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Comparative phylogeography and niche modeling for three species complexes of SE China (*Paradoxornis* spp., *Pycnonotus* spp., *Spizixos* spp.)

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Abstract Contrasting multiple organisms with similar contemporary distributions, researchers can identify shared evolutionary patterns and provide historical context for community composition. We used three species complexes with overlapping distributions in Southeastern China and surrounding islands to explore the phylogeographic history of the region. Despite similar geographic distributions, genetic data revealed few congruent patterns, but all complexes displayed genetic divergence for Taiwanese populations. Additionally, niche modeling and divergence dating did not find support for diversification associated with the Last Glacial Maximum [*Current Zoology* 61 (5): 943–950 , 2015].

Keywords Phylogeography, Niche modeling, *Paradoxornis*, *Pycnonotus*, *Spizixos*

Comparative phylogeography provides a framework to investigate external factors shaping population structure of co-distributed taxa (Arbogast and Kenagy, 2001). By contrasting multiple organisms with similar contemporary geographic ranges, comparative phylogeography can identify evolutionarily independent geographic regions, provide a historical context for species of a given community, understand responses to habitat alterations, and identify evolutionarily isolated areas of potential importance to conservation (Bermingham and Moritz, 1998). During the Pleistocene, glacial maxima reduced or expanded suitable habitat for mainland populations and potentially produced isolated refugia promoting species diversification. However, glacial maxima also exposed land bridges to continental islands, potentially promoting their colonization. As glaciers retreated and sea levels rose, island populations had the potential to differentiate in isolation. Distributional changes due to the Last Glacial Maximum (LGM) and Last Inter-Glacial (LIG) vary spatially, but were generally less extreme in mainland Southeast (SE) Asia compared to North America or Europe (Edwards et al. 2000). Therefore, determining the effects of LGM and LIG in mainland SE Asia is particularly difficult because taxa in allopatric refugia remained isolated for shorter periods of time.

Previous phylogeographic work has explored patterns of diversification and expansion across many floral and faunal populations in south China (Gong et al., 2008; Qian and Ricklefs, 2000; Shih et al., 2006). Many of these studies have uncovered a pattern of east/west intraspecific divergence (Huang et al., 2007; Huang et al., 2010; Lei et al., 2015; Song et al., 2009), but some taxa followed a latitudinal pattern of diversification (Zhang et al., 2008). In other parts of the world, Pleistocene refugia have been acknowledged as drivers of intraspecific diversification among multiple avian lineages (Hosner et al., 2014; Manthey et al., 2011). Recent studies have documented the impact of glacial cycles on the diversification of Chinese taxa (Li et al., 2009; Qu et al., 2015), yet the full impact of climate change on this region is still not very well understood. Here, we explored responses to the LGM and LIG for birds of mainland SE Asia.

In this study, we examined the phylogeographic history of three co-distributed species complexes: *Paradoxornis webbianus/alphonsianus*, *Pycnonotus sinensis/taivanus* and *Spizixos semitorques*. The study taxa are broadly distributed in Southeastern China with all taxa found on surrounding islands; for example, all three taxa have Taiwanese populations. Previous work has indicated both *Paradoxornis* spp. and *Pycnonotus* spp. complexes contain phylogeographic structure (Crottini et al.,

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2010; McKay et al., 2013; Qu et al., 2012). However, *S. semitorques* was characterized by Gao et al. (2011) to have extensive gene flow and lacking a phylogeographic pattern. By using available genetic data and ecological niche modeling techniques to establish a comparative framework, we were able to explore the effects that LGM and LIG mediated landscape fluctuations had on the population genetic structure of three SE Asian bird species complexes. Being able to understand how climate change shaped the current distribution and genetic diversity of these taxa will inform our understanding of the evolutionary history for these SE Asian biota. In turn, we can begin to uncover unified evolutionary processes that have shaped the extant biodiversity of SE Asia. Therefore, the goals of this project were: 1. Establish phylogeographic patterns using a consistent methodology and 2. Explore the effects of Pleistocene environmental fluctuations on population diversification.

1 Materials and Methods

Molecular datasets for *Paradoxornis webbianus/alphonsianus*, *Pycnonotus sinensis/taivanus* and *S. semitorques* were compiled from sequences available on Genbank (Table S1; Crottini et al., 2010; Gao et al., 2011; McKay et al., 2013; Qu et al., 2012; Yeung et al., 2011). Two mitochondrial regions, Cytochrome *b* (Cyt*b*) and NADH dehydrogenase subunit 2 (ND2) and one nuclear intron were available for *Paradoxornis webbianus/alphonsianus*; ND2, the nuclear intron MUSK, and 11 additional nuclear markers were available for *Pycnonotus sinensis/taivanus*; Cyt b and partial control region/tRNA-GLU were consolidated for *S. semitorques* (Table 1).

1.1 Phylogenetic Analyses

Mitochondrial loci and concatenated datasets were analyzed using both maximum likelihood (RAxML; Stamatakis, 2014) and Bayesian (BEAST v1.8.1; Drummond et al., 2012) approaches. Phylogenies were rooted using close relatives for each species of interest as determined by previously published work (Gao et al., 2011; McKay et al., 2013; Yeung et al., 2011). Models of molecular evolution for non-coding nuclear loci and codon positions for mtDNA loci were determined with jModelTest v 2.1.6 (Darriba et al., 2012; Guindon and Gascuel, 2003) using Akaike Information Criterion. BEAST input files were created in BEAUti v1.8.1 (Drummond et al., 2012) with a Markov chain Monte Carlo (MCMC) of 100,000,000 generations sampling every 10,000. The study taxa lacked fossil calibrations therefore relaxed lognormal molecular clocks were applied to both ND2 and Cytb analyses with substitution rates of 0.0115 (2.3% divergence my^{-1}, Klicka et al., 2011) and 0.01 (2% divergence my^{-1}, Sedano and Burns, 2010; Weir and Schluter, 2008), respectively. We determined convergence of model parameters by performing analyses in duplicate and examining the parameters in Tracer v 1.6 (Rambaut and Drummond, 2013). After examining log files, a 10% burn-in was determined to be sufficient for parameter convergence and then maximum clade credibility trees were generated with TREEANNOTATOR v1.8.1 (Drummond et al., 2012). We used RAxML to construct a ML tree, with nodal support assessed via 1000 bootstrap replicates. For RAxML analyses, we implemented a GTR + G model of sequence evolution with the datasets partitioned by locus and by codon position for coding loci (ND2, Cyt b). The best trees for both BEAST and RAxML analyses were visualized with FIGTREE v1.3.1.

