SUPPLEMENT TO:

Parallel Evolution of Bower-Building Behavior in Two Groups of Bowerbirds Suggested by Phylogenomics

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CONTENT

1. MATERIAL AND METHODS (DETAILED DESCRIPTION)

Taxon Sampling

In the study, we include all traditionally recognized bowerbird species as well as representatives for each of the morphologically and genetically distinct populations of the genus *Ailuroedus* that recently were elevated from status as subspecies to full species (Irestedt et al. 2016). The number of *Ailuroedus* species thus increased from the traditionally recognized three species (*buccoides, crassirostris* and *melanotis*; species epithets used for brevity when possible) to ten (*buccoides, stonii, geislerorum, crassirostris, maculosus, melanocephalus, astigmaticus, arfakianus, jobiensis* and *melanotis*). We used cryo-frozen tissue samples for most taxa, but for twelve individuals DNA was extracted from toe pad samples of museum study skins (Table S1 available on Dryad). We base our information on mating system, sexual plumage dimorphism, and building of courts and bowers on Gilliard (1969), Diamond (1986a), Kusmierski et al. (1997), Frith and Frith (2004), and Frith et al. (2019).

Extraction, Library Preparation and Sample Information

DNA from the frozen tissue samples was extracted using the KingFisher duo extraction robot and the KingFisher™ Cell and Tissue DNA Kit according to the manufacturer's instructions, while museum toe pad samples were extracted using the Qiagen QIAamp DNA Mini Kit following the protocol described in Irestedt et al. (2006). The sequencing libraries for Illumina sequencing from fresh tissue samples were prepared by National Genomics Infrastructure (NGI) using the Illumina TruSeq PCR- free (180/350bp) kit. The libraries from museum specimens were prepared using the protocol published by Meyer and Kircher (2010). In brief, the latter library preparation protocol for degraded DNA consisted of blunt-end repair, adapter ligation and adapter fill-in, followed by four independent index PCRs to reduce PCR bias. On each Illumina HiSeq X lane we pooled six species from fresh DNA-samples or two species from degraded museum samples. The samples were sequenced to a mean coverage of 19X (Table S1 available on Dryad).

DNA extracted from a frozen tissue sample of an unsexed individual of *Amblyornis subalaris* (Museum of Victoria Z43620, voucher held as ANWC B26561) collected on 23 May 1985 ca. 30 km east of Port Moresby, Owen Stanley Range, Efogi, Central Province, Papua New Guinea (9°10’S, 147°39’E) was used for de-novo sequencing. Four DNA libraries, one short-insert-sized, paired-end (180 bp) and three mate-pair (3 and 5-8 kb) DNA libraries, were sequenced on an Illumina HiSeq X platform at the National Genomics Institute. Low quality and duplicated reads were filtered out before assembly. The final genome was assembled by Science for Life Laboratory (National Genomics Institute, Stockholm) using their best-practice analysis for de novo assembly and assembly evaluation. Three different assemblers were used and their performances were evaluated by aligning a subset of Illumina reads back to the assembled sequence. The lowest number of scaffolds (2,429) and the highest scaffold N50 value (6.06 Mb) were obtained by the ALLPATHS_LG assembler and this assembly was used for the downstream analyses.

Filtering of Raw Reads and Reference Mapping

The Illumina sequencing reads were processed using a custom-designed workflow available at https://github.com/mozesblom to remove adapter contamination, low-quality bases and low-complexity reads. Overlapping read pairs were merged using PEAR (Zhang et

al. 2014) and SuperDeduper (Petersen et al. 2015) was used to remove PCR duplicates. Trimming and adapter removal was done with TRIMMOMATIC v.0.32 (Bolger et al. 2014); default settings) and overall quality and length distribution of sequence reads was inspected with FASTQC v.0.11.5 (Andrews 2010) before and after the cleaning. DNA degradation patterns in historical specimens could lead to a consistent signal of erroneous substitutions. This is normally not a problem for frozen tissue samples but may be so for the toepad samples. As erroneous DNA degradation patterns almost exclusively appears at the ends of sequence reads we shortened all reads obtained from museum study skins by deleting 5bp from both ends in order to avoid this "noise". We used BWA mem v.0.7.12 (Li and Durbin 2009) to map the polished reads against the whole genome of *Amblyornis subalaris*.

Extracting and Aligning Homologous Exonic and Intronic Loci

To obtain a large number of sequence homologs of nuclear exonic and intronic loci across the whole genome, we performed searches using profile hidden Markov models (HMM, Eddy 2011). Profile HMMs use information from variation in multiple sequence alignments, to seek similarities in databases, or as here, genome assemblies (Eddy 1998). The HMM profiles were based on the alignments of exonic and intronic loci generated by Jarvis et al. (2014) for 52 avian species (8,253 exonic and 11,013 intronic loci). The alignments were initially pruned to only include the four passerine species present in the original data set (*Acanthisitta chloris*, *Corvus brachyrhynchos*, *Geospiza fortis* and *Manacus vitellinus*). They were also pruned from gaps that resulted from the deletion of the non-passerine taxa. For each HMM query and taxon, the location on the genome for the most significant hit was identified, and the sequence parsed out using the genomic coordinates. These steps where carried out using a custom designed BirdScanner pipeline (available at github.com/Naturhistoriska/birdscanner). The extracted sequences were then aligned with the other taxa in separate files for exonic and intronic loci. Poorly aligned sequences were identified, based on a calculated distance matrix using OD-Seq (github.com/PeterJehl/OD-Seq), and excluded from the further analyses. We also checked the alignments manually and removed those that included non-homologous sequences for some taxa (indicated by an extreme proportion of variable positions in the alignment) and those that contained no phylogenetic information (no parsimony-informative sites). The number of misaligned loci was generally low, 2.5% for the exons and 0.1% for the introns. A total of 5,653 exonic and 7,020 intronic loci were kept for the phylogenetic analyses. The intra-familial variation in these data sets varies between 1.7 and 2.9% (Supplementary Table S2 available on Dryad).

