

Supporting Information

Evolutionary patterns of vane barb angles in birds

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Included:

1. Dataset and methods
2. Aves with different flight styles plotted in a wing phylomorphospace described by leading and trailing vane barb angles (Figure S1).
3. Aves with different flight styles plotted in a wing phylomorphospace described by trailing vane barb and barb angle asymmetry values. (Figure S2)
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8. Measurements used for extant birds from Feo et al. (2015) (Table S1)
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Dataset

Values for trailing vane angle and barb angle asymmetry for 25% feather length are significantly different for the Feo et al. sample. We chose to use the 50% values in this reanalysis since these were most similar to the measurement locations available for the majority fossil feathers sampled and because Feo et al. only provided 50% measurements for non-volant extant taxa. For Mesozoic taxa Measured values were compared to published values for specimens V15336, V13156, DNHM-D3078, BMNH-Ph000881 and Berlin specimen of *Archaeopteryx* utilized in that analysis.

Methods

(a) Phylogenetic signal and ancestral state reconstruction

Pagel's lambda [1] and Blomberg's K [2] were performed in R v. 3.0.1 [3] using the Phytools package (function `phylosig` [4]) to assess phylogenetic signal of barb angles. The influence of the phylogeny increases with lambda from 0 (no phylogenetic signal) and 1 (strong phylogenetic signal). When lambda = 0, a star phylogeny results with all tips radiating from a basal node, describing a model where traits evolve independent of the phylogeny. When lambda = 1, trait evolution followed a Brownian motion model, where branch lengths would be proportional to divergence. Blomberg's K statistic is used to test whether the observed distribution of traits exhibits more or less divergence than expected for traits evolving under Brownian motion. Values of K close to 1 indicate trait similarity is proportional to divergence and a Brownian motion model of evolution fits the data. $K > 1$ indicates that close relatives are more similar than expected, and $K < 1$ indicates more divergence between taxa than expected under a Brownian model.

Mesquite (v. 2.75 [5]) was used to map barb angles onto the reference phylogeny. Each character was traced onto the tree using the 'reconstruct ancestral state' module of Mesquite with weighted squared change parsimony [6]. Given the tree and observed character distribution, this method finds the ancestral states that minimize the number of steps of

character change.

1000 time-calibrated trees for the possible phylogenetic affinities of these 73 birds were sampled from the posterior distribution of Jetz et al [7] (<http://www.birdtree.org>). These trees use the Hackett et al [8] topology as a backbone. A majority rules consensus tree was built by Mesquite [5]. As taxa within passerines and rails are not fully resolved, the consensus tree was further resolved following recent phylogenetic hypotheses for passerines and rails [9, 10]. For Mesozoic taxa, we generate a fossil subtree with the timePaleoPhy function in paleotree [11] based on published fossil ages and branch [12, 13] (summarized in table S3). We grafted this time-calibrated tree of extinct taxa to the Aves tree with the bind.tip function in Phytools.

(b) Statistical analysis

All statistical analyses were conducted using the R statistical computing environment v.3.4.3 (R Development Core Team, 2017). To account for phylogeny via PGLS. ANOVA on PGLS models were conducted in R using the procD.pgls function in Geomorph package (residual randomisation permutation procedure) [14] and pairwise comparison was made in RRPP package [15]. The procD.pgls function performs ANOVA and regression models in a phylogenetic context under a Brownian motion model of evolution. The approach is derived from the statistical equivalency between parametric methods utilizing covariance matrices and methods based on distance matrices [14]. The randomization of residuals in a permutation procedure was used with 1000 iterations. F statistics are calculated from sums of squares based on coefficients that have appropriately accounted for phylogenetic relatedness. Effect-sizes (Z scores) are computed as standard deviates of the F sampling distributions generated [14].

The function Phylogenetic generalized least-squares (pGLS) were also performed in R package Caper [16] to assess the relationship between trailing vane barb angle and barb angle asymmetry. We categorized flight styles for living birds as those defined by Bruderer et al [17]. Specifically, “continuous flapping”, “flapping and soaring”, “flapping and gliding” and “passerine type flight”. Flightless species and fossils were categorized as distinct flight styles in this study. Measurements were log transformed to obtain a normal distribution as methods used have the assumption of normally distributed data.

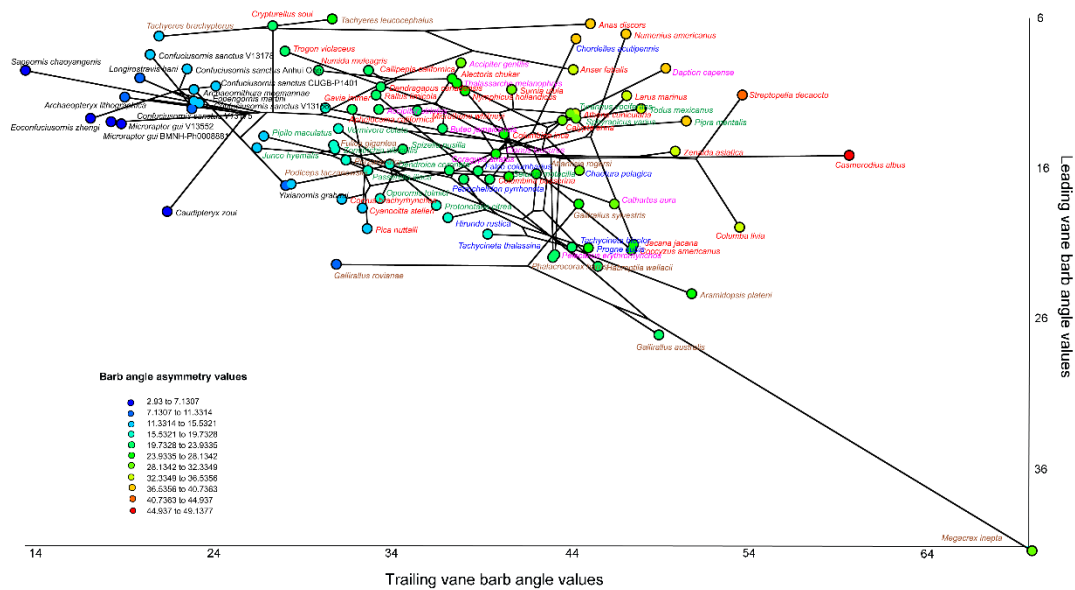


Figure S1. Aves with different flight styles and Mesozoic taxa plotted in a wing phylomorphospace described by leading and trailing vane barb angles. Red, continuous flapping “CF”; blue, flapping and soaring “FS”; purple, flapping and gliding “FG”; green, passerine type flight “PT”; brown, flightless “FL”; black, fossil data.