Phylogenetic relationships were further visualized by constructing haplotype networks. All nuclear sequences were phased in DnaSP (Librado and Rozas, 2009) per an output threshold of 0.7 utilizing PHASE algorithms (Stephens and Donnelly, 2003, Stephens et al., 2001). Median-joining networks (Bandelt et al., 1999) were

Table 1 Loci sample size and variation for each study taxa

Taxa	Locus	Variable Sites	Informative Sites	Sample Size
Paradoxornis spp.				
	ND2	124	64	157
	Cyt b	128	62	119
	TGFB2	27	13	51
Pycnonotus spp.				
	ND2	29	14	83
	Musk	12	10	25
	12630	15	8	25
	13403	16	9	25
	14572	17	13	25
	15463	20	14	25
	17898	17	15	25
	22187	11	6	25
	23361	7	4	25
	24972	24	18	25
	25442	16	11	25
	25613	10	6	25
	27331	23	11	25
	27818	18	12	25
Spizixos semitorques				
	Cyt *b*	58	17	121
	tRNA-Glu	43	18	121

created to visualize haplotype sorting using the program PopART (popart.otago.ac.nz).

1.2 Ecological niche modeling

Geo-referenced occurrence data were obtained via the Global Biodiversity Information Facility (GBIF; gbif.org) and VertNet (vertnet.org). Using custom R (RDC Team, 2012) scripts, localities within five km of each other were trimmed from the dataset to avoid sampling identical and neighboring raster cells of the climatic data. Points were visually inspected for accuracy and further trimmed for clustered points in areas of high-concentration observations using ArcMap v10 (ESRI). The final occurrence datasets consisted of 101, 287, and 74 points for *Paradoxornis, Pycnonotus*, and *Spizixos*, respectively. Fifty percent of each dataset was set aside for model evaluation; the remaining points were used for model calibration.

We obtained 19 "bioclimatic" layers from the WorldClim database (Hijmans et al., 2005) (worldclim.org). These layers contain minima, maxima, and ranges of worldwide temperature and precipitation information from the past 50 years. As many of these layers are not independent across geography, we limited our analysis to seven variables to reduce spatial non-independence: annual mean temperature, mean diurnal temperature range, maximum temperature of warmest month, minimum temperature of coldest month, annual precipitation, precipitation of wettest month, and precipitation of driest month. For use in projecting models to past climatic conditions, we obtained bioclimatic layers for the Last Glacial Maximum (LGM; ~21,000 ya) and the Last Inter-glacial (LIG; ~120,000-140,000 ya). These data sources were produced from model output of the Community Climate System Model (CCSM3; Collins et al., 2006) and the Model for Interdisciplinary Research on Climate (MIROC; Nozawa et al., 2005).

The accessible area (i.e., model calibration area) for each species was determined based on interpretation of each species' current range and the factors limiting range expansion (e.g., biogeographic barriers). For example, we used the Himalayas and oceanic regions for these species as barriers to the western lowlands (e.g., in India) and oceanic islands (e.g., the Philippines). The accessible areas for each species are presented in Fig. S1.

For each species, we created ecological niche models using Maxent (Phillips et al., 2006). Maxent utilizes presence-only occurrence data and environmental variables to estimate probability distributions of species occurrence in geography (Phillips et al., 2006). Here, we used the aforementioned environmental variables in conjunction with occurrence records for each species to train models within each species' given accessible area. For each species, we ran 100 bootstrap replicates with the calibration points. Using a partial-ROC analysis (Peterson et al., 2008), we evaluated the median output models with the points initially set aside for model evaluation with an acceptable omission error rate of 10%. Values from the partial-ROC analysis consistently above one indicate model performance exceeding null expectations. Because all AUC ratios were greater than 1.3 for each species—well above null expectations—we reran Maxent with all occurrence data, projecting models for each species to the LIG and LGM. Because of inherent error in biodiversity data that would act to place species in unsuitable environmental conditions (Peterson et al., 2008) we thresholded Maxent output models as inclusion of 90% of occurrences, allowing 10% omission.

2 Results

2.1 Phylogenetic Analyses

Paradoxornis webbianus/alphonsianus

Analysis of mtDNA for *Paradoxornis webbianus/alphonsianus* identified 252 variable characters (128 Cytb and 124 ND2) with 126 (62 Cytb and 64 ND2) parsimony informative sites. Nuclear genetic variation (TGFB2) included 27 variable characters and 13 phylogenetically informative sites. Maximum likelihood and Bayesian analyses of ND2, Cytb and concatenated datasets produced no strongly-supported conflicting relationships. The eastern and western populations, previously identified by Qu et al. (2012), were not particularly accurate delimitations because the clade with individuals from western areas like Sichuan also contained individuals from Taiwan, central China, and coastal China. Similarly, the "eastern" clade individuals originated from northeastern, southeastern, and central China. Therefore, we referred to the "western" group as Clade A and the "eastern" group as Clade B. BEAST estimated Clade A and B to have diverged 0.62–1.28mya (95% HPD) for Cytb and 0.70–1.42 (95% HBD) for ND2. Furthermore, all individuals from Taiwan form a clade that is estimated to have diverged 0.442mya (Cyt b; 95% HPD0.195–0.703mya) or 0.647 mya (ND2; 95% HPD 0.351–0.93 mya) from the mainland forms. Average number of nucleotide substitutions per site between the Taiwan clade and their sister clade (Fig. 1, node X) was estimated with D_{XY} (Wakeley 1996) to be 0.00412 (Cyt b) or .01124 (ND2). Nucleotide substitutions per site increased to 0.01156 (Cytb) or 0.01345 (ND2) when node X was collapsed and the two clades at node Y

were compared (Fig. 1) and finally, nucleotide diversity between Clade A and Clade B yielded 0.01788 (Cyt b) or 0.01594 (ND2) average nucleotide substitutions per site.

Pycnonotus sinensis/taivanus

The *Pycnonotus* dataset contained 235 variable and 151 informative characters from 13 nuclear loci (206

