Tropical island endemic birds' demographic responses to climate are modulated by habitat availability and species traits

Ratnesh Karjee[1, †], Vikram Iyer[1, †], Durbadal Chatterjee[1, †], Rajasri Ray[2], Kritika M. Garg[1,3], Balaji Chattopadhyay[4,*]

[1]Department of Biology, Ashoka University, Ashoka University, Sonipat, Haryana, India
[2]Centre for Studies in Ethnobiology, Biodiversity and sustainability (CEiBa), Malda, West Bengal, India
[3]Centre for Interdisciplinary Archaeological Research, Ashoka University, Sonipat, Haryana, India
[4]Trivedi School of Biosciences, Ashoka University, Sonipat, Haryana, India

[†] These authors contributed equally to this work
*Corresponding author: Dr. Balaji Chattopadhyay
Email address: balaji.chattopadhyay@ashoka.edu.in

Abstract

Tropical islands are ideal test sites for evolution in isolation. One reason for this is their complex geologic pasts which have affected their species distribution patterns. Birds are a well-studied model clade for this and have had complex, clade-wise colonisation and diversification pathways on tropical island archipelagos. Many such events occurred during periods of Quaternary sea-level fall resulting in many island landmasses connecting to each other and to continents, along with habitat availability changes. We reconstructed the demographic history of a panel of tropical, single-island endemics using Pairwise Sequential Markovian Coalescent (PSMC), reconstructed their habitat availability during the Last Glacial Period and Holocene, and checked for their correlations with species traits using bayesian multivariate regression models. We observed that 24 out of 28 species had an increase in habitat availability from the LIG to the LGM. From the LGM till present day, habitat decreased for 19 species. PSMC analyses revealed that most species experienced a decline in effective population size (Ne) from the LIG to the LGM, and that most species have entered the holocene with low values of genetic diversity. Diet specialists and large-bodied species showed a decrease in Ne between LIG to LGM. We also observed a strong passerine-specific signal for correlations between habitat availability and change in Ne. Our results indicate that tropical island endemics are sensitive to climatic fluctuations, their responses are dictated by species traits, and their plastic response to habitat availability could be a consequence of their ability to rapidly diversify.

Keywords: Climate change, Effective population size, Genetic diversity, Tropical endemic island birds, Demographic history, Species Distribution Modelling, PSMC

Introduction

Tropical islands of the Indo-Australian Archipelago (IAA), the Indo-Pacific, and the Caribbean and Atlantic have had complex geological pasts that have affected their species distribution patterns. While several Pacific islands are true oceanic islands arising *de novo* from the seafloor, many islands of the Caribbean and the IAA were once connected with each other or to the continental landmasses during periods of global sea-level fall in the Quaternary (Lohman et al., 2011; Voris, 2000). These make tropical islands an important natural system to study macroevolutionary processes. Birds are an ideal clade for this because they are taxonomically well-characterised, are ecologically well-studied, and charismatic. Many avian lineages have arisen on tropical islands during the Pleistocene (Andersen et al., 2015; Garg et al., 2018; Irestedt et al., 2013; Moyle et al., 2009), concomitant with complex, clade-wise colonisation and recolonisation trajectories (Filardi and Moyle, 2005; Jønsson et al., 2008, 2011b, 2014) including colonisations of the mainland (Jønsson et al., 2011a) and repeated, independent colonisation events (Cibois et al., 2011).

The formation of contiguous landmasses and subsequent increases in available habitat during periods of Quaternary sea-level fall facilitated many of these colonisation pathways (Andersen et al., 2015; Cros et al., 2020; Irestedt et al., 2013; Moyle et al., 2009; Ng et al., 2017; Pujolar et al., 2022), although non-conforming colonisations due to extreme dispersal events are documented as well (Moyle et al., 2013). The habitat type and quality of these intermittently exposed landmasses varied, ranging from open savannah biomes to lowland forests (Cannon et al., 2009; Lohman et al., 2011). In the case of stratified elevational gradients, with tropical upland montane

forests expanding onto lower slopes during periods of global cooling, upland montane species could disperse across otherwise persistent dual barriers of land and sea (Cannon et al., 2009).

