Supporting Information

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SI Results

Phylogenetic Results. A parameter-rich model of evolution (GTR + I + G) was selected for each partition of the data except the intron (GTR + G). Bayesian and ML approaches produced similar results (Fig. S1), although support indices differed dramatically at a few nodes. All *Yuhinas*, Philippine *Stachyris*, and Zosteropidae (except *Hypocryptadius*) formed a well-supported clade, which became the focus of diversification analysis (see below). *Yuhina* did not form a clade by itself, but rather branched off sequentially from the base of the radiation. White-eyes separated into two distinct groups in the phylogeny. Three small genera (*Lophozosterops*, *Oculocincta*, and *Cleptornis*), *Zosterops wallacei*, and the Philippine *Stachyris* formed a weakly supported clade (clade A, Fig. S1) sister to the remainder of the white-eyes. That clade received high support in all analyses (clade B, Fig. S1) and contained all *Zosterops* species except *Z. wallacei*, and species from four other genera (*Woodfordia*, *Rukia*, *Chlorocharis*, and *Speirops*) scattered among the *Zosterops*. Insertions and deletions (indels) within the nuclear intron data provided additional support for some relationships. Four indels could be mapped onto the tree unequivocally: *Macronous ptilosus* and *Stachyris erythroptera* shared a 2-bp indel; clade C (*Malacopteron magnirostre*, *Napothera crassa*, *Trichastoma rufipennis*, *Kenopia striata*, and *Pellorneum capistratum*) shared a 9-bp indel; *Yuhina*, Philippine *Stachyris*, and Zosteropidae shared a 3-bp indel; and a 1-bp indel separated *Yuhina everetti*, *Yuhina castaneiceps*, and *Yuhina diademata* from the rest of this last clade. One indel could not be mapped onto the ML tree as a single event. A 6-bp indel united clade C with *Hypocryptadius cinnamomeus* and the outgroup taxon, *Enicurus leschenaulti*. All analyses indicated that *Hypocryptadius* is not a white-eye and also may not be within the Timaliidae, although denser taxon sampling is necessary to decipher the relationships of this Mindanao endemic.

Divergence Times and Diversification Rate. The 2ln difference between likelihood scores for trees with and without a molecular clock enforced was 89.98, just over the critical value of 88 ($n - 2$ df = 68), indicating nonclocklike evolution. Cross validation within the r8s program indicated a smoothing parameter of 3.2.

The maximum uncorrected distance (ND2) between individuals sampled from throughout Kolombangara, New Georgia, and Kohingo was 0.0077, compared to a range of 0.024–0.029 between *Z. splendidus* (Ranongga) and its sister taxon. Thus, within population diversity is as high as 32% of that seen between species. This percentage was applied to 425,000 years (the more conservative of the two island age estimates, see above) to yield a calibration of 561,000 years, a conservative maximum age of the most recent common ancestor of *Z. splendidus* and its sister clade. Finally, the node depths and confidence intervals produced with penalized likelihood were converted into age estimates by multiplying by a scaling factor of (561,000/node depth of *Z. splendidus*).

Calibration of the tree and its bootstrapped confidence interval with the age of Rannonga Island produced a range of maximum estimated ages for nodes on the phylogeny (Table S1). One previous study estimated divergence times for nodes within the white-eye radiation. Warren *et al.* (1) also used island ages to calibrate the time estimates, but they used Indian Ocean islands rather than Pacific islands. Their calibration method did not provide confidence intervals and their taxon sampling overlapped little with ours, but some comparisons are possible. The basal node in their *Zosterops* radiation was estimated at 1.84 Ma, just inside our confidence interval (1.40–1.89). The origin of a large African clade (their node 14, 1.63 Ma) also lies within our confidence interval for that node (1.29–1.74). These comparisons provide independent support that our divergence time estimates accurately reflect the general time frame of diversification in the white-eyes.

Generation Time. A survey of incubation times in passerine birds (2) found that 11 or 12 days was the shortest documented span, shared by a few species including several *Zosterops*. More recently a study of *Zosterops rotensis* (3) reported incubation times as short as 8 days. Specimen data from recent collections in the New Georgia group revealed immature birds (bursa of Fabricius present and skulls <100% ossified) that were already in breeding condition (enlarged testes, enlarged and convoluted oviducts, enlarged ovaries, and/or developing ova). These specimens are housed in the Burke Museum at the University of Washington and include: UWBM-63044, UWBM-63047, UWBM-66029, UWBM-68096, and UWBM-76319. Taken together, these two lines of evidence suggest that *Zosterops* have among the shortest generation times among birds and at least some species of *Zosterops* may breed within 6 months of hatching.