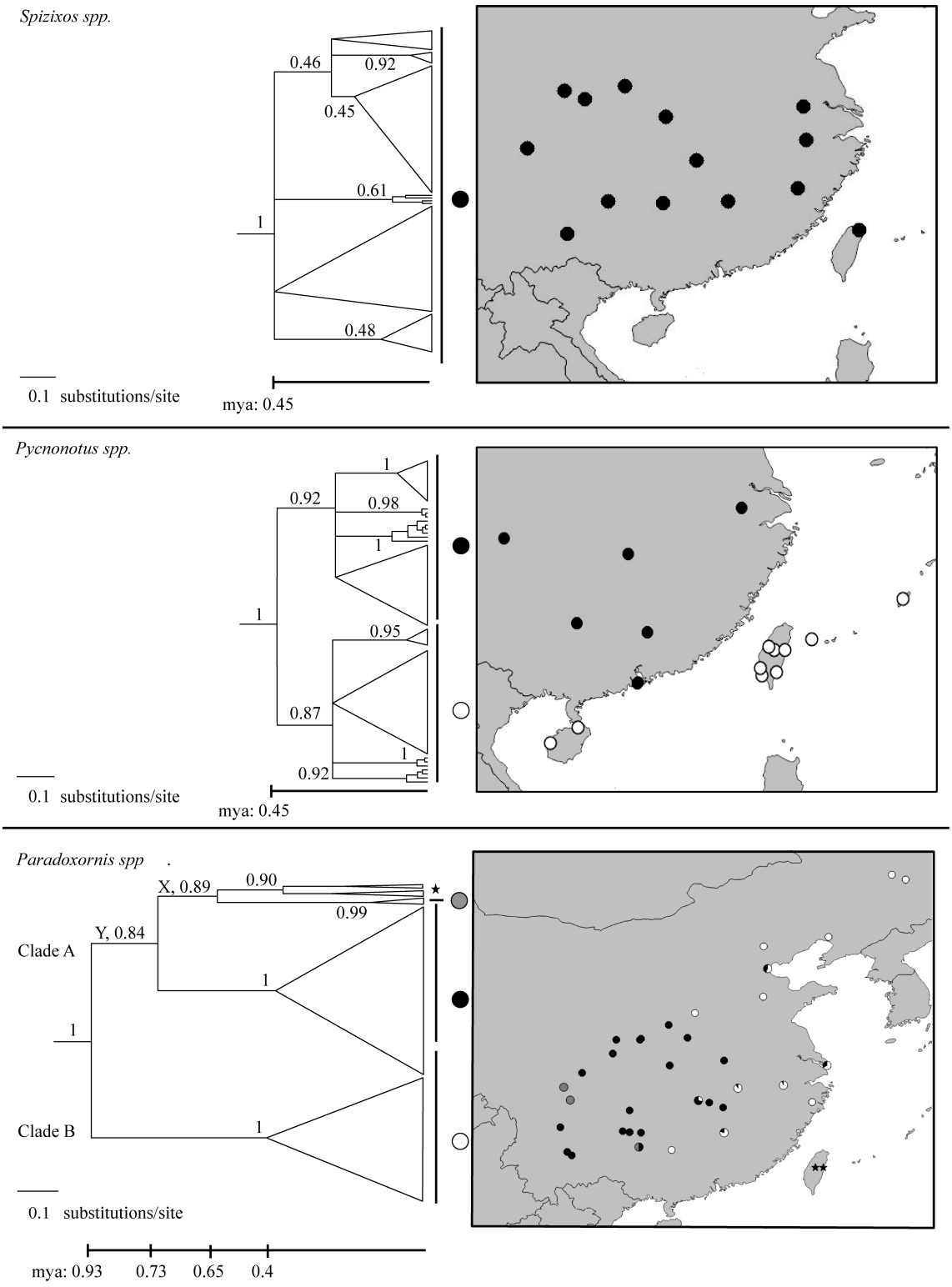

Fig. 1 Mitochondrial DNA maximum clade credibility trees with outgroups removed

Nodes receiving posterior probability below 0.45 were collapsed. Time scale bars are based on molecular clocks of Cyt b for *Spizixos* and *Paradoxornis* and ND2 for *Pycnonotus*.

variable, 137 informative) and one mitochondrial locus (ND2: 29 variable, 14 informative). Bayesian analyses recovered the same clades reported previously, with one clade of mainland taxa, *P. sinensis* and *P. hainanus*, and the other composed of island taxa: *P. taivanus*, *P. formosae*, *P. orii*. Maximum likelihood analyses produced less resolution for relationships, but the marginally supported nodes in the ML analyses did not strongly conflict with higher support observed for nodes in the Bayesian analyses, and average nucleotide substitutions per site between the island and mainland clades was estimated at 0.00662 (D_{XY}) for ND2. A divergence of 0.45 mya (0.25–0.68 mya 95% HBD) was estimated with BEAST using 2.3% divergence my^{-1} for the mainland and island clades. The ND2 haplotype network (Fig. S2) for *Pycnonotus* spp. corroborated the ML and Bayesian results of two clusters, island vs. mainland. The nuclear markers did not recover these groups, likely a result of incomplete lineage sorting.

Spizixos semitorques

Bayesian and ML analyses of *S. semitorques* did not produce any well-supported internal structure (Fig. 1, Supp. Fig 3). Cyt b had 58 variable and 17 informative sites, whereas tRNA-Glu and a portion of the control region had 43 variable and 18 informative sites. Although not recovered as a clade with ML or Bayesian analysis, *S. semitorques* individuals from Taiwan form a cluster (in haplotype network) and all exhibit unique Cytb haplotypes.

2.2 Ecological niche modeling

Ecological niche models for each species reconstructed the contemporary known breeding range accurately (Fig. 2). All predicted species models exhibited a widespread distribution across northern China, coastal southeast China, and Taiwan. Because all models performed well qualitatively and quantitatively (partial-ROC analysis), we were justified to interpret results from projections to past time periods. Models for the different climate scenarios (LGM) varied for each species (Fig. 2). Combining predictions for both climate scenarios during the LGM, the distributions of *Paradoxornis* and *Pycnonotus* remained widespread and largely contiguous