Mitochondrial Sequences

We assembled mitochondrial genomes from the resequenced data for each individual using MITObim 1.8 (Hahn et al. 2013), and used 11 of the 13 protein-coding genes (NCBI GenBank accession numbers MT249421-MT249794) to infer the phylogenetic tree. In most taxa the NADH3 and NADH6 genes were only partially reconstructed by MITObim and we excluded these from the analyses. The aligned mitochondrial data set used in the analyses consists of 10,560 bp (3,520 codons).

Phylogenetic Analyses

Individual trees were constructed for the 5,653 exonic and 7,020 intronic loci using IQ-TREE (Nguyen et al. 2015) that automatically selects the best substitution model for each loci alignment. We used ASTRAL-III v.5.6.3 (Zhang et al. 2018; Rabiee et al. 2019) to

construct species trees from the gene trees both for the exonic and intronic loci separately and for all loci combined. ASTRAL estimates a species tree given a set of unrooted gene trees and branch support is calculated using local posterior probabilities, LPP (Sayyari and Mirarab 2016).

The phylogenetic analysis of the mitogenomic data set was performed with MEGA X (Kumar et al. 2018). We estimated the maximum-likelihood tree for the mitochondrial data using 100 bootstrap replicates to assess the reliability of the branches. The data set was analyzed both with all codon positions present and with the third codon positions excluded.

Ancestral character reconstruction

We estimated ancestral character states across the phylogenetic tree for discretely valued traits using the "ace" function in the "APE" package (Paradis et al. 2004). The maximum-likelihood method (Pagel 1994) was used to estimate parameters for an explicit model of discrete character evolution and probabilities for the character states at every node of the phylogeny. Finally, the reconstructed states were plotted as a maximum clade credibility tree using the "phytools" package (Revell 2012).

Estimating Time of Divergence

Divergence time estimates were obtained by implementing a Bayesian relaxed clock model in BEAST 2 (Bouckaert et al. 2014). To make the BEAST 2 analysis feasible we used a custom-made python script to randomly sample 5% (24,390 bp) from the concatenation of all intron loci. We ran Markov chain Monte Carlo chains for 80 million generations (sampling every 100 generations) using a relaxed lognormal distribution for the molecular clock model and assuming a birth-death speciation process for the tree prior. The gamma substitution model was applied. The tree was calibrated with two calibration points obtained from Oliveros et al. (2019: figure 1): the split between Climacteridae and Ptilonorhynchidae was set to 31.6±5.5 Ma and the split between the clade including *Ptilonorhynchus* and the clade with *Ailuroedus* to 15.0±7.1 Ma. We checked for convergence between runs and analysis performance using Tracer v.1.5 and accepted the results if the values of the estimated sample size (ESS) were larger than 200, suggesting little autocorrelation between samples. The resulting trees were combined in TreeAnnotator v.1.7.5 and the consensus tree with the divergence dates was visualized in FigTree v.1.4.3.

2. FURTHER DETAILS ABOUT SYSTEMATIC RELATIONSHIPS OBSERVED

Phylogenetic analyses of the different data sets recovered almost the same pattern of relationships (Fig. 1, Supplementary Figs. S1-S3 available on Dryad). They suggest that all genera, except *Amblyornis*, are monophyletic. Monotypic *Archboldia* was nested within *Amblyornis*. Three distinct clades were recovered. Clade A comprises *Ptilonorhynchus*, *Chlamydera* and *Sericulus*, Clade B comprises *Scenopoeetes*, *Prionodura*, *Amblyornis* and *Archboldia*, while all *Ailuroedus* forms Clade C.

Within Clade A, *Ptilonorhynchus* and *Chlamydera* are sisters with 100% local posterior probability (LPP) in the analyses of both the intronic loci and the mitogenomes. The same topology is recovered also for the exonic loci but with a LPP (94%). Although *Chlamydera* is recovered as monophyletic by all analyses, the relationships among its species differ. *C. maculata* and *C. guttata* are consistently recovered as sister species. Both the exonic and intronic data place *C. nuchalis* as their sister, while the mitogenomic data place it with *C. cerviniventris*. The three individuals of *C. nuchalis* are recovered as monophyletic by both the intronic and mitogenomic data, but not by the exonic data, which instead places *C. nuchalis nuchalis* as sister to a clade consisting also of *C. nuchalis orientalis*, *C. maculata* and *C. guttata*. This is also the topology in the analysis of the combined nuclear data set. *Sericulus* forms the sister group to the *Ptilonorhynchus*-*Chlamydera* clade in all analyses. It consists of four species of which *S. chrysocephalus* is the sister to the other three. The mitogenomic and exonic data give high support for a sister group relationship between *S. aureus* and *S. ardens*, while the intronic data instead place *S. aureus* with *S. bakeri*. The analysis of the combined nuclear data set strongly support a sister group relationship between *S. aureus* and *S. ardens*.

In clade B, all analyses recovered monotypic *Scenopoeetes* as sister to the other species in the clade, and *Prionodura* as sister to *Amblyornis* and *Archboldia*. *Archboldia* is nested within *Amblyornis* in all analyses, but its relative position differs between data sets. In the analysis of the mitogenomic data set, it is sister to *Amblyornis inornata*, while the exonic and intronic data sets suggest it is sister to *Amblyornis macgregoriae*. Both the exonic and intronic data recover a sister pair of *Amblyornis flavifrons* and *Amblyornis inornata*. In the analyses of the mitogenomes and the intronic loci *Amblyornis subalaris* is sister to all other *Amblyornis* species and *Archboldia*. The exonic data instead shows 100% LPP for *Amblyornis subalaris* being sister to the *Amblyornis macgregoriae–Archboldia* clade. When combining all nuclear data *Amblyornis subalaris* is recovered as sister to *Archboldia* and the other *Amblyornis* species.