With such complex biogeographic pasts, tropical, single-island endemics represent either refugial populations, or *in-situ* diversifications as explained by taxon cycles (Ricklefs, 1970; Ricklefs and Cox, 1978, 1972). Being confined to single islands, these species are exceptionally vulnerable to ongoing anthropogenic climate change which is unprecedented and unlike past Pleistocene and early Holocene climatic changes (Crowley, 1990). In spite of this, knowing the past can inform future conservation efforts. This is exacerbated because we are currently experiencing a period of relatively high sea levels with reduced habitat availability for species resulting in population bottlenecks across taxa (Hewitt, 2000; Willis et al., 2004) including birds (Nadachowska-Brzyska et al., 2015; Smith et al., 2021).

Pairwise Sequential Markovian Coalescent (PSMC) is a powerful method to reconstruct the effective population size (Ne) for a species using a single diploid genome (Li and Durbin, 2011a) and has been used to infer demographic history across taxa (Chattopadhyay et al., 2019; Kim et al., 2016; Kozma et al., 2016; Murray et al., 2017; Nadachowska-Brzyska et al., 2015). Using this along with paleo-ecological niche modelling allows us to directly correlate the demographic history of a species with its distributional range at different time points (Chattopadhyay et al., 2019). We perform these analyses on a global panel of tropical single-island endemics to understand the effects of past climatic changes on species with assumed low genetic diversity owing to their status as refugial species or newly arisen lineages.

Methods:

Species selection

We queried Avibase (Lepage et al., 2014) for all species endemic to tropical islands and selected all species for which assembled whole genome sequences were available on GenBank using short-read data from the Illumina platform. We only selected species that had not been analysed using similar methods already. We excluded genomes assembled from museum specimens. This resulted in a panel of 30 species (Table 1).

Pairwise Sequential Markovian Coalescent (PSMC) analyses

For each assembled diploid genome, we identified the contigs corresponding to the sex chromosomes using Satsuma ver. 2.0 (Grabherr et al., 2010) by aligning contigs to a *Gallus gallus* (chicken; BioSample: SAMN02981218) genome as a reference. All contigs mapping to the sex chromosomes were removed. Next, we obtained all available Illumina short reads for each species from the Sequence Read Archive (SRA) database of the NCBI, and checked them for errors using FastQC (Andrews, 2010). We used Trimmomatic Bolger et al., 2014) for preprocessing and trimming the reads. The cleaned reads were aligned to the autosomes using BWA-MEM ver. 0.7.17 (Li, 2013). Next, we used SAMtools ver. 1.10 (Danecek et al., 2021) to merge all the resulting files to generate a single bam file for each species. We further sorted and removed duplicates using SAMtools and estimated the depth of coverage for each species. We excluded species with a depth of coverage < 18X. This is a sufficient value of coverage for PSMC analyses (Li and Durbin, 2011b). Next, we implemented the SAMtools mpileup-bcftools

pipeline to identify SNPs. The minimum and maximum depths for calling SNPs was set to one-third and double the mean depth respectively following Nadachowska-Brzyska et al., (Nadachowska-Brzyska et al., 2015).

We used three sets of parameters for PSMC analyses and looked for consensus trends amongst them because PSMC analyses can result in spurious peaks of effective population size (Hilgers et al., 2024). We used the following parameter sets for PSMC analyses: –t5 –b –r1 –p "4 + 30 * 2 + 4 + 6 + 10", –t5 –b –r1 –p "2 + 2 + 30 * 2 + 4 + 6 + 10", and –t5 –b –r1 –p "1 + 1 + 1 + 1 + 30 * 2 + 4 + 6 + 10". We performed 30 iterations for parameter optimisation and ran 100 bootstrap replicates to judge the uncertainty in our estimates. Bootstrapping was done by randomly sampling chromosome segments with replacement and running PSMC on them. To plot the results from the PSMC analyses, we used previously estimated values of mutation rates and generation times for passerines (1.4 x 10e–9 years/site and 2 years respectively; (Ellegren et al., 2012; Nadachowska-Brzyska et al., 2016) and non-passerines (1.91 x 10e–9 years/site and 1 year respectively) (Nam et al., 2010) (Supplementary material S1, supplementary table S4).

Species and climate records

We performed reconstructions of paleohabitats through ecological niche models and reconstructed species distributions from four time periods: the Last Interglacial (LIG, approx. 110,000–130,000 years ago), the Last Glacial Maximum (LGM, approx. 20,000 years ago), the Mid-Holocene (MDH, approx. 6000 years ago) and Current (CUR, present day).