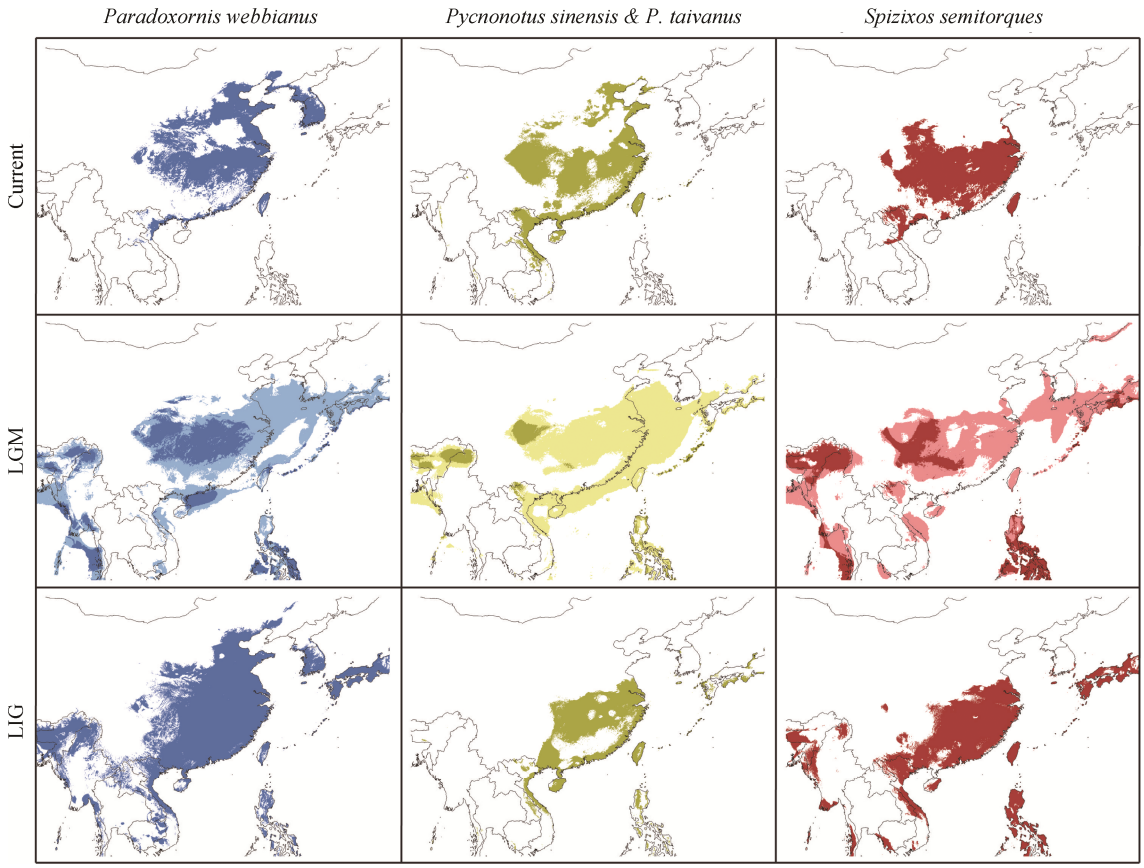

Fig. 2 The top row (Current) is the predicted range for each species under contemporary climate patterns

The middle row (LGM) predicts the distribution for each taxa under two climate scenarios (CCSM3, MIROC), agreement between models is shown with darker colors and areas predicted by only one climate scenario are lighter. The bottom row depicts the predicted distribution for taxa at the last inter-glacial (LIG)

within their known contemporary distributions, east of the Himalayas, whereas *S. semitorques* was slightly fragmented in the southern portion of its range (Fig. 2). During the LIG, the distribution of each species was predicted as widespread with few disjunct suitable areas (Fig. 2). For all species, projections indicated potential suitable habitat west of Myanmar, as well as in Japan and the Philippines. Oceanic and montane (e.g., Arakan and Himalayan ranges) biogeographic barriers likely limited dispersal to these regions.

3 Discussion

Pleistocene climatic fluctuation and fragmented suitable habitats isolated many populations in North America and Europe, but climatic shifts were less extreme in Southeast Asia (Edwards et al., 2000); therefore, signatures of these events on the genetic structure of species in this region are harder to detect. Thus, deciphering the impact of Pleistocene glaciation on populations of mainland Southeast Asia is aided by a multi-taxon approach that allows direct comparisons among co-distributed species. Three species complexes were selected to explore the historical influences of Pleistocene glaciation: *Paradoxornis webbianus/alphonsianus*, *Pycnonotus sinensis/taivanus* and *S. semitorques*. Contemporary distributions are largely congruent among the three study complexes, with year-round ranges throughout mainland South China (W to Yunnan/Sichuan and E to the Coast) and many surrounding continental islands. Despite similar geographic distributions, the genetic data revealed disparate phylogeographic patterns for each of the species groups. Below we discuss the details of these data in light of biogeography and niche modeling.

3.1 Biogeography

Strikingly different phylogeographic patterns for three focal taxa preclude generalizations about the forces driving intraspecific diversification in birds of mainland Southeast Asia. A lack of comparable phylogeographic histories suggests a corresponding lack of strong environmental or geological forces promoting co-diversification events in the recent past (last 1 my). Of the three taxa examined, only the *Paradoxornis* spp. complex had structure among the mainland populations. This divergence was estimated to have occurred during the Pleistocene (ca. 0.58–1.03 mya), but the data did not support a simple separation between "eastern" and "western" clades. Taiwanese lineages of *Paradoxornis* spp. and the island clade of *Pycnonotus* spp. both had qualitatively similar divergence dates for ND2 (0.35–0.93 mya and 0.25–0.68 mya, respectively), and *S. semitorques* individuals from Taiwan formed a cluster in our haplotype analyses. Thus, all three examined taxa had a genetically differentiated population on Taiwan. Evidence suggests the Taiwan Strait was most likely a savannah during LGM (Li et al., 2010; Yu et al., 2000), other studies have indicated that land bridges do not always result in an interchange between previously "isolated" populations (Hosner et al., 2014). Therefore, it is possible that environmental or habitat factors may have restricted gene flow across the straits, leaving the Taiwan populations isolated. Furthermore, the divergence dates for *Paradoxornis* spp. and *Pycnonotus* spp. island clades pre-date the LGM, suggesting an older origin for these clades. Voris (2000) showed that Taiwan has been connected to the Chinese mainland for a small proportion of time over the last 250,000 years. Instead, the majority of Taiwan's late Pleistocene history is one of isolation intermixed with short intervals of land bridge connectivity. This complex geologic history is potentially the reason for the varied divergence estimates for Taiwanese lineages.

Lei et al. (2006) studied the endemic avifauna of Taiwan and mainland China by subdividing the two landmasses into 19 sub-regions; from this they concluded that the most endemics restricted to one sub-region were from the Taiwanese sub-region. Other investigations also found strong phylogenetic support for endemism in Taiwan lineages (Qu et al., 2015; Song et al., 2009). However, Qu et al. (2015) estimated isolation of the Taiwanese lineages of *Alcippe morrisonia* and *Stachyridopsis ruficeps* around 2 mya, approximately four times older than our estimates. Therefore, it is unlikely that a single event isolated the endemic avian taxa of Taiwan.

Paradoxornis spp. is the only complex examined to have mainland phylogenetic structure and the only complex with potentially isolated LGM refugia. Similar phylogeographic structure was previously described for the Chinese Bamboo Partridge (*Bambusicola thoracica*, Huang et al., 2010); exploring ENM for the Chinese Bamboo Partridge may reveal common LGM refugia that could have produced their similar phylogeographic structure.

3.2 Niche modeling

Predictably, currently co-distributed and ecologically similar taxa produced largely concordant historical niche model predictions for LGM and LIG distributions, but close examination of the projection for *Paradoxornis* spp. reveals isolated refugia in central and south

China. It may be tempting to correlate these refugia to divergence patterns in the phylogeny (Fig. 1), however, we did not recover any divergence estimates between well-supported clades dating to the LGM. Thus, although the pattern suggests how diversification could have happened within *Paradoxornis* spp. we did not have the evidence to support an LGM induced vicariance event. In this case, over interpretation of niche model based LGM refugia would be misinformed lacking other sources of information to corroborate recent allopatric divergence in refugia. Overall, our results suggest caution when interpreting niche models to infer evolutionary process because despite similar niche models among species, phylogenetic structure varied widely between study taxa (Fig. 1).