Within clade C all analyses recovered *Ailuroedus buccoides*, *A. geislerorum* and *A. stonii* as sister to the other seven taxa. Among the latter, *A. crassirostris* and *A. maculosus* fall outside the rest, but the relationship between these two is unclear. The exonic data places *A. maculosus* as sister to *A. crassirostris* and the other taxa, the intronic data recovers *A. maculosus* and *A. crassirostris* as sisters, and the mitogenomic data places *A. crassirostris* as sister to *A. maculosus* and the other. Each of these arrangements receives highest support in its respective data set. The combined nuclear data set strongly supports a sister group relationship between *A. crassirostris* and *A. maculosus*.

The phylogenetic analyses show that *Scenopoeetes* and *Prionodura* are successively more distantly related to *Amblyornis* and *Archboldia*. However, in the only previously published phylogeny of this clade, *Prionodura* was nested within *Amblyornis* species (Kusmierski et al. 1997). Our analyses indicate that this unexpected position of *Prionodura*, as noted by Schodde and Mason (1999) and Beehler and Pratt (2016), most likely is a

consequence of the small size of the mitochondrial data analyzed. We rule out a sample mix-up as explanation of this finding as the sequence of *Prionodura newtoniana* published by Kusmierski et al. (1997) is almost identical (differing in two positions only) to the corresponding segment of cytochrome *b* obtained from the two individuals included in the present study. With considerably more mitochondrial data we can confidently show that *Prionodura* is sister to the *Amblyornis-Archboldia* clade. This topology is also obtained in the analyses of both the exonic and intronic data. The genetic and morphological distinctiveness of *Prionodura newtoniana* relative to the *Amblyornis-Archboldia* clade supports the retention of *newtoniana* in the monotypic genus *Prionodura*, contra Storr (1984) and Christidis and Boles (2008) who merged it with *Amblyornis*.

Another key result was our affirmation of Kusmierski et al.'s (1993, 1997) finding that *Archboldia* is nested within *Amblyornis*. *Archboldia* differs from *Amblyornis* species by having sooty grey to jet-black plumage unlike the more brownish-olive plumage of the *Amblyornis* species, which nonetheless may have a simple genetic basis, a forked not square tail in adult males, and by being considerably larger and differently proportioned. In addition, *Archboldia* clears and decorates a large mat for display whereas *Amblyornis* are maypole-builders. This structure differs from the typical maypole bowers, albeit a variant of maypole structure (Frith and Frith 2004). The phylogenetic results show that the character combination that sets *Archboldia* apart from *Amblyornis* species are either losses (building bower of a typical maypole-style) or gains (different body size and proportions; melanistic plumage). Some of the morphological changes as large size and melanistic plumage (cf. Sandoval and Barrantes 2019) may be adaptations to living at elevations up to 3,660 meters above sea level, no other bowerbird living at higher elevations than *Archboldia*. Conversely, there are character that link the two genera. Colored crest are shared by of some species of *Amblyornis* and *Archboldia*, shares distal black tipping to the feathers and female *Archboldia* displays a few wing-coverts feathers concolorous with the brown of *Amblyornis*. Furthermore, females and immature birds of Archboldia differ from adult males by having shorter, squarer tails as in *Amblyornis*. The yellow crest of *Archboldia* and *Amblyornis flavifrons* may also be homologous. We suggest that the phenotypic and behavioral differences between *Archboldia* and *Amblyornis*, while superficially seeming so great as to generate the understandable skepticism expressed by Beehler and Pratt (2016), may in fact not indicate genetic differences so great as to prevent *Archboldia* being subsumed within *Amblyornis*.

Although the inferred phylogenetic relationships suggest that bowerbirds group according to major characteristics in their mating system and bower construction, the results also indicate that several sexually selected traits (e.g., details of the bower design and decoration, head crest and other plumage characters) are less reliable for phylogenetic inference at the family-level. This is in agreement with previous molecular studies (Kusmierski et al. 1997; Zwiers et al. 2008), which have stressed how evolutionary labile these traits seem to be. It has been suggested that major components of the courtship behavior, including bower design, decoration type and the accompanying female preferences, are culturally transmitted traits (Diamond 1986a). It takes several years of practice of bower construction and decoration (at least four years in *Ptilonorhynchus violaceus* [Frith and Frith 2004]) until males build bowers suitable for attracting females. Young males spend considerable time watching the bowers of older males. Likewise, young females visit bowers together with older females and may learn from them which males to choose (Diamond 1986a). Another observation indicating the lability of reproductive traits is that one population of *Amblyornis inornata* (Fakfak and Kumawa Mts) builds and decorates its bowers

in a style that is very different from those of the nearby populations in Vogelkop and Wandammen Mts (Diamond 1986b, 1987; Diamond and Bishop 2015). It has been questioned whether these populations in fact may represent different species (Gibbs 1994; Frith and Frith 2004). These populations differ little in their mitochondrial DNA (an average difference of only 0.5% [Uy and Borgia 2000]), which suggests that they share a recent common ancestor. However, as pointed out by Rheindt (2012), this could also be the result of gene flow and a more detailed study of the nuclear genome would be desirable. Unfortunately, no sample from the Fakfak or Kumawa Mts was available for inclusion here.

3. DATA REPOSITORIES

The datasets supporting the conclusions of this article are available in the Dryad repository, doi:10.5061/dryad.6hdr7sqwp. Raw Illumina sequences and the *Amblyornis subalaris* genome assembly are deposited in Sequence Reads Archive, National Center for Biotechnology Information, SRA accession PRJNA601961 (https://www.ncbi.nlm.nih.gov/sra/PRJNA601961). Mitochondrial sequences have GenBank accession nos. MT249421-MT249794.