Species records:

We used R (ver. 4.2.1; R Core Team, 2021) for all paleo-habitat modelling analyses. We accessed the location records of 20 bird species from the Global Biodiversity Information Forum (GBIF) in September, 2023 using the "rbgif" package (ver. 3.7.9) (Chamberlain and Boettiger, 2017) in R. We discarded duplicates and retained only human observed records using the "tidyverse" (v-2.0.0) package (Wickham and RStudio, 2023) followed by the 'CoordinateCleaner' package (v-3.0.1) (Zizka et al., 2023). We used the "spThin" package (Aiello-Lammens et al., 2014) to account for spatial autocorrelation and finally discarded spurious distribution records like records overlaying water bodies, buildings, roadways, and railways using QGIS (v-3.34+; https://www.qgis.org/).

Climatic variable selection:

We used 19 climate variables (labelled BIO1 – BIO19; see supplementary file) for the four different time periods. We downloaded CHELSA (https://chelsa-climate.org/; Karger et al., 2021) climate predictors at a resolution of 2.5 arc-minutes (~5 km) for all regions except for *Amazona guildingii* from Saint Vincent where we used a resolution of 30 arc-seconds (~1km). For the latter, we used WORLDCLIM (https://www.worldclim.org/; Fick and Hijmans, 2017) for data for the LIG and MDH while CHELSA was used for the LGM and CUR.

We followed Chattopadhyay et al., (2019) and used a global dataset approach to account for idiosyncratic biases due to smaller datasets to extract the location points of each endemic-island group against each climatic variable. We tested for multicollinearity using variance inflation

factor (VIF) using the 'usdm' R package (Naimi, 2023) and considered variables for further analyses if their VIF value was ≤ 5.

Habitat Suitability Modelling and Area Calculation:

We used R to reconstruct paleo-climatic suitable habitat for 28 endemic island birds through ecological niche models for the four time periods considered. For this, we accessed the Global Biodiversity Information Forum (GBIF) to extract our species' occurrence records. We could not perform ENM analyses for two species due to a paucity in the number of GBIF occurrence points for them (Table 1).

Data partitioning and model evaluation

For each species, we used available occurrence records from the present day to generate pseudo-absence data points. We generated 500-10,000 pseudo-absence/background points for each species depending upon the area of the island (Supplementary table S5), except for *Amazona guildingii* endemic to Saint Vincent where we generated 40 points. Saint Vincent's small land area could not accommodate more points than this. We used a subset of bioclimatic variables to generate a weighted average ensemble species distribution model (eSDM) for each island group. eSDMs were implemented in the R package "sdm" (v-1.2.37; Naimi and Araujo, 2016) applying the 'MaxEnt', 'GLM', and 'BRT' algorithms. eSDMs account for the limitations of different models by generating a weighted average of multiple models (Araújo and New, 2007; Dormann et al., 2018; Naimi and Araujo, 2016). We used k-fold cross-validation (CV) with replication for each method for training and test datasets across each endemic island group (Supplementary table S5). Model accuracy was measured using the Area Under the Curve

(AUC) and True Skill Statistics (TSS) metrics. We first performed the above analyses for the present-day (CUR) distribution using the weighted-average of AUC and TSS. AUC and TSS values greater than 0.9 and 0.75 respectively have been shown to be indicators of superior model performance (Ahmad et al., 2019) and we chose a similar threshold (AUC ≥ 0.9 & TSS ≥ 0.8) to get the best ensemble model for most of the species except for 10 species for which data quality was poor (Supplementary table S5). Models for the other time points: the LIG, LGM, and MDH, were generated using the eSDM model generated based on CUR data.

Suitable area analysis

All spatial analyses were carried out using the R package 'terra' (ver. 1.7.13) (Hijmans et al., 2024). Equal area projections were used to calculate the absolute suitable area of each species across the four time-periods. To account for a spherical Earth and the limitations of landmass depiction of the original eSDM raster (World Geodetic System 1984) we reprojected it into a pseudocylindrical projection (Eckert IV). Further, we used the average quantile threshold pixels to measure the availability of absolute suitable areas for the LIG, LGM, MDH, and CUR periods (Supplementary table S6).

Statistical Analyses

We checked for associations between Ne and habitat change during the Last Glacial Period (from LIG to LGM) (LGP) using Cramer's V implemented in the"polycor" package in R (Fox, 2022). Cramver's V varies between -1 to 1, with values closer to 0 suggesting no-correlation. This was done for the entire dataset, and then for passerines and non-passerines separately.