In conclusion, although many studies have shown the influence of glaciation mediated range shifts and subsequent vicariance (Petit et al., 2003; Provan and Bennett, 2008), this should not be considered the only driver of current avian diversity. Research has shown that divergence of extant taxa most likely began during the Late Pliocene or Early Pleistocene, well before the LGM and LIG (Cheviron et al., 2005; Klicka and Zink, 1997; Moritz et al., 2000). Conversely, Milá et al. (2007) demonstrated that LGM factors could influence avian diversity in a widespread polytypic species *Junco hyemalis*. In this and other cases (Arbogast and Kenagy, 2001; Demboski and Cook, 2001; Weir and Schluter, 2004) in North America, LGM-mediated range-shifts were the driving force behind the rapid genetic and morphological divergence seen among extant sister taxa, with many patterns shared between species (the Rocky Mountain/Pacific/boreal and east clades). These examples relied on mitochondrial DNA sequences, so their findings (on a different continent) are directly comparable to ours. In our study, all estimated divergence times are much earlier than the start of the LGM (23,000 to 18,000 years ago); also, none of our phylogenetic reconstructions showed any recent divergence between intraspecific taxa. This suggests that the climate and habitat shifts throughout the last glacial cycle had no observable effect on the mtDNA structure of the three species complexes discussed in this study, and is in direct contrast with the aforementioned patterns of intraspecific co-diversification in North America.

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Supplementary materials

Table S1 Specimen information (catalogue number, species name, locality) for individuals used for this project and the publication that produced the data

Catalog number	Taxon	Country	Population	Publication
SCIEA S00036	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00040*	*Pycnonotus sinensis sinensis*	China	Chongqing	McKay et al., 2013
SCIEA S00042	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00043	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00045	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00046	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00047	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00067	*Pycnonotus sinensis sinensis*	China	Macao	McKay et al., 2013
SCIEA S00145*	*Pycnonotus sinensis sinensis*	China	Langxi, Anhui	McKay et al., 2013
SCIEA S00146	*Pycnonotus sinensis sinensis*	China	Langxi, Anhui	McKay et al., 2013
SCIEA S00147	*Pycnonotus sinensis sinensis*	China	Langxi, Anhui	McKay et al., 2013
SCIEA S00148	*Pycnonotus sinensis sinensis*	China	Langxi, Anhui	McKay et al., 2013
SCIEA S00150	*Pycnonotus sinensis sinensis*	China	Langxi, Anhui	McKay et al., 2013
SCIEA S00221	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00227	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00228*	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00229	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00230	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00231	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00232	*Pycnonotus sinensis sinensis*	China	Miluo, Hunan	McKay et al., 2013
SCIEA S00262	*Pycnonotus sinensis sinensis*	China	Guilin, Guangxi	McKay et al., 2013
SCIEA S00264*	*Pycnonotus sinensis sinensis*	China	Guilin, Guangxi	McKay et al., 2013
SCIEA S00266	*Pycnonotus sinensis sinensis*	China	Guilin, Guangxi	McKay et al., 2013
SCIEA S00268	*Pycnonotus sinensis sinensis*	China	Guilin, Guangxi	McKay et al., 2013
SCIEA S00755*	*Pycnonotus sinensis sinensis*	China	Zhuhai, Guangdong	McKay et al., 2013
SCIEA S00759	*Pycnonotus sinensis sinensis*	China	Zhuhai, Guangdong	McKay et al., 2013
SCIEA S00760	*Pycnonotus sinensis sinensis*	China	Zhuhai, Guangdong	McKay et al., 2013
SCIEA S00761	*Pycnonotus sinensis sinensis*	China	Zhuhai, Guangdong	McKay et al., 2013
SCIEA S00763	*Pycnonotus sinensis sinensis*	China	Zhuhai, Guangdong	McKay et al., 2013
SCIEA S01565	*Pycnonotus sinensis sinensis*	China	Shixing, Guangdong	McKay et al., 2013
SCIEA S01566	*Pycnonotus sinensis sinensis*	China	Shixing, Guangdong	McKay et al., 2013
SCIEA S01567	*Pycnonotus sinensis sinensis*	China	Shixing, Guangdong	McKay et al., 2013
SCIEA S01568	*Pycnonotus sinensis sinensis*	China	Shixing, Guangdong	McKay et al., 2013
SCIEA S00012*	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00158	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00162*	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00165*	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00167*	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00168	*Pycnonotus sinensis hainanus*	China	Datian, Hainan	McKay et al., 2013
SCIEA S00174	*Pycnonotus sinensis hainanus*	China	Fanjia, Hainan	McKay et al., 2013
SCIEA S00184	*Pycnonotus sinensis hainanus*	China	Fanjia, Hainan	McKay et al., 2013
SCIEA S00274*	*Pycnonotus sinensis hainanus*	China	Fanjia, Hainan	McKay et al., 2013
NTNU 5454	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5455	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5457	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
NTNU 5458	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5459	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5460	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5462	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5463	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5465	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5466	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5467	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
NTNU 5468	*Pycnonotus sinensis formosae*	China	Tainan, Taiwan	McKay et al., 2013
TESRI 3606	*Pycnonotus sinensis formosae*	China	Taichung, Taiwan	McKay et al., 2013
TESRI 3680*	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
TESRI 3870	*Pycnonotus sinensis formosae*	China	Taichung, Taiwan	McKay et al., 2013
TESRI 3919	*Pycnonotus sinensis formosae*	China	Taichung, Taiwan	McKay et al., 2013
TESRI 6301*	*Pycnonotus sinensis formosae*	China	Taichung, Taiwan	McKay et al., 2013
TESRI 6324*	*Pycnonotus sinensis formosae*	China	Kaohsiung, Taiwan	McKay et al., 2013
TESRI 6380	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
TESRI 6445*	*Pycnonotus sinensis formosae*	China	Kaohsiung, Taiwan	McKay et al., 2013
TESRI 6486	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5236	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5237*	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5238	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5239	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5240	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
AMNH DOT5241	*Pycnonotus sinensis formosae*	China	Nantou, Taiwan	McKay et al., 2013
TESRI 2261	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
TESRI 2440	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
TESRI 2456*	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
TESRI 2666*	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
TESRI 2667	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
TESRI 4211	*Pycnonotus taivanus*	China	Hwalien, Taiwan	McKay et al., 2013
TESRI 4443*	*Pycnonotus taivanus*	China	Hwalien, Taiwan	McKay et al., 2013
TESRI 5042*	*Pycnonotus taivanus*	China	Hwalien, Taiwan	McKay et al., 2013
TESRI 5169*	*Pycnonotus taivanus*	China	Taitung, Taiwan	McKay et al., 2013
NSMT YA86*	*Pycnonotus sinensis orii*	Japan	Yonaguni Island, Okinawa prefecture	McKay et al., 2013
NSMT 2008.95*	*Pycnonotus sinensis orii*	Japan	Okinawa Island, Okinawa prefecture	McKay et al., 2013
NSMT YA36*	*Pycnonotus sinensis orii*	Japan	Okinawa Island, Okinawa prefecture	McKay et al., 2013
KU 13691*	*Pycnonotus xanthorrhous*	China	Libo, Guizhou	McKay et al., 2013
KU 13728*	*Pycnonotus xanthorrhous*	China	Libo, Guizhou	McKay et al., 2013
MIB_zpl_1124	*Paradoxornis alphonsianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1128	*Paradoxornis alphonsianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1129	*Paradoxornis alphonsianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1122	*Paradoxornis alphonsianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1132	*Paradoxornis alphonsianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1125	*Paradoxornis webbianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1126	*Paradoxornis webbianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1123	*Paradoxornis webbianus*	Italy	Introduced population	Crottini et al., 2010

