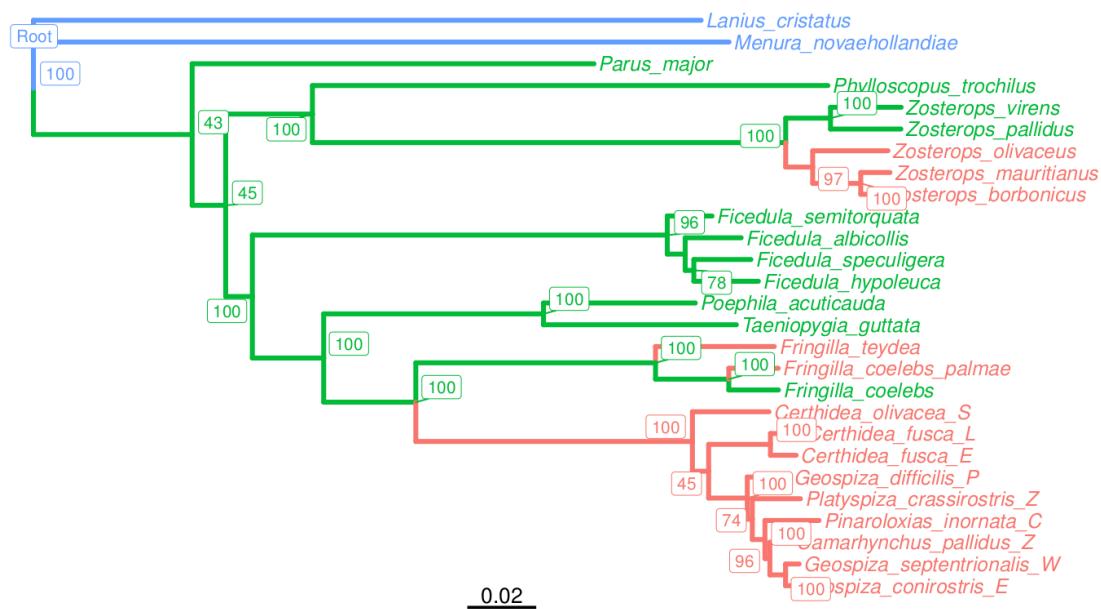


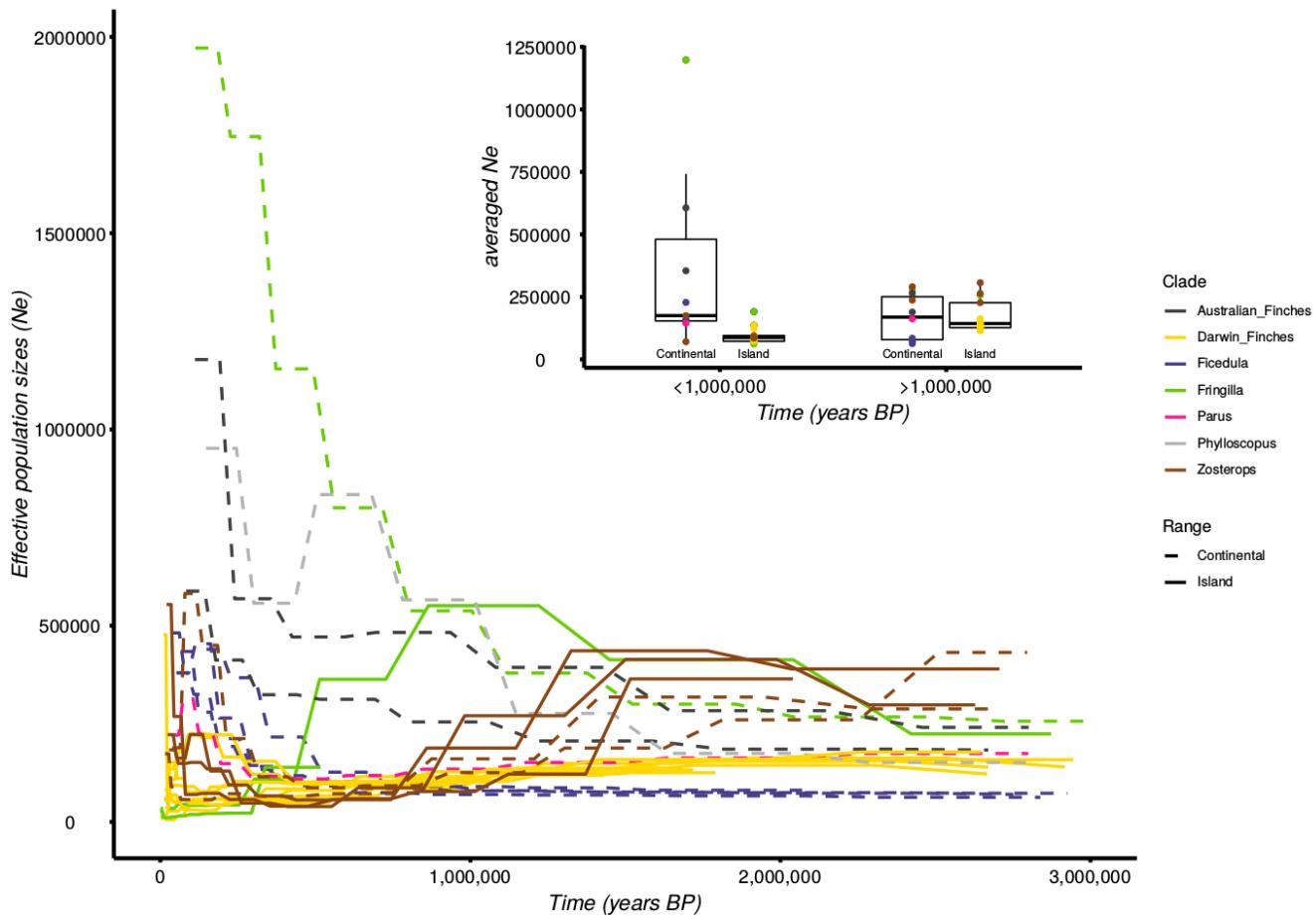
**Supplemental Information**

**Island songbirds as windows  
into evolution in small populations**

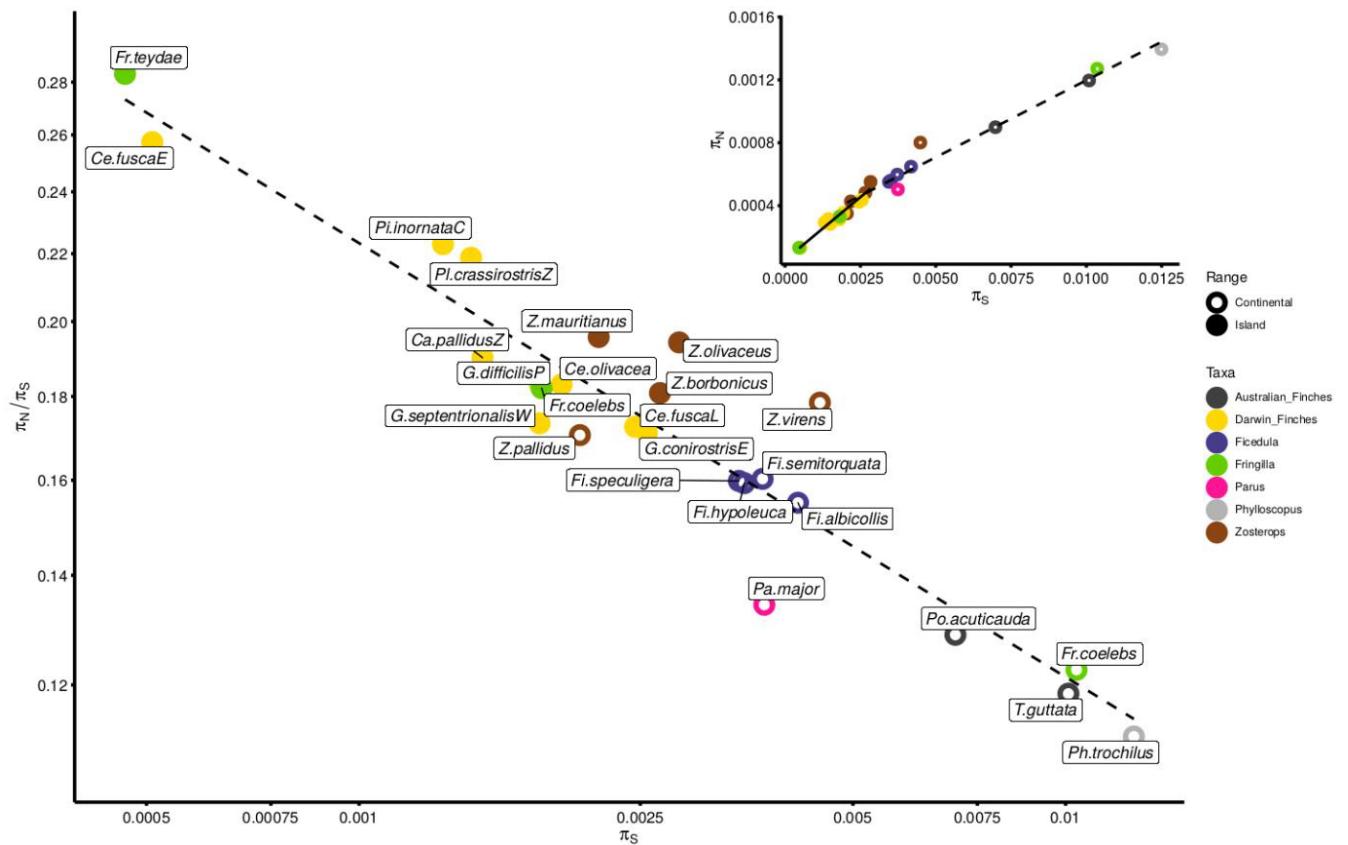