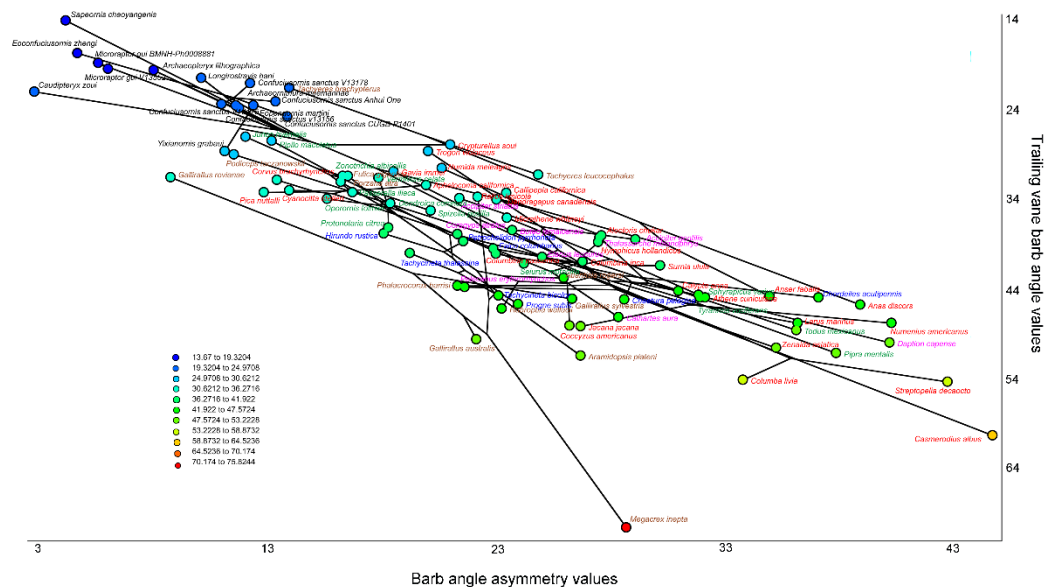


Figure S2. Aves with different flight styles and Mesozoic taxa plotted in a wing phylomorphospace described by trailing vane barb and barb angle asymmetry values. Red, continuous flapping “CF”; blue, flapping and soaring “FS”; purple, flapping and gliding “FG”; green, passerine type flight “PT”; brown, flightless “FL”; black, fossil data.

Interestingly, we found that distinct from other water birds, loons showed very reduced barb angles and angle asymmetry (11.829 and 30.508 for leading and trailing vane barb angles), similar to those of grebes (Figures 1,2, S2).

As barb angles were measured from different feathers and positions, we also mapped the values of barb angle variance across modern flight species. Similar patterns were recovered in ancestral state reconstructions of angle variance values. The leading vane and angle asymmetry values show reduced variance in galloanseres and passerines. Variance for trailing vane barb angles is also small in passerines (Figures S3-S5).

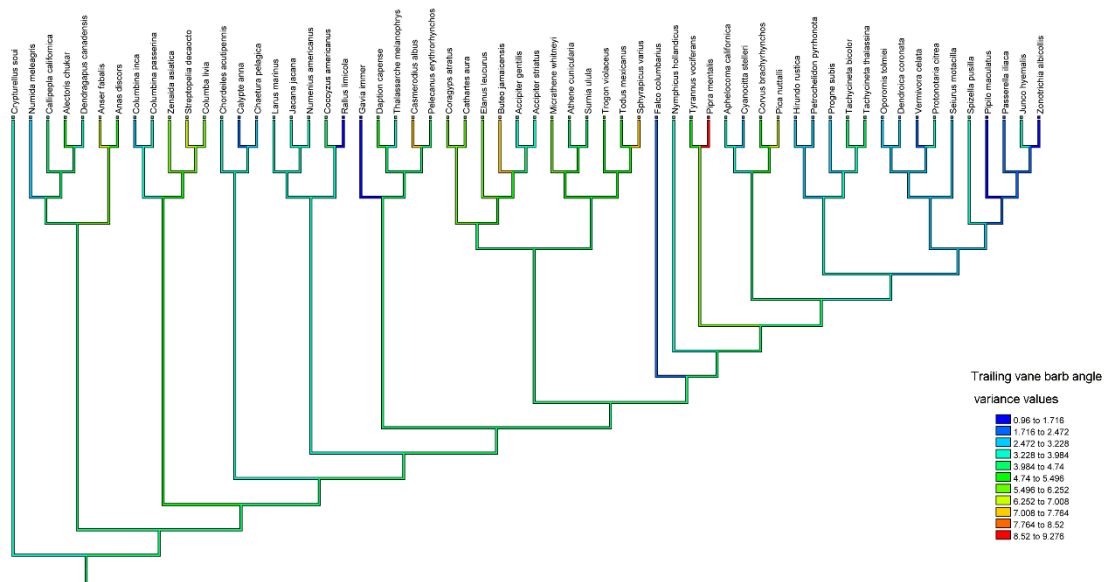


Fig S3. Changes in trailing vane barb angle variance from different feathers (inner, middle and outer) and positions (25% and 50% from feather tip) across extant flight species.