We further explored the effects of species biology, habitat, and phylogenetic constraint on the fluctuation in Ne during the LGP using Bayesian Multilevel Models (MLMs), using the "brms" package in R (Bürkner, 2018). Our fixed effect predictors were habitat change from the LIG to LGM, diet (invertivore, frugivore, or omnivore), body mass, and clade identity (passerine and non-passerine). The latter allows us to check if belonging to the rapidly diversifying passerine clade results in a signal. We also included country (the island/archipelago a species is endemic to) as a random effect variable for the analysis to account for country-specific effects. For the response variable i.e., the change in Ne, a Bernoulli distribution with a logit link because it is a binary response variable.

We ran a series of models (n=12) to find the best-fit model (brms11, S8) based on leave-one-out cross-validation. We generated a total of 16,000 posterior samples by using the No-U-Turn Sampler (Hamiltonian Monte Carlo) algorithm with 4 chains with 5000 iterations each (with 1000 warm-up iterations; supplementary information S3). Further, we estimated the posterior parameters with 95% confidence intervals to find negative or positive associations between the Ne and its predictors. In addition, we assessed the posterior convergence of the sample through R-hat statistics ($\hat{R} = 1$) where values close to 1 suggest an ideal convergence. We also reported the effective sample size for bulk and tail distributions (Supplementary table S7).

Results

Bird species panel

Our final species panel comprises 30 tropical single-island endemic bird species. Out of these, PSMC analyses were possible for 22 species and ENM was possible for 28 species. Both PSMC and ENM analyses could be done successfully for 20 species (Table 1). These included seven Papuan species, five Philippine species, three Caribbean species, and three species from the Bismarck Archipelago. Of these 20 species, 13 species are passerines, with two from the white-eye family (Zosteropidae). Of the non-passerines, two species are parrots (family Psittacidae). All other families are represented by single species.

Paleo-habitat reconstruction

Among the 19 climatic variables used, we observed precipitation of the warmest quarter (BIO18) to contribute the most for each island endemic bird species except for the Caribbean species *Amazona guildingii*. 24 out of the 28 bird species experienced an increase in suitable habitat from the LIG to the LGM (Supplementary table S6). 11 out of 13 Papuan species showed an increase in habitat availability from the LIG to the LGM, with *Cicinnurus regius* and *Pseudorectus ferrugineus* as exceptions. All Philippine species showed an increase in habitat from the LIG to the LGM as well (Figure 1, Supplementary information S2). Two out of the three Caribbean species experienced a decline in suitable habitat during this period. Of the remaining species, all showed an increase in available habitat. Upland Papuan species remained confined to upland montane regions at all the time points we reconstructed available habitat, with

Rhagologus leucostigma as a notable exception (Supplementary information S2). Papuan lowland species remained largely confined to regions which were not newly-exposed landbridges at all times as well. From the LGM to the present day, habitat decreased for 19 out of the 28 bird species, and two species experienced no change (Supplementary table S6). For the present study, we primarily concentrate on habitat fluctuation between the LIG and the LGM as this is the period for which we have comparative evidence of fluctuations of both habitat as well as genetic diversity.

Strong Quaternary fluctuations in genetic diversity

PSMC analyses could be successfully done for 22 species (Table 1). Results indicate large genetic diversity variations in almost all bird species, corresponding to the Quaternary climate shifts (Figure 2). The demographic history of these species reconstructed using Pairwise Sequentially Markovian Coalescent (PSMC) analyses extends back over a million years (Supplementary information S1). Reconstructed Ne values were generally concordant across the three PSMC settings used, except for five species where Ne values had large differences across PSMC settings for Ne values at the LIG and LGM. However, in these species as well, trends of Ne increase or decrease from the LIG to LGM were robust across all three PSMC models considered. *Centropus unirufus, Dicaeum eximium, Irena cyanogastra, Sterrhoptilus dennistouni, Zosterops hypoxanthus* were the six species which had large differences (Supplementary information S1). We found no significant difference between the different sets of PSMC settings used (Kruskal-Wallis test, χ^2= 0.217, DF = 2, p = 0.897).