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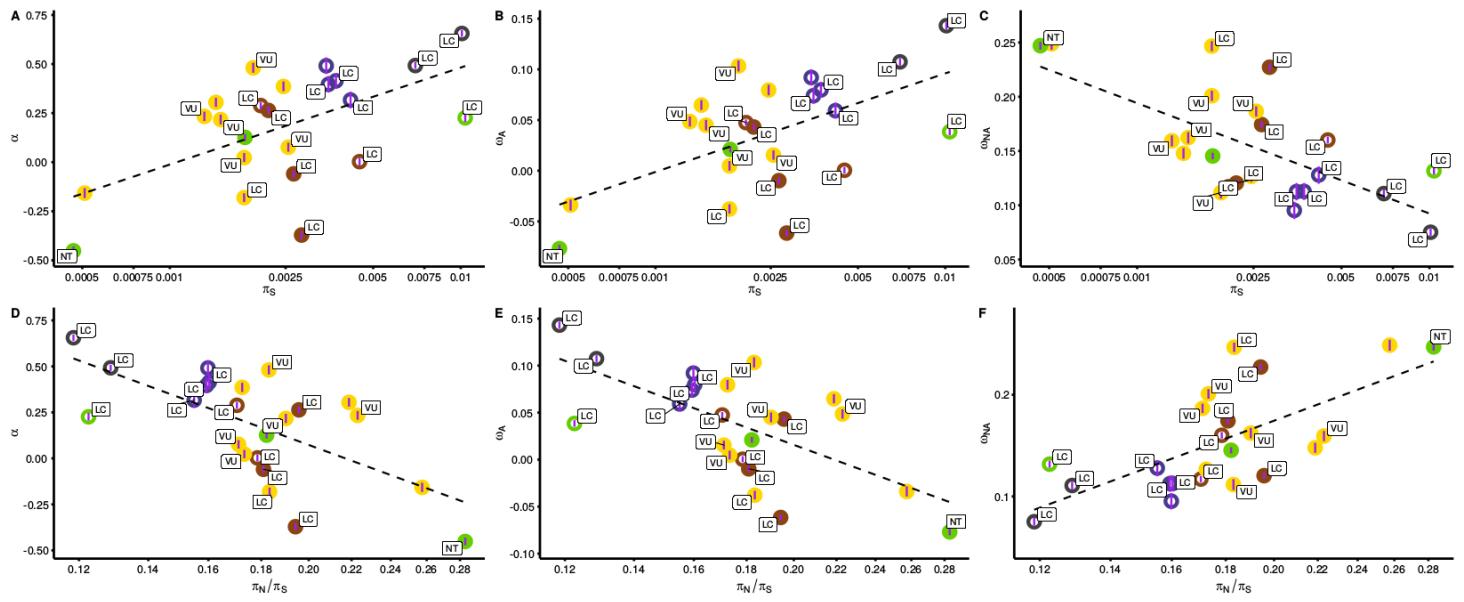
**Figure S1: Phylogenetic relationship estimated using complete mitochondrial sequences and a maximum likelihood approach (Related to Figure 1).** Island, continental and outlier species are shown in red, green and blue, respectively. Numbers shown in boxes indicated ultrafast bootstrap supports estimated by IQTREE.