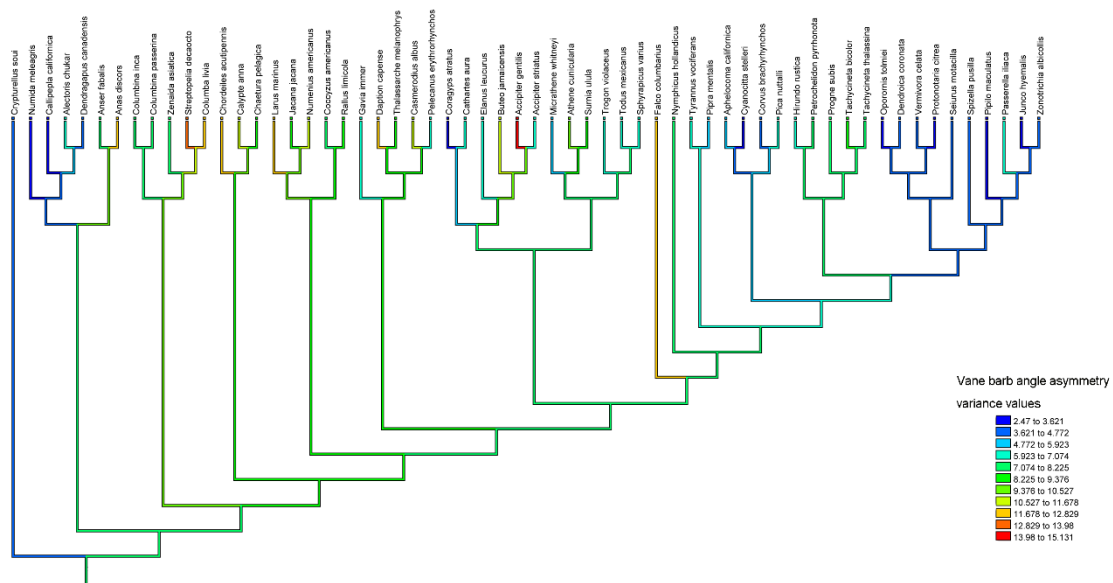


Fig. S4 Changes in vane barb angle asymmetry variance from different (inner, middle and outer) and positions (25% and 50% from feather tip) across extant flight species.

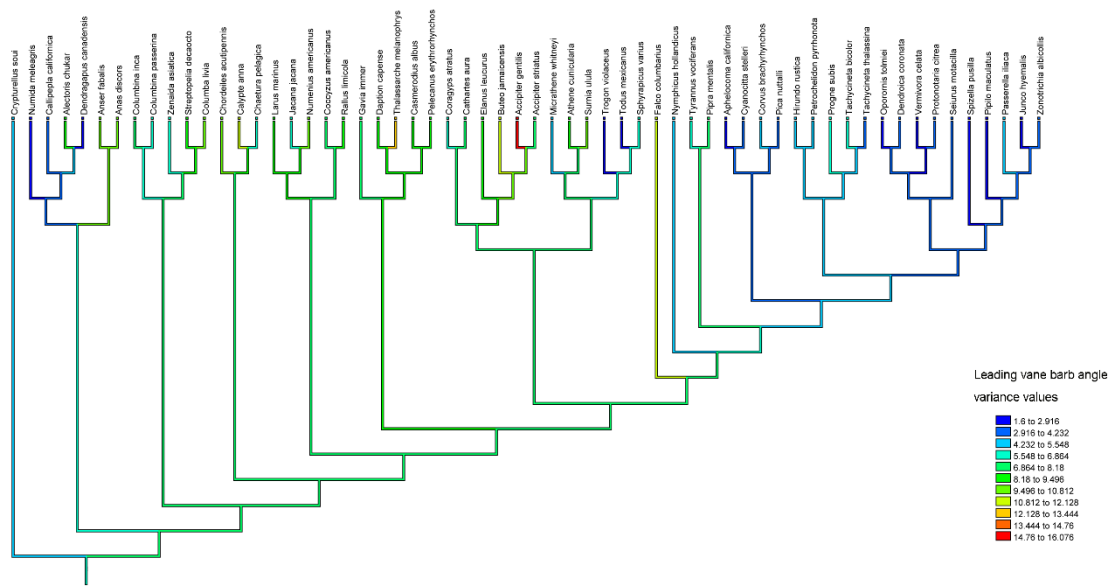


Fig. S5 Changes in Leading vane barb angle variance from different (inner, middle and outer) and positions (25% and 50% from feather tip) across extant flight species.