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4. SUPPLEMENTARY FIGURES S1-S5

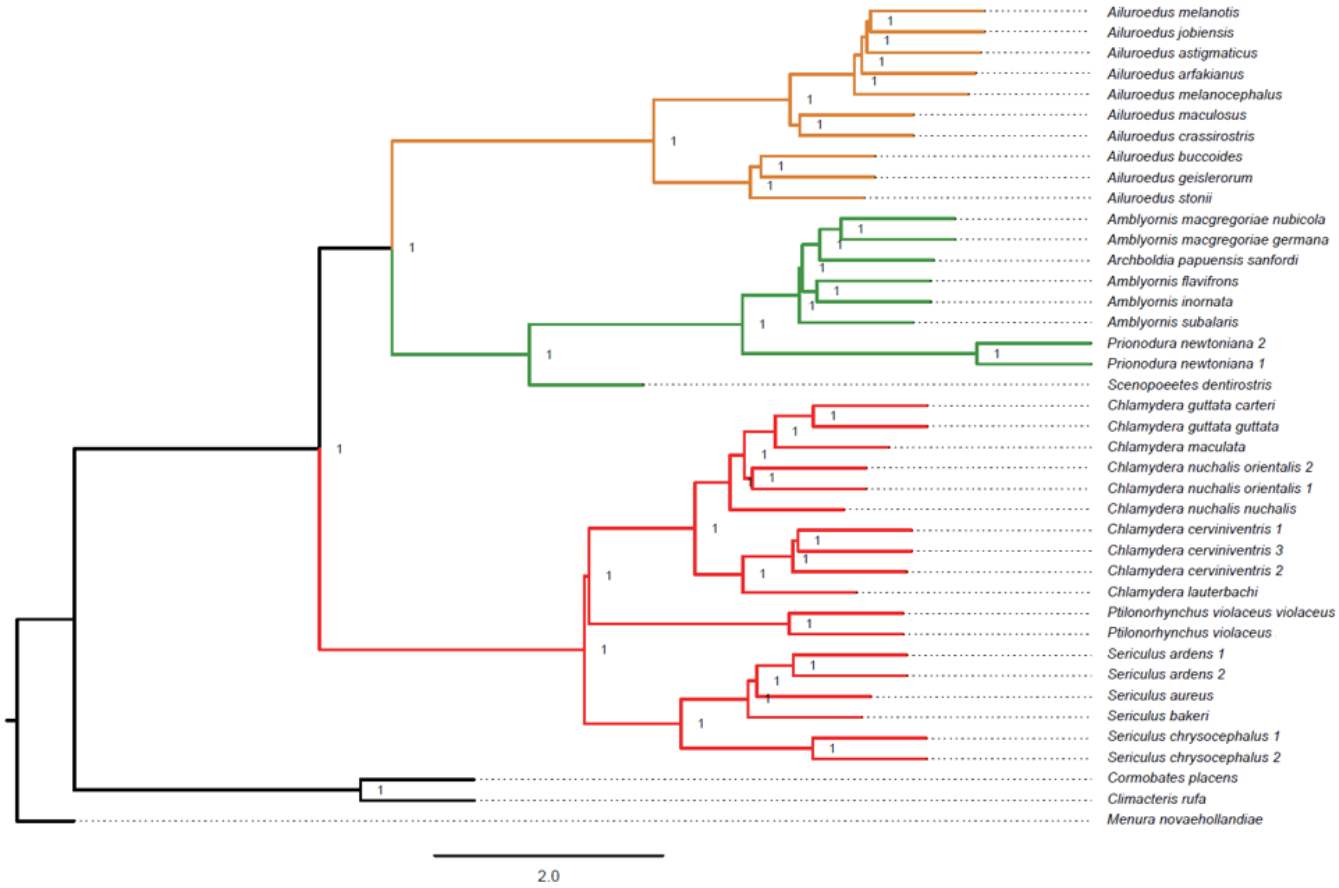

Figure S1: ASTRAL tree based on 12,673 individual trees (5,653 exonic and 7,020 intronic regions).