**Figure S2: PSMC estimates of the changes in effective population size ( $N_e$ ) over time for each species (outer plot) (Related to Figure 1).** Each line represents the historical changes of  $N_e$  for one individual randomly selected among all individuals of each species. The inner boxplot shows the averaged mean  $N_e$  for all island and continental species over the last million years or estimates for older times. Estimates for the last million year exclude the last 4 estimates (see the STAR Methods), because PSMC can generate inaccurate estimates for present-day or very recent  $N_e$ .



**Figure S3: Linear regression between the log-transformed ratio of nonsynonymous to synonymous nucleotide diversity ( $\pi_N/\pi_S$ ) and the log-transformed levels of nucleotide diversity ( $\pi_S$ ), used as an indicator of effective population sizes (outer plot) (Related to Figures 1 and 2). Species genera are: Ca=Camarhynchus, Ce=Certhidea, Fi=Ficedula, Fr=Fringilla, G=Geospiza, Pa=Parus, Ph=Phylloscopus, Pi=Pinaroloxias, Pl=Platyspiza, Po= Poephila, T=Taeniopygia, Z= Zosterops. Inner plot: linear regressions between  $\pi_N$  and  $\pi_S$  for insular species (solid line) vs. continental species (dotted line).**



**Figure S4: Scatterplots of proportion of amino-acid substitutions that result from positive selection ( $\alpha$ , A and C), adaptive ratio of nonsynonymous over synonymous ( $\omega_A$ , B and E) & non-adaptive ratio of non-synonymous over synonymous substitutions ( $\omega_{NA}$ , C and F) with regards to the levels of nucleotide diversity ( $\pi_S$ ; A, B and C) and the observed ratios of nonsynonymous to synonymous mutations in the polymorphism data ( $\pi_N/\pi_S$ ; D, E and F) (Related to Figure 3).**