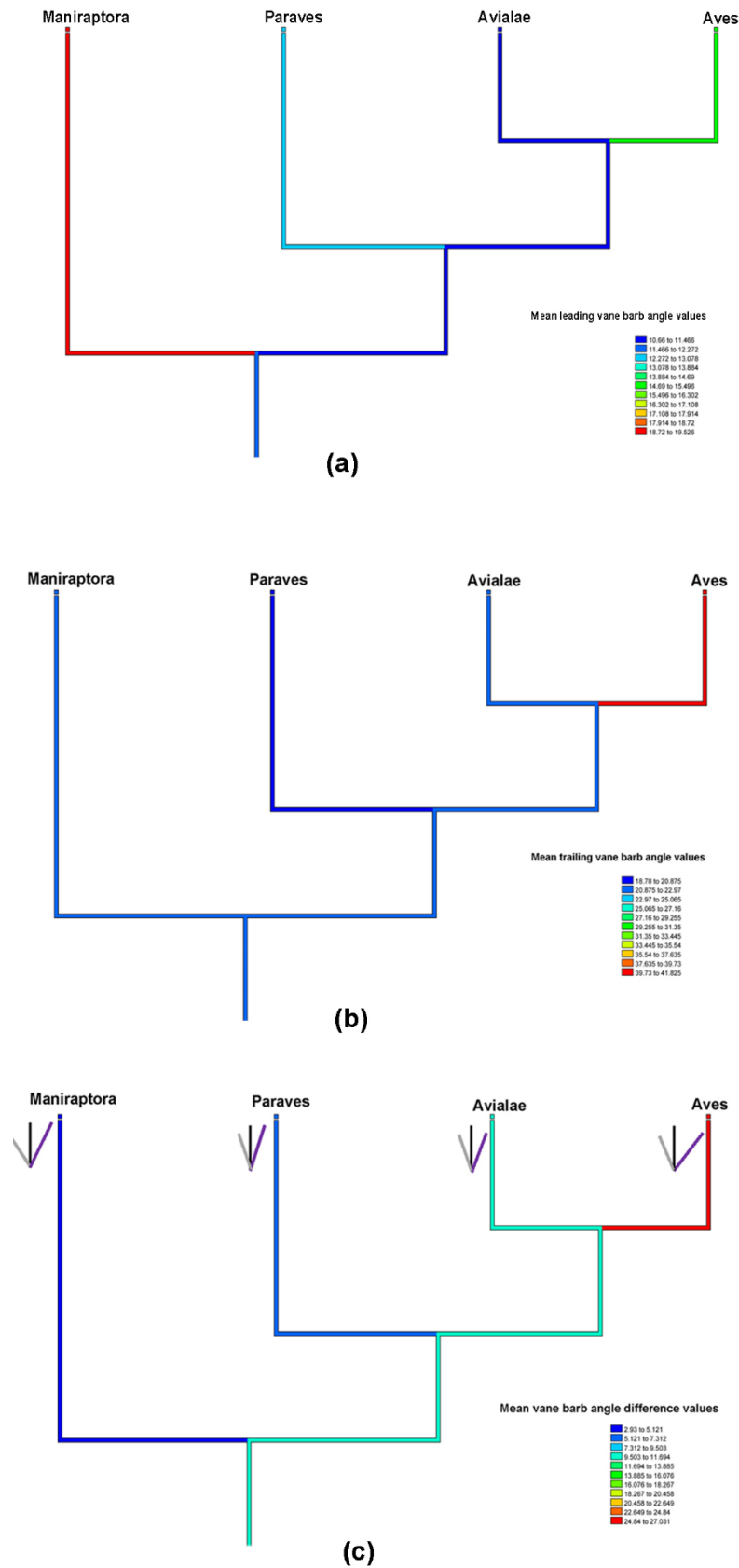


Fig. S6 Ancestral state reconstruction for leading (a), trailing (b) vane barb angles and barb angle asymmetry (c) showing the general evolutionary pattern for simplified phylogeny. Diagrams show the barb geometry. Grey, leading vane barb; purple, trailing vane barb.

Table S1. Measurements used for extant birds from Feo et al. (2015)*

Species	Ld	Tr	Diff	flight style
<i>Coragyps atratus</i>	16.008	37.495	21.488	FS
<i>Cathartes aura</i>	18.222	46.757	28.535	FS
<i>Elanus leucurus</i>	14.887	40.099	25.212	FS
<i>Buteo jamaicensis</i>	13.223	37.100	23.878	FS
<i>Accipiter gentilis</i>	8.849	38.133	29.284	FS
<i>Accipiter striatus</i>	11.916	33.505	21.589	FS
<i>Anser fabalis</i>	9.269	44.457	35.187	CF
<i>Anas discors</i>	6.226	45.384	39.158	CF
<i>Tachyeres brachypterus</i>	7.067	21.171	14.104	FL
<i>Tachyeres leucocephalus</i>	5.885	30.917	25.031	FL
<i>Calypte anna</i>	12.664	43.836	31.172	CF
<i>Chaetura pelagica</i>	15.973	44.779	28.806	FG
<i>Chordeiles acutipennis</i>	7.250	44.577	37.327	FG
<i>Jacana jacana</i>	20.919	47.810	26.891	CF
<i>Numenius americanus</i>	6.903	47.417	40.514	CF
<i>Larus marinus</i>	11.022	47.423	36.401	CF
<i>Zenaida asiatica</i>	14.690	50.156	35.466	CF
<i>Streptopelia decaocto</i>	10.968	53.943	42.975	CF
<i>Columba livia</i>	19.787	53.782	33.996	CF
<i>Columbina inca</i>	13.582	40.570	26.989	CF
<i>Columbina passerina</i>	16.558	39.732	23.175	CF
<i>Todus mexicanus</i>	11.874	48.230	36.356	PT
<i>Coccyzus americanus</i>	21.291	47.710	26.419	CF
<i>Falco columbarius</i>	16.050	39.114	23.064	FG
<i>Callipepla californica</i>	9.340	32.963	23.623	CF
<i>Alectoris chukar</i>	9.855	37.650	27.794	CF
<i>Dendragapus canadensis</i>	10.427	33.645	23.218	CF
<i>Numida meleagris</i>	9.331	30.138	20.807	CF
<i>Gavia immer</i>	11.829	30.508	18.679	CF
<i>Habroptila wallacii</i>	22.393	45.832	23.440	FL
<i>Atlantisia rogersi</i>	16.218	42.375	26.156	FL
<i>Fulica gigantea</i>	14.321	31.000	16.679	FL
<i>Porzana atra</i>	15.295	31.664	16.369	FL
<i>Aramidopsis plateni</i>	24.205	51.094	26.890	FL
<i>Megacrex inepta</i>	41.273	70.174	28.901	FL
<i>Gallirallus australis</i>	26.919	49.250	22.331	FL
<i>Gallirallus sylvestris</i>	18.205	44.733	26.528	FL
<i>Gallirallus roviae</i>	22.229	31.150	8.921	FL
<i>Rallus limicola</i>	10.985	33.354	22.369	CF
<i>Tyrannus vociferans</i>	12.215	44.285	32.070	PT
<i>Pipra mentalis</i>	12.715	50.799	38.085	PT
<i>Aphelocoma californica</i>	11.925	32.040	20.115	CF
<i>Cyanocitta stelleri</i>	18.498	32.615	14.118	CF
<i>Corvus brachyrhynchos</i>	17.885	31.449	13.564	CF
<i>Pica nuttalli</i>	19.881	32.875	12.995	CF
<i>Hirundo rustica</i>	19.154	37.410	18.256	FG
<i>Petrochelidon pyrrhonota</i>	16.564	38.299	21.736	FG
<i>Progne subis</i>	21.154	45.293	24.139	FG