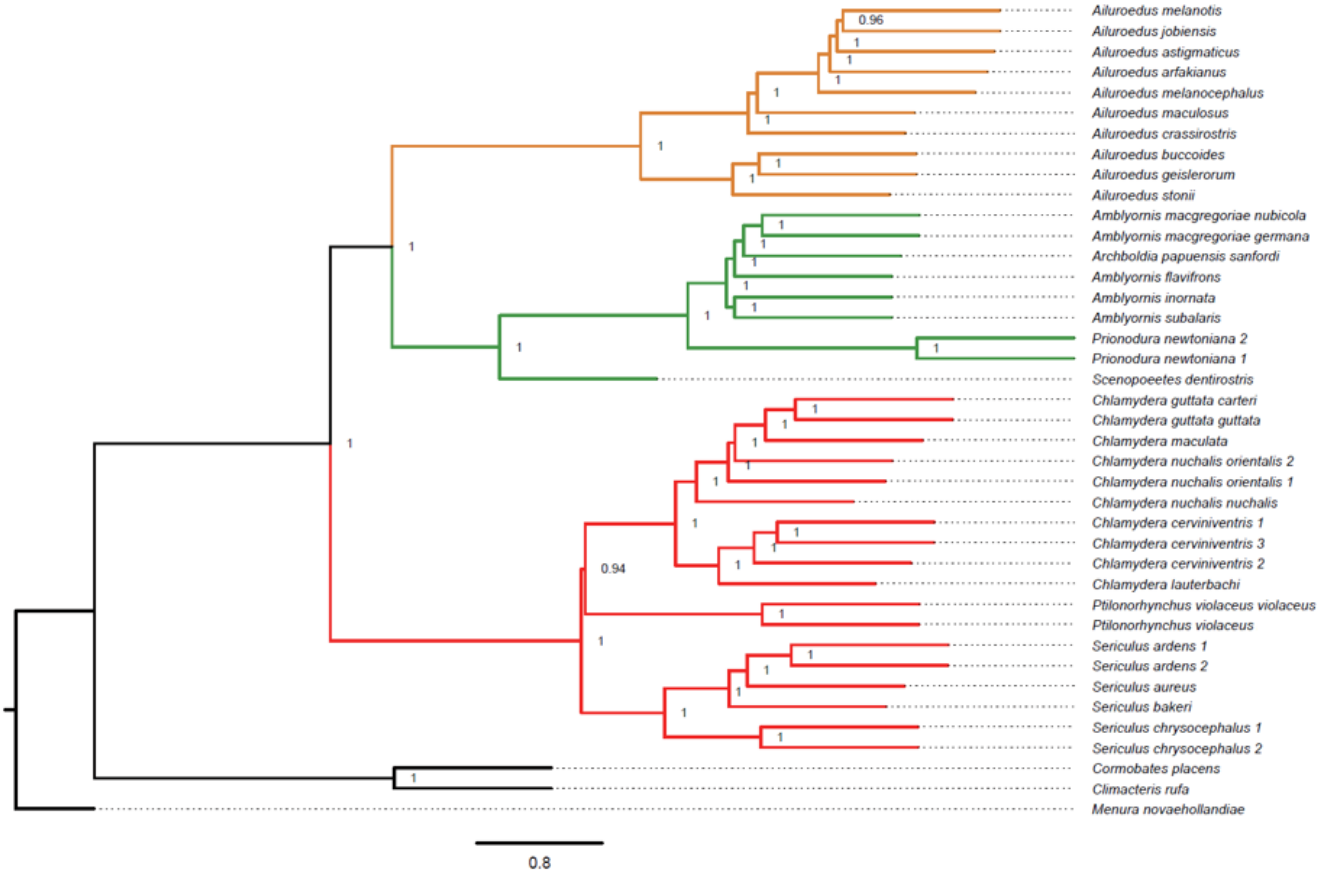

Figure S2: ASTRAL tree based on individual trees calculated for 5,653 exonic regions. Average alignment length is 591 bp and average proportion parsimony-informative positions in the alignment is 4.8%.

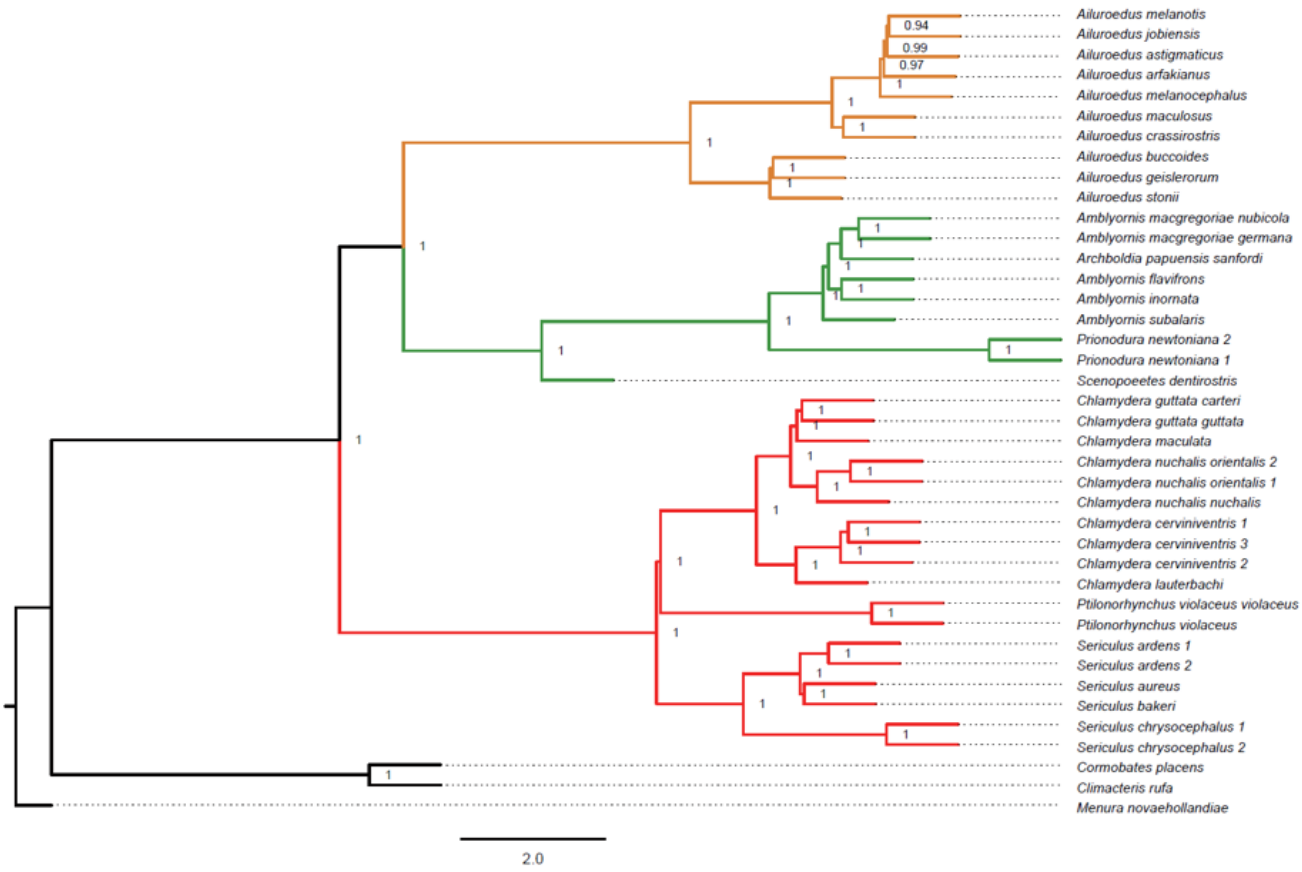

Figure S3: ASTRAL tree based on individual trees calculated for 7,020 exonic regions. Average alignment length is 1087 bp and average proportion parsimony-informative positions in the alignment is 10.0%.