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
MIB_zpl_1120	*Paradoxornis webbianus*	Italy	Introduced population	Crottini et al., 2010
MIB_zpl_1130	*Paradoxornis webbianus*	Italy	Introduced population	Crottini et al., 2010
NTNU_T5341	*Paradoxornis alphonsianus*	China*	Leipo, Sichuan	Yeung et al., 2011
IOZ_8779	*Paradoxornis webbianus*	China	Luding, Sichuan	Qu et al., 2012
IOZ_8780	*Paradoxornis webbianus*	China	Luding, Sichuan	Qu et al., 2012
web_a_1634	*Paradoxornis alphonsianus*	China	Kumming, Yunnan	Crottini et al., 2010
web_a_1652	*Paradoxornis alphonsianus*	China	Kumming, Yunnan	Crottini et al., 2010
NTNU_T5349	*Paradoxornis webbianus*	China*	Ganluo, Sichuan	Qu et al., 2012
NTNU_T5350	*Paradoxornis webbianus*	China*	Ganluo, Sichuan	Qu et al., 2012
NTNU_T1634	*Paradoxornis alphonsianus*	China*	Kunming, Yunnan	Qu et al., 2012
NTNU_T1652	*Paradoxornis alphonsianus*	China*	Kunming, Yunnan	Qu et al., 2012
113601136	*Paradoxornis alphonsianus*	China	Dunjiangyan, Sichuan	Crottini et al., 2010
MIB_zpl_2276	*Paradoxornis alphonsianus*	China	Dunjiangyan, Sichuan	Crottini et al., 2010
228302283	*Paradoxornis alphonsianus*	China	Dunjiangyan, Sichuan	Crottini et al., 2010
113801138	*Paradoxornis alphonsianus*	China	Dunjiangyan, Sichuan	Crottini et al., 2010
113301133	*Paradoxornis alphonsianus*	China	Dunjiangyan, Sichuan	Crottini et al., 2010
IOZ_8892	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8862	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_5546	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_5548	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8889	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8900	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8891	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8863	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_8857	*Paradoxornis webbianus*	China	Guangyuan, Sichuan	Qu et al., 2012
IOZ_11034	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_2071	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_3571	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_11052	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_3572	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_11054	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_11049	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_11030	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_2546	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_2540	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
IOZ_11028	*Paradoxornis webbianus*	China	Mountain Villa Li, Shaanxi	Qu et al., 2012
NTNU_T3163	*Paradoxornis alphonsianus*	China*	Guiyang, Guichou	Yeung et al., 2011
IOZ_12935	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12928	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12930	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12936	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12934	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12932	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
IOZ_12929	*Paradoxornis webbianus*	China	Machanghexiang, Guizhou	Qu et al., 2012
KUNHM_11096	*Paradoxornis alphonsianus*	China	Datu, Guizhou	Moyle et al., 2011
IOZ_8776	*Paradoxornis webbianus*	China	Shuijia, Guizhou	Qu et al., 2012