<i>Tachycineta_bicolor</i>	21.071	44.374	23.303	FG
<i>Tachycineta_thalassina</i>	20.222	39.624	19.402	FG
<i>Oporornis_tolmiei</i>	17.854	33.617	15.762	PT
<i>Protonotaria_citrea</i>	18.292	36.756	18.464	PT
<i>Dendroica_coronata</i>	15.581	34.123	18.542	PT
<i>Seiurus_motacilla</i>	16.396	40.809	24.414	PT
<i>Vermivora_celata</i>	13.224	31.267	18.043	PT
<i>Junco_hyemalis</i>	14.478	26.672	12.194	PT
<i>Zonotrichia_albicollis</i>	14.593	31.064	16.471	PT
<i>Passerella_iliaca</i>	16.000	32.891	16.891	PT
<i>Pipilo_maculatus</i>	13.719	27.074	13.354	PT
<i>Spizella_pusilla</i>	14.567	34.880	20.313	PT
<i>Casmerodius_albus</i>	14.982	59.920	44.937	CF
<i>Pelecanus_erythrorhynchos</i>	21.610	43.411	21.801	FS
<i>Phalacrocorax_harrisi</i>	21.789	43.270	21.481	FL
<i>Sphyrapicus_varius</i>	12.498	44.609	32.112	PT
<i>Podiceps_taczanowskii</i>	16.903	28.605	11.702	FL
<i>Daption_capense</i>	9.175	49.622	40.447	FS
<i>Thalassarche_melanophrys</i>	10.181	37.892	27.711	FS
<i>Nymphicus_hollandicus</i>	10.707	38.358	27.652	CF
<i>Micrathene_whitneyi</i>	12.011	35.665	23.655	CF
<i>Athene_cunicularia</i>	12.207	44.568	32.361	CF
<i>Surnia_ulula</i>	10.595	40.984	30.389	CF
<i>Crypturellus_soui</i>	6.378	27.558	21.180	CF
<i>Trogon_violaceus</i>	8.041	28.254	20.213	CF

Ld, leading vane angle; Tr, trailing vane angle; Diff, barb angle differences; CF, continours flapping; FS, flapping and soaring; FG, flapping and gliding; PT, passerine type flight; FL, flightless
*Specimen numbers and localities can be found from Feo et al. (2015).

Table S2 Measurements used for fossil taxa

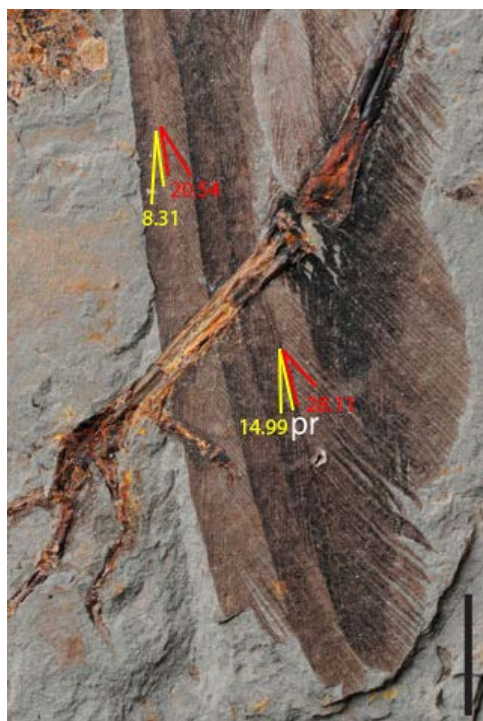
Specimen No.	Species	Ld	Tr	Diff
STM-7-145	<i>Archaeornithura meemannae</i>	10.62	23.16	12.54
V13631	<i>Yixianornis grabau</i>	17.00	28.29	11.29
V11309	<i>Longirostravis hani</i>	9.85	20.12	10.27
STM-24-1	<i>Eopengornis martini</i>	7.42	23.59	16.16
V15336	<i>Eopengornis martini</i>	11.13	19.46	8.33
V13156	<i>Confuciusornis sanctus</i>	11.37	23.14	11.77
CUGB-P1401	<i>Confuciusornis sanctus</i>	10.36	24.38	14.03
AGB5488	<i>Confuciusornis sanctus</i>	9.22	22.75	13.53
V13178	<i>Confuciusornis sanctus</i>	8.27	20.69	12.41
V13175	<i>Confuciusornis sanctus</i>	11.87	23.02	11.15
V11977	<i>Eoconfuciusornis zhengi</i>	12.50	17.34	4.84
DNHM-D3078	<i>Sapeornis chaoyangensis</i>	7.84	13.78	5.93
Berlin specimen	<i>Archaeopteryx lithographica</i>	11.11	19.27	8.17
BMNH-Ph000881	<i>Microraptor gui</i>	12.74	18.48	5.74
V13352	<i>Microraptor gui</i>	12.90	19.08	6.18
NGMC 97-4-A DSC2551	<i>Caudipteryx zoui</i>	18.72	21.66	2.93

Ld, leading vane angle; Tr, trailing vane angle; Diff, barb angle differences; STM, Shandong Tianyu Natural History Museum; V, Institute of Vertebrate Paleontology and Paleoanthropology; CUGB, China University of Geosciences (Beijing); DNHM, Dalian Natural History Museum; BMNH, Beijing Museum of Natural History; NGMC, National Geological Museum of China.

Table S3 Fossil age (Ma) data for paleotree [31].