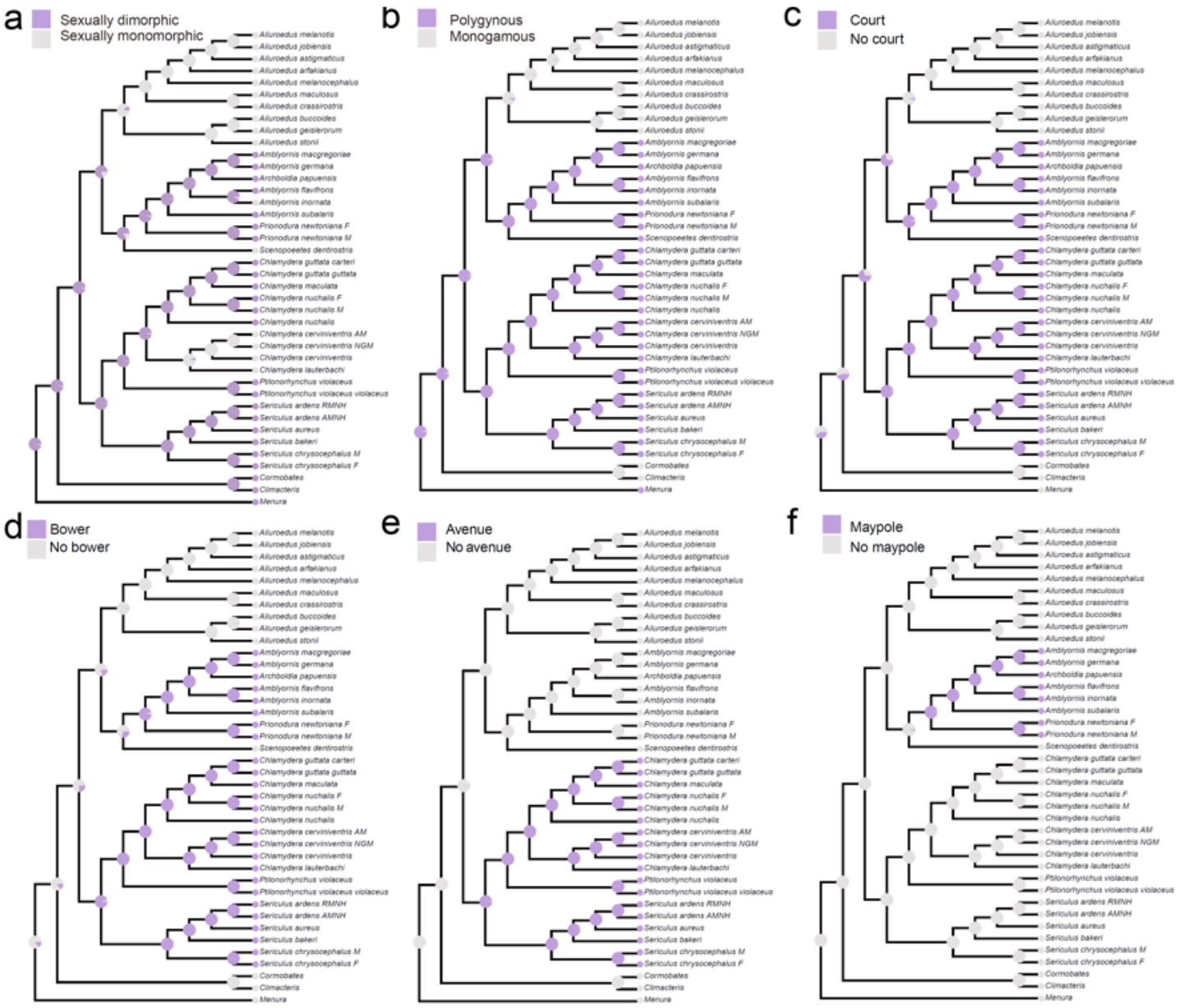

Figure S4: Reconstruction of ancestral character states.