1. Warren BH, Bermingham E, Prys-Jones RP, Thébaud C (2006) Immigration, species radiation and extinction in a highly diverse songbird lineage: White-eyes on Indian Ocean islands. *Mol Ecol* 15:3769–3786.
2. Nice MM (1953) The question of ten-day incubation periods. *Wilson Bull* 65:81–93.
3. Amidon FA (2000) Habitat relationships and life history of the Rota bridled white-eye (*Zosterops rotensis*). Master's thesis (Virginia Polytechnic Institute and State University, Blacksburg, VA).

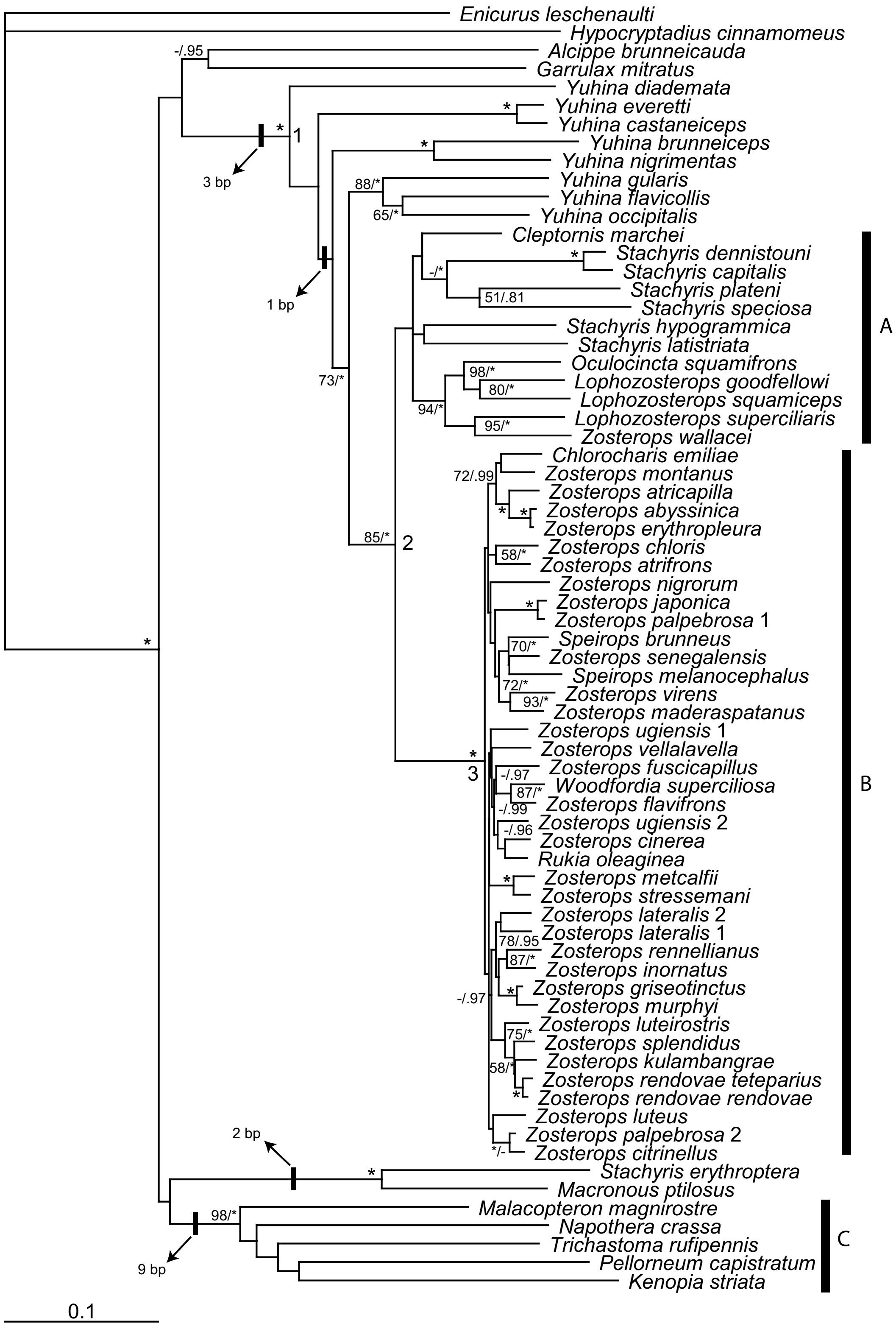

Fig. S1. Maximum likelihood phylogenetic estimate of white-eye relationships. Numbers at nodes indicate ML bootstrap support/Bayesian posterior probability. Asterisks (*) indicate 100% bootstrap support or 1.0 posterior probability. Hyphens (-) indicate <50% bootstrap support or <0.95 posterior probability. Inferred insertions and deletions are mapped onto the phylogeny along with the length (in base pairs) of each indel. Labeled clades are discussed in the text. For estimated ages of numbered nodes (1–3) see Table S1.

Table S1. Age estimate for selected nodes in the phylogeny

Node	Description	Age, Ma	Confidence interval
1	*Yuhina* diversifies	7.19	6.31–8.06
2	Zosteropidae + *Stachyris*	5.01	4.46–5.57
3	*Zosterops* radiation	1.65	1.40–1.89
	Origin of endemic genera:		
	Chlorocharis	1.13	0.88–1.39
	Speirops	1.12	0.89–1.35
	Rukia	0.76	0.50–1.03
	Woodfordia	0.79	0.61–0.97

Ages are maximum estimates based on penalized likelihood and island age calibration. See text for details.

Table S2. Samples included in the study

Genus	Species	Locality	Source	Voucher
Zosteropidae				
Zosterops	*erythropleura*	Captive	LSUMNS	B20626
	japonicus	Vietnam	AMNH	DOT10981
	palpebrosus 1	Nepal	AMNH	DOT5746
	palpebrosus 2	Flores Is., Indonesia	WAM	23218
	nigrorum	Luzon, Philippines	FMNH	432997
	montanus	Sulawesi, Indonesia	AMNH	DOT12552
	chloris	Sulawesi, Indonesia	AMNH	DOT12558
	atrifrons	Sulawesi, Indonesia	AMNH	DOT12620
	citrinellus	Roti Is., Indonesia	WAM	23542
	wallacei	Sumba Is., Indonesia	WAM	22903
	flavifrons	Vanuatu	LSUMNS	B45805
	atricapilla	Borneo	LSUMNS	B36444