Species	Min_age	Max_age	Start	End	Midpoint
<i>Yixianornis_grabau</i>	Aptian	Aptian	126.3	113	119.65
<i>Longirostravis_hani</i>	Late_Barremian	Early_Aptian	128.55	119.65	124.1
<i>Eopengornis_martini</i>	Hauterivian	Hauterivian	133.9	130.8	132.35
<i>Confuciusornis_sanctus</i>	Late_Barremian	Early_Aptian	128.55	119.65	124.1
<i>Eoconfuciusornis_zhengi</i>	Hauterivian	Hauterivian	133.9	130.8	132.35
<i>Sapeornis_chaoyangensis</i>	Aptian	Aptian	126.3	113	119.65
<i>Archaeopteryx_lithographica</i>	Early_Tithonian	Early_Tithonian	152.1	147.7	149.9
<i>Microraptor_gui</i>	Aptian	Aptian	126.3	113	119.65
<i>Caudipteryx_zoui</i>	Aptian	Aptian	126.3	113	119.65
<i>Archaeornithura_meemannae</i>	Hauterivian	Hauterivian	133.9	130.8	132.35

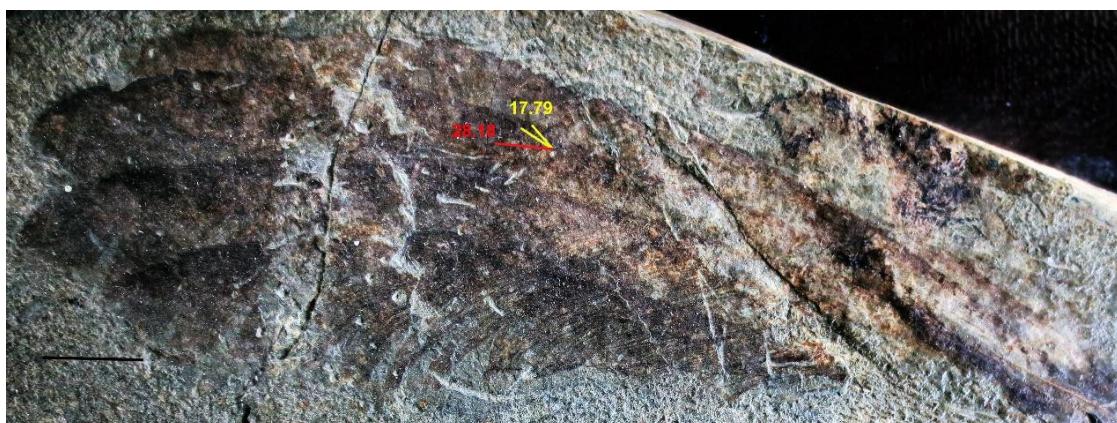
10. Images showing the angle measurements of Mesozoic fossil taxa.



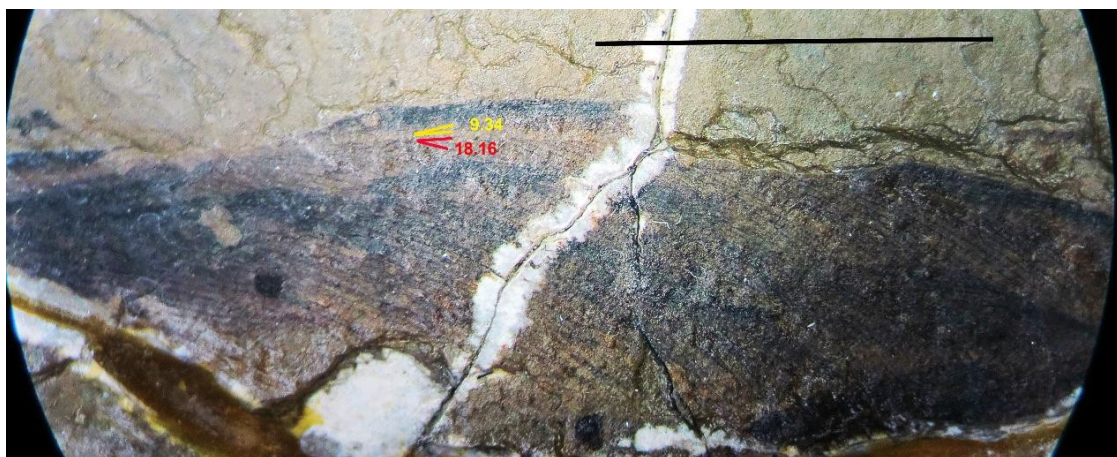
Archaeornithura meemannae (STM7-145)



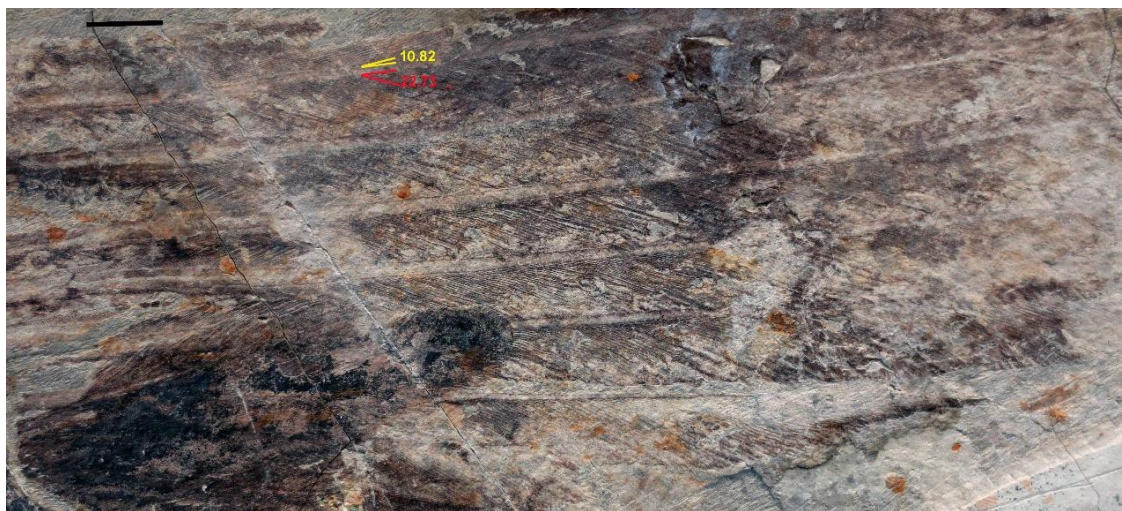
Eopengornis martini (V15336)