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
KUNHM_13794	*Paradoxornis webbianus*	China	Shuijia, Guizhou	Moyle et al., 2011
IOZ_11882	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11872	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_4672	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_4635	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11865	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11847	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11814	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11843	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11842	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11811	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_10613	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_8739	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_4681	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11854	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_4660	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_11864	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
IOZ_8736	*Paradoxornis webbianus*	China	Haoping, Shaanxi	Qu et al., 2012
NTNU_T4285	*Paradoxornis alphonsianus*	China*	Kaili, Guichou	Yeung et al., 2011
NTNU_T4290	*Paradoxornis alphonsianus*	China*	Kaili, Guichou	Yeung et al., 2011
web_s_3159	*Paradoxornis webbianus*	China	Qinling Mt, Shaanxi	Crottini et al., 2010
web_s_834	*Paradoxornis webbianus*	China	Qinling Mt, Shaanxi	Crottini et al., 2010
web_s_836	*Paradoxornis webbianus*	China	Qinling Mt, Shaanxi	Crottini et al., 2010
web_s_3158	*Paradoxornis webbianus*	China	Qinling Mt, Shaanxi	Crottini et al., 2010
IOZ_11343	*Paradoxornis webbianus*	China	Nanyin, Shaanxi	Qu et al., 2012
IOZ_1934	*Paradoxornis webbianus*	China	Nanyin, Shaanxi	Qu et al., 2012
IOZ_1886	*Paradoxornis webbianus*	China	Nanyin, Shaanxi	Qu et al., 2012
IOZ_11344	*Paradoxornis webbianus*	China	Nanyin, Shaanxi	Qu et al., 2012
IOZ_2205	*Paradoxornis webbianus*	China	Nanyin, Shaanxi	Qu et al., 2012
IOZ_8543	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8540	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8471	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8330	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8495	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8542	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8541	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8498	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8473	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8297	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8285	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8541	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
IOZ_8261	*Paradoxornis webbianus*	China	Chaojiaping, Hubei	Qu et al., 2012
NTNU_T5742	*Paradoxornis webbianus*	China*	Kuilin, Guanxi	Yeung et al., 2011
NTNU_T6118	*Paradoxornis webbianus*	China*	Kuilin, Guanxi	Yeung et al., 2011
NTNU_T0834	*Paradoxornis webbianus*	China*	Foping, Shanxi	Yeung et al., 2011
NTNU_T0836	*Paradoxornis webbianus*	China*	Foping, Shanxi	Yeung et al., 2011
NTNU_T3159	*Paradoxornis webbianus*	China*	Foping, Shanxi	Yeung et al., 2011
NTNU_T3158	*Paradoxornis webbianus*	China*	Foping, Shanxi	Yeung et al., 2011
IOZ_8676	*Paradoxornis webbianus*	China	Xiachuan, Shanxi	Qu et al., 2012
IOZ_8639	*Paradoxornis webbianus*	China	Xiachuan, Shanxi	Qu et al., 2012
IOZ_13283	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
IOZ_13284	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_13281	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_3207	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_3206	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_3209	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_3205	*Paradoxornis webbianus*	China	Lujiacun, Hunan	Qu et al., 2012
IOZ_11420	*Paradoxornis webbianus*	China	Chengnancun, Hunan	Qu et al., 2012
KUNHM_6740	*Paradoxornis webbianus*	China	Yuquan Mt. Villa, Hunan	Moyle et al., 2011
IOZ_1515	*Paradoxornis webbianus*	China	Nanhu Lake, Jiangxi	Qu et al., 2012
IOZ_14758	*Paradoxornis webbianus*	China	Nanhu Lake, Jiangxi	Qu et al., 2012
IOZ_14769	*Paradoxornis webbianus*	China	Nanhu Lake, Jiangxi	Qu et al., 2012
IOZ_14770	*Paradoxornis webbianus*	China	Nanhu Lake, Jiangxi	Qu et al., 2012
IOZ_1500	*Paradoxornis webbianus*	China	Nanhu Lake, Jiangxi	Qu et al., 2012
113701137	*Paradoxornis webbianus*	China	Dongzhai NR, Henan	Crottini et al., 2010
113901139	*Paradoxornis webbianus*	China	Dongzhai NR, Henan	Crottini et al., 2010
114001140	*Paradoxornis webbianus*	China	Dongzhai NR, Henan	Crottini et al., 2010
114101141	*Paradoxornis webbianus*	China	Dongzhai NR, Henan	Crottini et al., 2010
IOZ_2844	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2843	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2851	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2853	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2846	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2845	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2854	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2766	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2855	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2849	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2848	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_2845	*Paradoxornis webbianus*	China	Beihu Lake, Henan	Qu et al., 2012
IOZ_13882	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13878	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13876	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13880	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13872	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13883	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13886	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13879	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13887	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13877	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_13871	*Paradoxornis webbianus*	China	Jinan, Hebei	Qu et al., 2012
IOZ_12174	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
IOZ_12171	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
IOZ_12180	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
IOZ_2361	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
IOZ_12173	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
IOZ_2362	*Paradoxornis webbianus*	China	Heituwan, Hebei	Qu et al., 2012
228402284	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
114201142	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
113401134	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
228202282	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
MIB_zpl_2277	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
MIB_zpl_2278	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
228102281	*Paradoxornis webbianus*	China	East Tianjin	Crottini et al., 2010
IOZ_12656	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12657	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12556	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_13783	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12655	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_10095	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12660	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12625	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_11417	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12622	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_10094	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12658	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_10096	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_10064	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12623	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12588	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_12555	*Paradoxornis webbianus*	China	Jixi, Anhui	Qu et al., 2012
IOZ_11014	*Paradoxornis webbianus*	China	Yinghuimen, Jiangsu	Qu et al., 2012
IOZ_10997	*Paradoxornis webbianus*	China	Yinghuimen, Jiangsu	Qu et al., 2012
IOZ_11015	*Paradoxornis webbianus*	China	Yinghuimen, Jiangsu	Qu et al., 2012
IOZ_10985	*Paradoxornis webbianus*	China	Yinghuimen, Jiangsu	Qu et al., 2012
IOZ_11016	*Paradoxornis webbianus*	China	Yinghuimen, Jiangsu	Qu et al., 2012
NTNU_T2225	*Paradoxornis webbianus*	Taiwan, China	Nantou,Taiwan	Yeung et al., 2011
NTNU_T0666	*Paradoxornis webbianus*	Taiwan, China	Hwalian	Yeung et al., 2011
113501135	*Paradoxornis webbianus*	China	Dong, Chongming Island, Shanghai	Crottini et al., 2010
MIB_zpl_2279	*Paradoxornis webbianus*	China	Dong, Chongming Island, Shanghai	Crottini et al., 2010
228002280	*Paradoxornis webbianus*	China	Dong, Chongming Island, Shanghai	Crottini et al., 2010
IOZ_10716	*Paradoxornis webbianus*	China	Panjin, Liaoning	Qu et al., 2012
IOZ_10690	*Paradoxornis webbianus*	China	Panjin, Liaoning	Qu et al., 2012
IOZ_10658	*Paradoxornis webbianus*	China	Panjin, Liaoning	Qu et al., 2012
IOZ_10625	*Paradoxornis webbianus*	China	Panjin, Liaoning	Qu et al., 2012
NTNU_T3161	*Paradoxornis webbianus*	China*	Heilongjiang	Yeung et al., 2011
NTNU_T6135	*Paradoxornis webbianus*	China*	Heilongjiang	Yeung et al., 2011
IOZ_10868	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_5838	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9607	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9010	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_6742	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9006	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9368	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9369	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_9366	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_10859	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_5839	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_5838	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_6743	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
IOZ_5881	*Paradoxornis webbianus*	China	Heilongjiang	Qu et al., 2012
T5280	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T2628	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
T1877	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T5283	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T6152	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T6157	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T2627	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
T5281	*Paradoxornis webbianus*	China	Nantou, Taiwan	Qu et al., 2012
KUNHM 11037	*Paradoxornis gularis*	Outgroup	NA	
NTNU T3023	*Paradoxornis guttaticollis*	Outgroup	NA	
NTNU T3089	*Paradoxornis heudei*	Outgroup	NA	
12671	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12670	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12672	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12674	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12675	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12676	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12678	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12673	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
12677	*S. s. semitorques*	China	Dongjiecun, Anhui	Gao et al., 2011
3073	*S. s. semitorques*	China	Jianyang, Fujian	Gao et al., 2011
10351	*S. s. semitorques*	China	Jianyang, Fujian	Gao et al., 2011
10352	*S. s. semitorques*	China	Jianyang, Fujian	Gao et al., 2011
3090	*S. s. semitorques*	China	Jianyang, Fujian	Gao et al., 2011
2968	*S. s. semitorques*	China	Jianyang, Fujian	Gao et al., 2011
1156	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1213	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1157	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1162	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1175	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1188	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1180	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1160	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
1211	*S. s. semitorques*	China	Wenxian, Gansu	Gao et al., 2011
12865	*S. s. semitorques*	China	Suoling, Guangxi	Gao et al., 2011
13004	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
12998	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13001	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13002	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13003	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13005	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13006	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13007	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
12999	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
12866	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
13000	*S. s. semitorques*	China	Guiding, Guizhou	Gao et al., 2011
1533	*S. s. semitorques*	China	Shihuiyao, Hunan	Gao et al., 2011
6099	*S. s. semitorques*	China	Shihuiyao, Hunan	Gao et al., 2011