	luteus	Australia	KUNHM	8904
	lateralis 1	Australia	KUNHM	6094
	lateralis 2	Vanuatu	LSUMNS	B45835
	abyssinicus	Captive	LSUMNS	B20825
	[*pallidus*] *virens*	South Africa	FMNH	390165
	senegalensis	Ghana	LSUMNS	B39250
	maderaspatanus	Madagascar	FMNH	345980
	metcalfi	Choiseul, Solomon Is.	UWBM	63177
	rennelianus	Rennel, Solomon Is.	UWBM	69808
	stresemanni	Malaita, Solomon Is.	UWBM	66034
	griseotinctus	Louisiade Is.	NMNH	2003–067
	rendovae rendovae	Rendova, Solomon Is.	UWBM	76258
	rendovae tetepare	Tetepare, Solomon Is.	UWBM	76356
	kulambangarae	Kohingo, Solomon Is.	UWBM	76278
	splendidus	Rannonga, Solomon Is.	AMNH	DOT171
	luteirostris	Ghizo Is, Solomon Is.	AMNH	DOT113
	inornatus	Lifou, Loyalty Is.	AMNH	337461*
	cinerea	Palau Is.	AMNH	332201*
	murphyi	Kolombangara, Solomon Is.	AMNH	DOT193
	fuscicapillus	Louisiade Is.	NMNH	2003–062
	vellalavella	Vellalavella, Solomon Is.	AMNH	DOT166
	ugiensis 1	Bougainville Is.	AMNH	222105*
	ugiensis 2	Makira, Solomon Is.	KUNHM	12803
Rukia	*oleaginea*	Yap Is., Micronesia	LSUMNS	B48626*
Cleptornis	*marchei*	Saipan Is., Micronesia	LSUMNS	B48623*
Woodfordia	*superciliosa*	Rennell, Solomon Is.	UWBM	58818
Lophozosterops	*goodfellowi*	Mindanao, Philippines	FMNH	357641
	squamiceps	Sulawesi, Indonesia	AMNH	DOT12549
	superciliaris	Flores, Indonesia	WAM	223291
Oculocincta	*squamifrons*	Borneo	LSUMNS	B51197
Chlorocharis	*emiliae*	Borneo	LSUMNS	B51361
Hypocryptadius	*cinnamomeus*	Mindanao, Philippines	FMNH	357652
Speirops	*brunneus*	Fernando Po	AMNH	706105*
	melanocephalus	Mt. Cameroon, Cameroon	AMNH	461540*
Timaliidae				
Yuhina	*everetti*	Borneo	LSUMNS	B36290
	nigrimentas	Vietnam	AMNH	DOT12297
	brunneiceps	Taiwan	AMNH	DOT5230
	occipitalis	Nepal	AMNH	DOT5588
	gularis	Nepal	AMNH	DOT5639
	flavicollis	Nepal	AMNH	DOT5550
	diademata	China	KUNHM	11118
	castaniceps	China	KUNHM	6676
Stachyris	*erythroptera*	Borneo	LSUMNS	B36417
	hypogrammica	Palawan, Philippines	CMNH	37765
	dennistouni	Luzon, Philippines	CMNH	38201
	plateni	Mindanao, Philippines	CMNH	37768
	speciosa	Negros, Philippines	CMNH	37091
	latistriata	Panay, Philippines	CMNH	34221