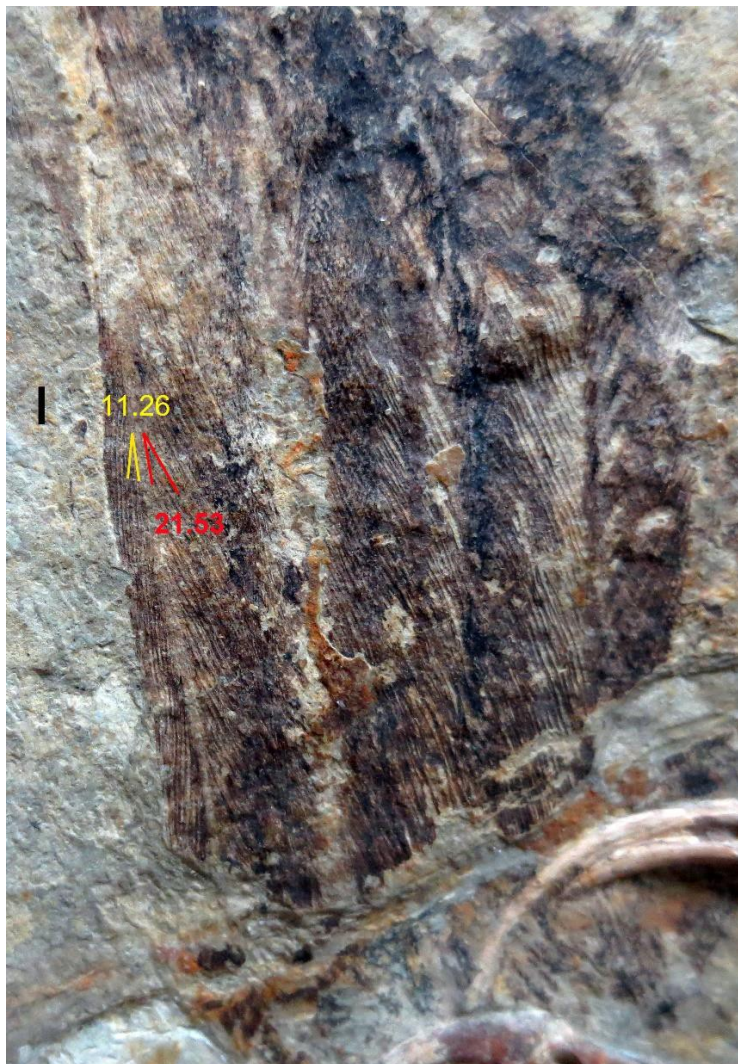
Yixianornis grabau (V13631)



Longirostravis hani (V11309)



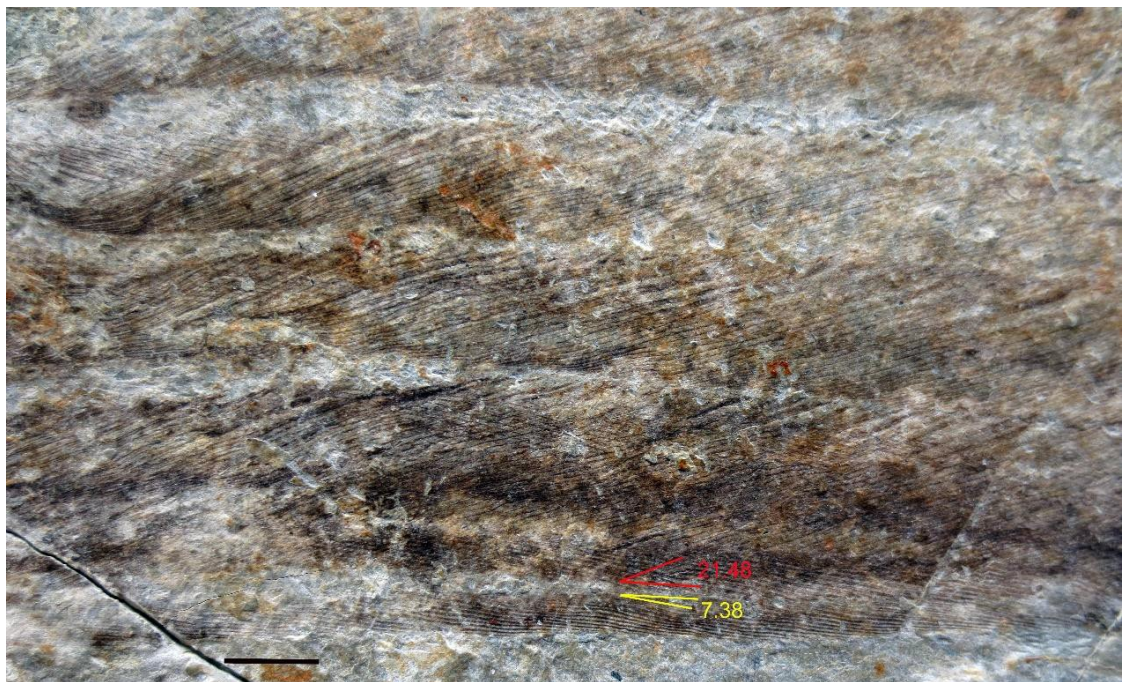
Confuciusornis sanctus(V13156)



Confuciusornis sanctus (V13175)