Groups	species	outgroup	Range	$\pi_S$ (meth1)	$\pi_N$ (meth1)	$\pi_N/\pi_S$ (meth1)	$\pi_S$ (meth2)	$\pi_N$ (meth2)	$\pi_N/\pi_S$ (meth2)
Zosterops	<i>Z.borbonicus</i>	<i>Z.pallidus</i>	Island	0.00267	0.00048	0.18086	0.00049	0.00239	0.20353
Zosterops	<i>Z.olivaceus</i>	<i>Z.virens</i>	Island	0.00284	0.00055	0.19422	0.00061	0.00268	0.22600
Zosterops	<i>Z.mauritianus</i>	<i>Z.virens</i>	Island	0.00218	0.00043	0.19569	0.00038	0.00166	0.22898
Zosterops	<i>Z.pallidus</i>	<i>Z.borbonicus</i>	Continental	0.00205	0.00035	0.17048	0.00029	0.00141	0.20435
Zosterops	<i>Z.virens</i>	<i>Z.borbonicus</i>	Continental	0.004490	0.00080	0.17844	0.00097	0.00463	0.20842
Ficedula	<i>Fi.albicollis</i>	<i>Fi.speculigera</i>	Continental	0.00418	0.00065	0.15502	0.00151	0.00830	0.18185
Ficedula	<i>Fi.semitorquata</i>	<i>Fi.speculigera</i>	Continental	0.00372	0.00060	0.16031	0.00269	0.01384	0.19446
Ficedula	<i>Fi.hypoleuca</i>	<i>Fi.speculigera</i>	Continental	0.00351	0.00056	0.15935	0.00175	0.00904	0.19362
Ficedula	<i>Fi.speculigera</i>	<i>Fi.albicollis</i>	Continental	0.00345	0.00055	0.15985	0.00097	0.00493	0.19631
Darwin Finches	<i>Ce.olivacea</i>	<i>Ce.fuscaE</i>	Island	0.00193	0.00035	0.18304	0.00027	0.00118	0.22832
Darwin Finches	<i>G.septentrionalisW</i>	<i>Ce.olivacea</i>	Island	0.00180	0.00031	0.17333	0.00033	0.00149	0.21897
Darwin Finches	<i>Ce.fuscaE</i>	<i>Ce.olivacea</i>	Island	0.00051	0.00013	0.25737	0.00019	0.00057	0.33101
Darwin Finches	<i>Pl.crassirostrisZ</i>	<i>Ce.olivacea</i>	Island	0.00144	0.00032	0.21875	0.00022	0.00079	0.27822
Darwin Finches	<i>Pi.inornataC</i>	<i>Ce.olivacea</i>	Island	0.00131	0.00029	0.22298	0.00036	0.00133	0.27235
Darwin Finches	<i>Ce.fuscaL</i>	<i>Ce.olivacea</i>	Island	0.00246	0.00042	0.17250	0.00070	0.00327	0.21465
Darwin Finches	<i>Ca.pallidusZ</i>	<i>Ce.olivacea</i>	Island	0.00149	0.00028	0.19009	0.00010	0.00041	0.23349
Darwin Finches	<i>G.conirostrisE</i>	<i>Ce.olivacea</i>	Island	0.00255	0.00044	0.17110	0.00041	0.00195	0.20801
Darwin Finches	<i>G.difficilisP</i>	<i>Ce.olivacea</i>	Island	0.00180	0.00033	0.18333	0.00038	0.00167	0.22543
Parus	<i>Pa.major</i>	NA	Continental	0.00375	0.00050	0.13431	NA	NA	NA
Phylloscopus	<i>Ph.trochilus</i>	NA	Continental	0.01249	0.00139	0.1116	NA	NA	NA
Australian Finches	<i>T.guttata castanodis</i>	<i>Po.acuticauda</i>	Continental	0.01009	0.00120	0.11853	0.00109	0.00856	0.12702
Australian Finches	<i>Po.acuticauda</i>	<i>T.guttata castanodis</i>	Continental	0.00698	0.00090	0.12876	0.00076	0.00526	0.14493
Fringilla	<i>Fr.coelebs</i>	<i>Fr.teydae</i>	Continental	0.01036	0.00127	0.12258	0.00119	0.00869	0.13703
Fringilla	<i>Fr.coelebs</i>	<i>Fr.teydae</i>	Island	0.00181	0.00033	0.18212	0.00032	0.00151	0.21456
Fringilla	<i>Fr.teydae</i>	<i>Fr.coelebs(M)</i>	Island	0.00047	0.00013	0.28326	0.00010	0.00029	0.34870

**Table S2:  $\pi_N$ ,  $\pi_S$  and  $\pi_N/\pi_S$  as estimated by the diversity-based (meth.1) and the SFS-based (meth.2) methods (Related to Figures 1 and 2).** For the method 2, *P. major* and *P. trochilus* were not excluded for the computations (no phylogenetically relevant outgroup information available).

<https://tinyurl.com/OSFWithinGenomeVariation> for additional information regarding the method 2.

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