Table S2. Cont.

Genus	Species	Locality	Source	Voucher
	capitalis	Mindanao, Philippines	CMNH	37769
Garrulax	*mitratus*	Borneo	LSUMNS	B36460
Macronous	*ptilosus*	Borneo	LSUMNS	B36391
Napothera	*crassa*	Borneo	LSUMNS	B36469
Pellorneum	*capistratum*	Borneo	LSUMNS	B36430
Alcippe	*brunneicauda*	Borneo	LSUMNS	B36359
Kenopia	*striata*	Borneo	LSUMNS	B36395
Trichastoma	*rufipennis*	Ghana	LSUMNS	B39437
Malacopteron	*magnirostre*	Borneo	LSUMNS	B36421
Outgroup				
Enicurus	*leschenaulti*	Borneo	LSUMNS	B36442

Source abbreviations: LSUMNS, Louisiana State University Museum of Natural Science; AMNH, American Museum of Natural History; WAM, Western Australian Museum; FMNH, Field Museum of Natural History; KUNHM, University of Kansas Natural History Museum; UWBM, Burke Museum University of Washington; CMNH, Cincinnati Museum of Natural History; NMNH, National Museum of Natural History.

*Samples for which DNA was extracted from museum study skins.

Table S3. List of published and newly developed primers used in the study

Primer	Sequence (5′-3′) or ref.
L10755	1
H11151	1
L5215	2
ND2-SwH	3
H6313	4
TGF5	5
TGF6	5
TGF-5alt	ATCTGGGGTGATTCCCACATGC
TGF-6alt	ACTCAAGTGTWTTTCTCCAGGTCC
Zost190H	ACTAATGCRGARGCAGCTGC
Zost754H	GTTAGTGGTGGAAGTCCTGC
Zost371H	CCTTGGAGGACTTCTGGRAATCA
Zost351L	CAGCAATTGCAATAAAACTAGG

1. Chesser RT (1999) Molecular systematics of the rhinocryptid genus *Pteroptochos. Condor* 101:439–446.
2. Hackett SJ (1996) Molecular phylogenetics and biogeography of tanagers in the genus *Ramphocelus* (Aves). *Mol Phylogenet Evol* 5:368–382.
3. Sheldon FH, Whittingham LA, Moyle RG, Slikas B, Winkler DW (2005) Phylogeny of swallows (Aves: Hirundinidae) estimated from nuclear and mitochondrial DNA sequences. *Mol Phylogenet Evol* 35:254–270.
4. Johnson KP, Sorenson MD (1998) Comparing molecular evolution in two mitochondrial protein-coding genes (cytochrome *b* and ND2) in the dabbling ducks (Tribe: Anatini). *Mol Phylogenet Evol* 10:82–94.
5. Primmer CR, Borge T, Lindell J, Saetre GP (2002) Single-nucleotide polymorphism characterization in species with limited available sequence information: High nucleotide diversity revealed in the avian genome. *Mol Ecol* 11:603–612.