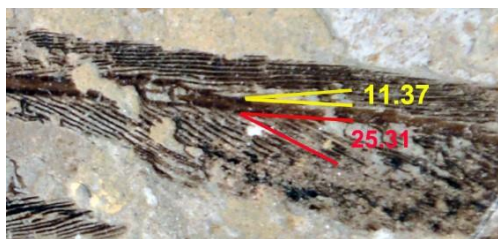
Confuciusornis sanctus (V13178a)



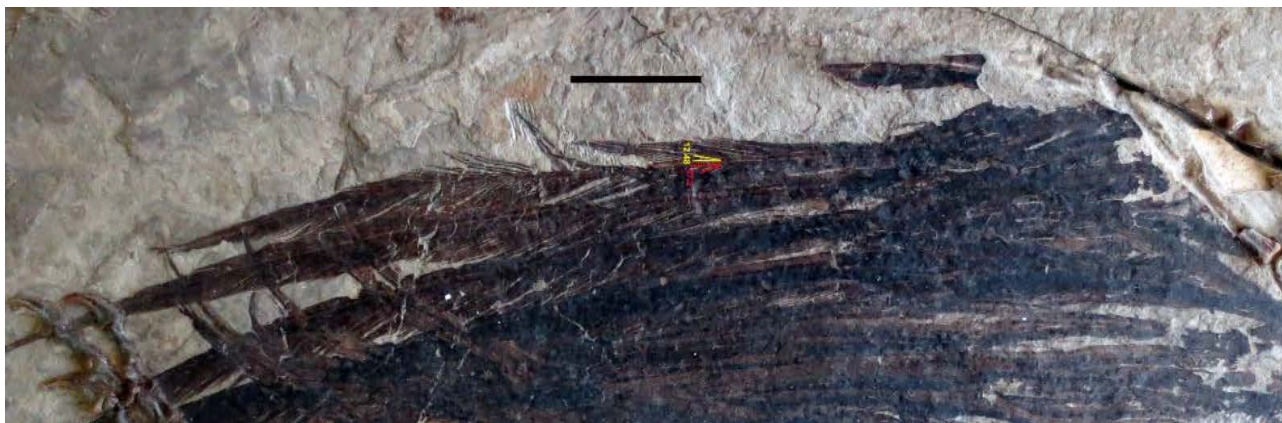
Confuciusornis sanctus (V13178b)



Confuciusornis sanctus (AGB5488)



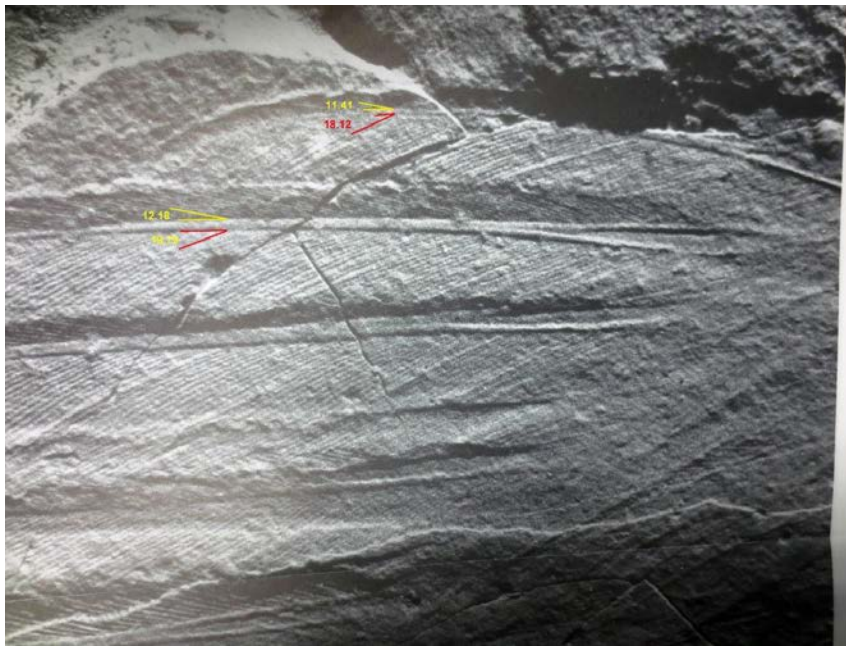
Confuciusornis sanctus (CUGB-P1401)



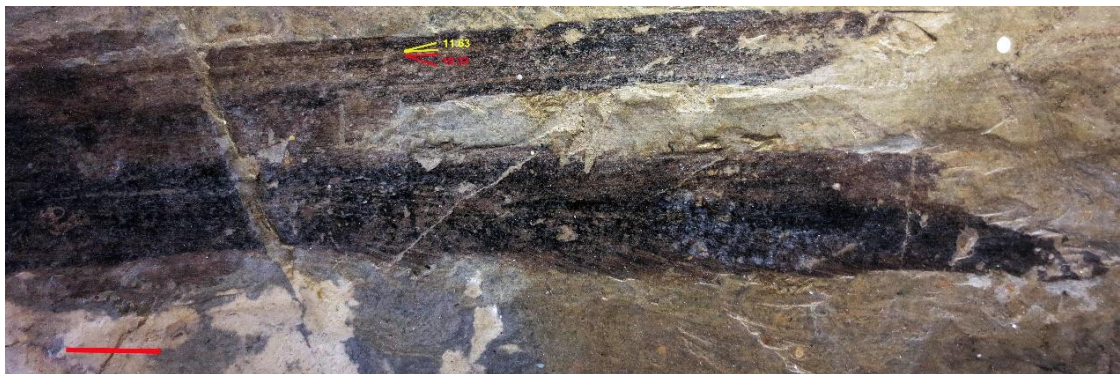
Eoconfuciusornis zhengi (V11977)



Sapeornis chaoyangensis (DNHM-D3078)



***Archaeopteryx lithographica* (Berlin specimen)**



***Microraptor gui* (V13352)**



***Caudipteryx zoui* (NGMC 97-4-A DSC2551)**

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