	
Isle of Wight specimen	England	MFGG96	127	103	8	MFGG96	Pterodactyloidea	<i>undetermined</i>	
Noriopterus complicidens	China	p118	120	110	2	p120	Pterodactyloidea	<i>dsungaripteridae</i>	
Arthurdactylus conan-doylei	Brazil	FM94	120	110	4.6	FM94	Pterodactyloidea	<i>ornithocheiridae</i>	
Jeholopterus ningchengensis	Jehol	J_104	124	106	0.9	J_100	Ramphorhynch	<i>anurognathidae</i>	
Eosipterus yangi	Jehol	J_22	122	108	1.2	J_100	Pterodactyloidea	<i>pterodactylidae</i>	
Haopterus gracilis	Jehol	J_22	122	108	1.35	J_100	Pterodactyloidea		subadult?
Sinopterus dongi	Jehol	J_106	115	115	1.2	J_104	Pterodactyloidea	<i>tapejaridae</i>	young indiv Well04
Chaoyangopterus zhangii	Jehol	J_106	115	115	1.85	J_104	Pterodactyloidea	<i>nyctosauridae</i>	
Liaoningopterus gui	Jehol	J_106	115	115	5	J_104	Pterodactyloidea	<i>anhangueridae</i>	
Anhanguera blittersdorffi	Brazil	p128	115	115	4	p129	Pterodactyloidea	<i>anhangueridae</i>	
Anhanguera santanae	Brazil	p128	115	115	4.15	p125	Pterodactyloidea	<i>anhangueridae</i>	
Anhanguera piscator	Brazil	KT2000	105	125	5	Kell2004a	Pterodactyloidea	<i>anhangueridae</i>	very young indiv
Cearadactylus atrox	Brazil	p128	115	115	5.5	p129	Pterodactyloidea	<i>ctenochasmatidae</i>	Unwin02
Cearadactylus' ligabuei	Brazil	KT2000	105	125	5.5	KT2000	Pterodactyloidea	<i>ctenochasmatidae</i>	
Tropeognathus mesembrinis	Brazil	p128	115	115	6.2	p129	Pterodactyloidea	<i>criorhynchidae</i>	
Tropeognathus robustus	Brazil	p128	117	113	5.5	p129	Pterodactyloidea	<i>criorhynchidae</i>	in proportion
Santanadactylus araripensis	Brazil	p128	115	115	3	p124	Pterodactyloidea	<i>ornithocheiridae</i>	
Tapejara wellnhoferi	Brazil	p128	115	115	1.5	Kell04	Pterodactyloidea	<i>tapejaridae</i>	

Tupuxuara longicristatus	Brazil	p130	115	115	2.8	Kell04	Pterodacyloidea	<i>tapejaridae</i>	toothless
Tupuxuara leonardii	Brazil	Well04	116	114	4.5	Kell04	Pterodacyloidea	<i>tapejaridae</i>	
Araripesaurus castilboi	Brazil	p124	115	115	2.2	p124	Pterodacyloidea		
Araripedactylus debmi	Brazil	p124	115	115	4.8	p124	Pterodacyloidea	indeterm	
ornithocheirid'	Mongolia	U&B426	112	118	5.5	U&B426	Pterodacyloidea	<i>ornithocheiridae</i>	
Bennett 1989	Argentina	p134	115	115	4	p134	Pterodacyloidea		
Coloborhynchus spielbergi	Brazil	Veld03	108	122	5.9	Veld03	Pterodacyloidea	<i>anhangueridae</i>	
Thalassodromeus sethi	Brazil	KC02	110	120	4.4	KC02	Pterodacyloidea	<i>tapejaridae</i>	
<u>Pterodaustro guinazui</u>	Argentina	Chiappe04	100	130	3	Chiappe04	Pterodacyloidea	<i>pterodaustriidae</i>	filter feeder
Ornithostoma orientalis	England	p110	97	133	2.5	p111	Pterodacyloidea	<i>pteranodontidae</i>	
cf. Anhanguera	Russia	U&B425	95	135	3.5	U&B425	Pterodacyloidea	<i>ornithocheiridae</i>	
cf. Anhanguera	Russia	U&B425	95	135	3.5	U&B425	Pterodacyloidea	<i>ornithocheiridae</i>	
Ornithocheirus sp	Zaire	p121	90	140	4.5	p121			
Pteranodon sternbergi	Kansas	p134	85	145	9	p139	Pterodacyloidea	<i>pteranodontidae</i>	toothless
Pteranodon ingens	Kansas	p134	85	145	7	p139	Pterodacyloidea	<i>pteranodontidae</i>	toothless
"Pteranodon sp"	Japan	p145	83	147	6	UBLML	Pterodacyloidea	<i>azhdarchid</i>	
Haenamichnus footprint	Korea	KHCLC03	81	149	10	KHCLC03	Pterodacyloidea	<i>footprints!</i>	
Ornithocheirus bunzeli	Austria	p116	80	150	1.7	117	Pterodacyloidea	<i>ornithocheiridae</i>	may be Azhdarch
Azhdarcho lancicollis	Uzbekistan	U&B426	87	143	5	U&B426	Pterodacyloidea	<i>azhdarchid</i>	
Azhdarchid	Russia	U&B427	85	145	3.5	U&B427	Pterodacyloidea	<i>azhdarchid</i>	
Wairoa specimen	NZ	WM88	76	154	3.5	WM88	Pterodacyloidea	indeterm	
Ornithocheiridae indet	Russia	AY04	75	155	5	AY04	Pterodacyloidea	<i>ornithocheiridae</i>	
Nyctosaurus gracilis	Kansas	p138	80	150	2.9	p139	Pterodacyloidea	<i>nyctosauridae</i>	
Nyctosaurus lamegoi	Brazil	p145	75	155	3.5	p122	Pterodacyloidea	<i>nyctosauridae</i>	
Quetzalcoatlus northropi	Texas	p142	66	164	11	p143	Pterodacyloidea	<i>azhdarchid</i>	
Quetzalcoatlus sp	Texas	p142	66	164	5.5	p142	Pterodacyloidea	<i>azhdarchid</i>	p142
Phosphatodraco mauritanicus	Morocco	B_M80	68	162	5	B_M87	Pterodacyloidea	<i>azhdarchid</i>	
Arambourgiania philadelphiae	Jordan	MSFK96	69	161	12	FM96	Pterodacyloidea	<i>azhdarchid</i>	formerly Titanopteryx B_M86
Zhejiangopterus linhaiensis	China	U_J97	81	149	3.5	B_M87	Pterodacyloidea	<i>azhdarchid</i>	
cf. Quetzalcoatlus	France	BLLB97	67	163	9	BLLB97	Pterodacyloidea	<i>azhdarchid</i>	
Azhdarchidae indet.	Spain	Company99	69	161	5.5	Company99	Pterodacyloidea	<i>azhdarchid</i>	
Hatzegopteryx thambema	Romania	Buffet02	68	162	12	Buffet02	Pterodacyloidea	<i>azhdarchid</i>	
Montplaisir pterosaur	France	Buffet96	67	163	5	Buffet96	Pterodacyloidea	<i>azhdarchid</i>	
largest ever'	Spain	Company01	67	163	12.2	Company01	Pterodacyloidea	<i>azhdarchid</i>	

Data for Figure 3, Panel A, pterosaur diversity through time. The data in Figure 3A was taken directly from Figure 21 of Unwin (2003), but that figure is redrawn and shown here for convenience.



The following references were used for the data in Figure 3 (other references were consulted, but not used for the primary data).

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