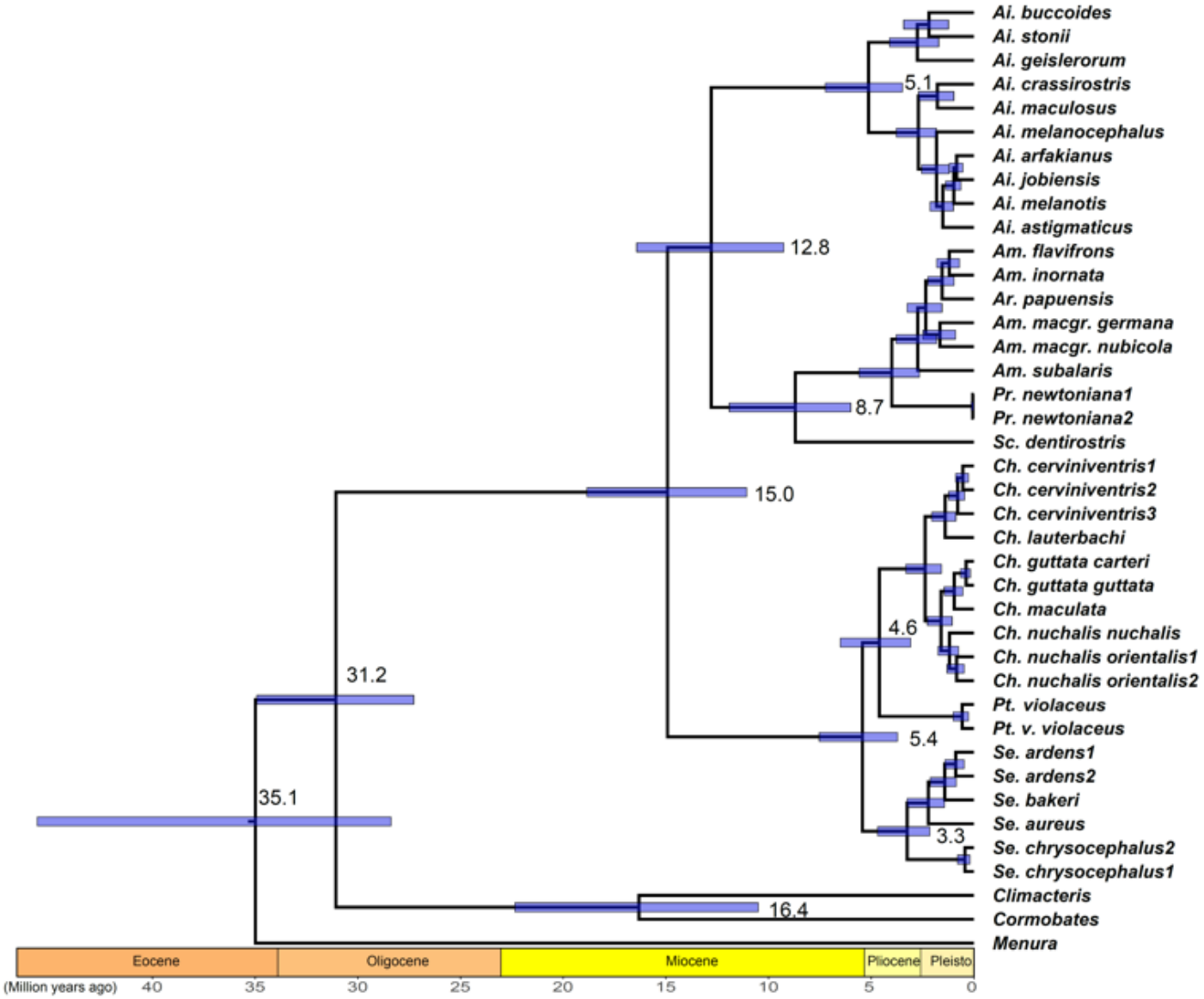

Figure S5: Time-tree for the bowerbird radiation.

5. SUPPLEMENTARY TABLES S1-S2

Table S1. Samples sequenced in the study. Abbreviations: AM, Australian Museum, Sydney; AMNH, American Museum of Natural History, New York; ANWC, Australian National Wildlife Collection, Canberra; BMNH, Natural History Museum, London; MV, Museum Victoria, Melbourne; NHMD, Natural History Museum of Denmark; NRM, Swedish Museum of Natural History, Stockholm; RMNH, National Museum of Natural History, Leiden.