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
1534	*S. s. semitorques*	China	Shihuiyao, Hunan	Gao et al., 2011
3224	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3219	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3225	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
1776	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3220	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
1495	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3223	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3221	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3222	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
3226	*S. s. semitorques*	China	Lujiacun, Hunan	Gao et al., 2011
4728	*S. s. semitorques*	China	Luozhuang, Jiangsu	Gao et al., 2011
4730	*S. s. semitorques*	China	Luozhuang, Jiangsu	Gao et al., 2011
4731	*S. s. semitorques*	China	Luozhuang, Jiangsu	Gao et al., 2011
13340	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13338	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13344	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13346	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13347	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13348	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13354	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13359	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13360	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13339	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13345	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
13358	*S. s. semitorques*	China	Shangduan, Jiangxi	Gao et al., 2011
4723	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
4732	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
8910	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
8911	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
8912	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
8913	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
8914	*S. s. semitorques*	China	Quanjialing, Sichuan	Gao et al., 2011
5178	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5183	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5161	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5163	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5180	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5179	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5181	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5182	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
5162	*S. s. semitorques*	China	Niushipo, Sichuan	Gao et al., 2011
8250	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8476	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8195	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8091	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011

Continued Table S1

Catalog number	Taxon	Country	Population	Publication
8450	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8551	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8194	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8059	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8090	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8420	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
8280	*S. s. semitorques*	China	Wanjiagou, Hubei	Gao et al., 2011
1962	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2131	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2001	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2028	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2130	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2141	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
1952	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2010	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2016	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2135	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2136	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
1970	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2017	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2020	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2050	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
1941	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2029	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2121	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
3527	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
3526	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
3530	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
4563	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
4636	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
4574	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
8752	*S. s. semitorques*	China	Sanchahecun, Shaanxi	Gao et al., 2011
2828	*S. s. cinereicapillus*	China	Taipei, Taiwan	Gao et al., 2011
36	*S. s. cinereicapillus*	China	Taipei, Taiwan	Gao et al., 2011
1883	*S. s. cinereicapillus*	China	Taipei, Taiwan	Gao et al., 2011
3288	*S. s. cinereicapillus*	China	Taipei, Taiwan	Gao et al., 2011
882	*S. s. cinereicapillus*	China	Taipei, Taiwan	Gao et al., 2011

Fig. S1 Accessible areas used for niche modeling are tan, blue, and purple for *Paradoxornis* spp., *Pycnonotus* spp., and *Spizixoz* sp., respectively

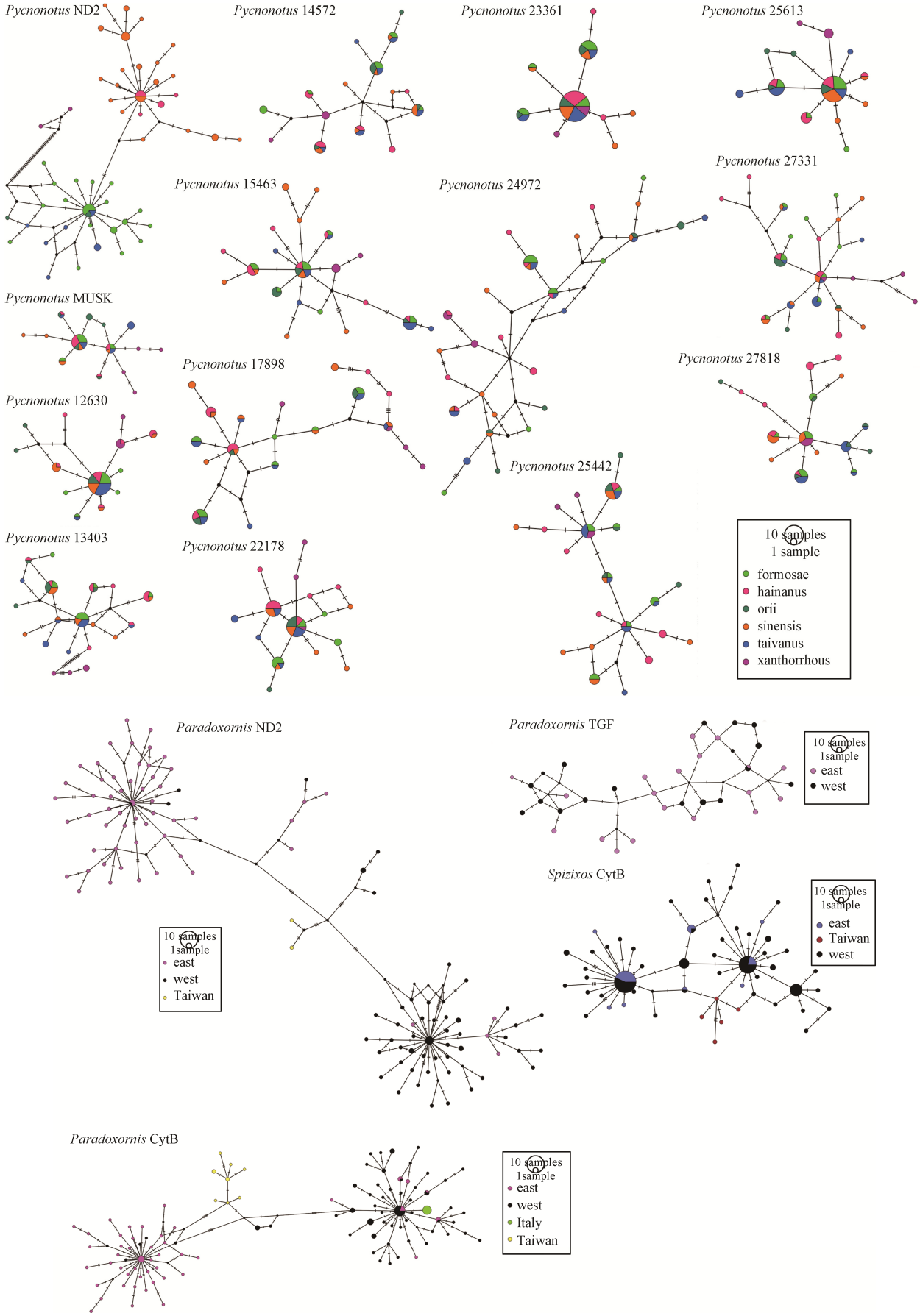

Fig. S2 Median-joining haplotype networks for all loci for each species complex