Taxon	Sample ID	Locality	Year	Sex	Material	Coverage
Ailuroedus buccoides	NRM 566714	Indonesia, West Papua Prov., Sorong Regency, Sorong District	1949	female	toe pad	20
Ailuroedus geislerorum	MV Z43749	Papua New Guinea, Oro Prov., Kokoda environs (8 53 00 S, 147 44 00 E)	1987	male	fresh	21.7
Ailuroedus stonii	MV Z43608	Papua New Guinea, Central Prov., Kerea, 50 km N of Port Moresby on Vanapa River (9 04 30 S, 147 10 30 E)	1985	male	fresh	22.7
Ailuroedus crassirostris	MV Z38638	Australia, New South Wales, Kangaroo Valley (23 42 S, 133 52 E)	1984	female	fresh	22.1
Ailuroedus arfakianus	AMNH 294642	Papua New Guinea, Mts. nr. Siwi	1928	male	toe pad	7.5
Ailuroedus astigmaticus	AMNH 268274	New Guinea, Sevia or Zakaheme	1929	female	toe pad	12.6
Ailuroedus melanotis	MV Z38684	Australia, Queensland, McIlwraith Range (13 45 S, 143 20 E)	1985	female	fresh	19.2
Ailuroedus jobiensis	AMNH 830415	New Guinea, Torricelli Mtns, Mt. Nibo	1966	female	toe pad	15.3
Ailuroedus maculosus	MV Z38675	Australia, Queensland, Mt Lewis (16 35 S, 145 17 E)	1985	male	fresh	19.9
Ailuroedus melanocephalus	MV Z43724	Papua New Guinea, Oro Prov., Teyebedi Environs, Upper Kumusi River (9 10 S, 148 05 E)	1987	male	fresh	23.3
Amblyornis flavifrons	AMNH 679121	Indonesia, New Guinea	no date	unknown	toe pad	11.3
Amblyornis inornata	NRM 566731	Indonesia, West Papua Prov., Pegunungan Arfak Regency, Anggi Gida District, Tombrok (1°21′ S 133°57′ E)	1949	male	toe pad	16.3
Amblyornis macgregoriae germana	NHMD 217716	Papua New Guinea, Morobe Prov., Wasaunon (-6.09, 146.92)	2016	unknown	fresh	14.9
Amblyornis macgregoriae nubicola	MV Z43644	Papua New Guinea, Oro Prov., Giliageda Environs, Gulugawa Ridge S above Awoma, Mountain Camp (8 04 S, 146 08 E)	1987	male	fresh	17.4
Amblyornis subalaris	MV Z43618	Papua New Guinea, Central Prov., Efogi, c.30 km E of Port Moresby, Owen Stanley Range (9 10 00 S, 147 39 00 E)	1985	female	fresh	16.6
Archboldia papuensis sanfordi	BMNH 195317217	Papua New Guinea, Mount Giluwe	1953	male	toe pad	20
Chlamydera cerviniventris	ANWC B55923	Papua New Guinea, 3 km N of Agevairu, 90 km NW of Port Moresby	2013	male	fresh	19.5
Chlamydera cerviniventris	ANWC B56356	Papua New Guinea, Bensbach River, 3.2 km S of Bensbach Airport	2014	female	fresh	23.1
Chlamydera cerviniventris	MV Z38686	Australia, Queensland, Massey Creek (17 37 S, 145 34 E)	1990	male	fresh	24
Chlamydera guttata carteri	MV Z1583	Australia, Western Australia, Mandu Mandu Gorge, Cape Range NP (22 09 S, 113 54 E)	1996	male	fresh	19.4
Chlamydera guttata guttata	ANWC B32839	Australia, 6 km N of Kulgera Roadhouse	2002	male	fresh	20.6
Chlamydera lauterbachi	NRM 566721	Papua New Guinea, Jiwaka Prov., Wahgi Valley, Nondugl (05° 52' S, 144° 46' E)	1951	female	toe pad	12.1
Chlamydera maculata	MV Z41572	Australia, Queensland, 13 km e. of Windorah (25 25 S, 142 39 E)	1988	female	fresh	23.7
Chlamydera nuchalis nuchalis	MV Z24331	Australia, Northern Territory, South Alligator River (13 09 S, 132 16 E)	1987	female	fresh	22.7
Chlamydera nuchalis orientalis	MV Z126	Australia, Queensland, 100km s. of Charters Towers (20 05 S, 146 15 E)	1994	male	fresh	18
Chlamydera nuchalis orientalis	MV Z38670	Australia, Queensland, Silver Plains (13 59 S, 143 33 E)	1990	female	fresh	24.2
Prionodura newtoniana	ANWC B32313	Australia, Mt Baldy, Herberton Range, c. 8 km WSW of Atherton	2000	male	fresh	21.3
Prionodura newtoniana	MV Z41566	Australia, Queensland, Atherton (17 16 S, 145 29 E)	1988	female	fresh	21.4
Ptilonorhynchus violaceus	ANWC B41557	Australia, Summit of Mt Baldy, Atherton, Atherton Tableland	1988	male	fresh	22.3
Ptilonorhynchus violaceus violaceus	MV Z38674	Australia, Queensland	1985	female	fresh	20.8
Scenopoeetes dentirostris	MV Z41564	Australia, Queensland, Atherton (17 16 S, 145 29 E)	1988	male	fresh	21
Sericulus ardens	AMNH 427632	Papua New Guinea, 2 m. below juct. of Black & Palmer R's	1936	male	toe pad	21.1
Sericulus ardens	RMNH 143263	Indonesia, Papua Prov., Noord River (=Lorentz River), Sabang	1907	male	toe pad	7.9
Sericulus aureus	NRM 566726	Indonesia,West Papua Prov., Pegunungan Arfak Regency, Membey District, Bivak October (1°26′ S 134°0′ E)	1949	male	toe pad	7.7
Sericulus bakeri	AMNH 791269	Indonesia, New Guinea, Memenga forest, Adelbert Mts.	1959	male	toe pad	18.5
Sericulus chrysocephalus	MV Z38672	Australia, Queensland, Conondale Range (26 45 S, 152 37 E)	1985	male	fresh	21.4
Sericulus chrysocephalus	MV Z38687	Australia, Queensland, Eungella, Dalrymple Plateau (21 02 S, 148 38 E)	1985	female	fresh	20.9
Climacteris rufa	MV Z1696	Australia, South Australia, Sinclair Gap (-34.5, 135.12)	1989	male	fresh	16.9
Cormobates placens	MV Z44207	Papua New Guinea, Oro Prov., Daleatana Environ, Gulugawa Ridge S above Awoma (-9.07, 148.13)	1987	unknown	fresh	16.2
Menura novaehollandiae	AM LAB1112	Australia	1999	female	fresh	18.3

Table S2. Summary statistics for pairwise sequence distances (p-values) within clades of bowerbird taxa.

	concatenation of 5,653 exons				concatenation of 7,020 introns				mitochondrial coding genes			
	number of comparisons	mean	min	max	number of comparisons	mean	min	max	number of comparisons	mean	min	max
Within family Ptilonorhynchidae (bowerbirds)	666	1.70%	0.1%	2.5%	666	2.93%	0.0%	4.2%	561	14.63%	0.0%	19.0%
Within genus *Aiuroedus*	45	0.62%	0.2%	1.0%	45	0.92%	0.3%	1.6%	35	10.41%	5.1%	13.7%
Within genus *Amblyornis* (including *Archboldia*)	15	0.44%	0.4%	0.5%	15	0.59%	0.4%	0.7%	10	7.15%	4.7%	8.9%
Within genus *Chlamydera*	45	0.40%	0.2%	0.6%	45	0.48%	0.1%	0.7%	36	3.47%	10.0%	5.0%
Within genus *Sericulus*	15	0.50%	0.3%	0.7%	15	0.63%	0.1%	0.9%	15	7.83%	0.2%	10.3%
Within *Prionodura newtonia*	1	0.10%			1	0.03%			1	0.09%		
Within *Ptilonorhynchus violacea*	1	0.24%			1	0.17%			1	0.15%		
Within *Chlamydera guttata*	1	0.20%			1	0.11%			1	0.18%		
Within *Chlamydera nuchalis*	3	0.30%	0.3%	0.3%	3	0.32%	0.3%	0.3%	3	1.31%	0.1%	1.9%
Within *Chlamydera cerviniventris*	3	0.22%	0.2%	0.3%	3	0.17%	0.2%	0.2%	3	0.51%	0.0%	0.8%