The 14 passerine species we analysed showed overall lower Ne values in the LGM as compared to the LIG (Figure 1). We obtained similar results for non-passerines as well, with *Rhynochetos*

jubatus as a notable exception using the –p "4 + 30 * 2 + 4 + 6 + 10" setting, displaying a large peak followed by a crash in Ne (Supplementary information S1). This is likely a PSMC artefact, because plots using other parameter settings did not show peak (Supplementary information S1). Along with overall lower values, we also see a smaller range of Ne values in the LGM as compared to the LIG (Figure 2).

Correlation between historical fluctuations in Ne and distribution

Habitat change was poorly associated with change in Ne for the 20 species for which both PSMC and ENM analyses were possible (Cramer's V = 0.15). However, passerine species only showed a strong association (Cramer's V = 0.96), while non-passerines showed a weak negative association (Cramer's V = –0.15).

Bayesian multivariate regression models revealed an overall fluctuation in Ne was associated with species biology and habitat change during the LGP even after controlling for the geographical island group (Figure 3). Most confidence intervals and beta coefficients did not overlap with zero (Figure 3) suggesting significant relationships. We found a positive association between change in habitat area (LIG to LGM) and Ne (β = 9.45, 95% CI: [1.95, 21.1]). This means that species with increasing habitat area in the LGP also showed an increase in Ne. Change in Ne and body mass showed a significant negative association (β = −8.63, 95% CI: [16.27, –2.61]). That is, large-bodied species showed decreases in Ne during the LGP. Diet specialists like frugivores (β = –11.89, 95% CI: [–22.65, –2.99]) and invertivores (β = –11.7, 95% CI: [–22.66, –2.94]) also showed significant negative associations with population change. However, omnivores (β = –1.39, 95% CI: [–13.38, 11.5]) did not show any association with population change. Whether or not a species was a passerine was an important predictor of Ne

only in combination with the change in habitat from LIG to LGM (β = 7.97, 95% CI: [1.82, 16.91], suggesting that passerines respond positively to habitat change, as suggested by Cramer's V as well. The interaction between habitat change and body mass (β = 10.05, 95% CI: [–0.3, 24.41) suggests that there is no impact of habitat change in larger species. Finally, the random intercept for Country (sd(Intercept)) showed a marginal positive influence (β = 0.85, 95% CI: [0.04, 2.24]) (Figure 3, Supplementary table S9)

Discussion

Island birds are vulnerable to the effects of climate change

Our results on the reconstruction of the fluctuations in paleohabitat and genetic diversity (Ne) during the Last Glacial Period from bird species across islands like the Caribbean, the Philippines, and Papua (Figure 2, Supplementary information S2) points towards the vulnerability of island birds to climatic fluctuations. While habitat change is a more direct consequence of climate change, changes in genetic diversity depend on such shifts in habitat, making these species particularly sensitive to a changing environment. In response to landmass expansion, most species in our panel across islands showed an overall increase in their genetic diversity from the LIG to the LGM (Figure 1, Supplementary information S1). The current climate crisis has greatly imperilled biodiversity with the documented loss of many vertebrate species (Steadman and Martin, 2003; Tan et al., 2023; Willis et al., 2004). Island birds are particularly vulnerable to fluctuations in climate and associated habitat changes. For example, fossil evidence has revealed the extinction of several species in the Caribbean since the LGM (Morgan and Woods, 1986; Orihuela et al., 2020; Steadman et al., 1984). Climate warming, sea

level rise and changes in vegetation are all associated with this loss and flightless birds and endemics are particularly prone to extinction (Fromm and Meiri, 2021).

Habitat loss, rise in sea level and warming temperatures can rapidly accelerate species extinction, particularly in the tropics (Şekercioğlu et al., 2012). Our study provides indirect evidence of the susceptibility of island birds to climate change using effective population size as an indicator of genetic diversity. Effective population size, and in extension genetic diversity are associated with survival of a species and its extinction risks (Frankham, 2005). Coalescent effective population size as used in PSMC is an important predictor of species vulnerability to extinction (Brüniche-Olsen et al., 2021; Wilder et al., 2023). Thus an evolution-informed understanding of species vulnerability to climate change and their associations with paleohabitats can be an important tool to predict species vulnerability to the current climate crisis and future extinction risk (Brüniche-Olsen et al., 2021; Chattopadhyay et al., 2019; Gabrielli et al., 2024; Germain et al., 2023).

Island birds entered the Holocene with low genetic diversity

Our overall results show that both passerine and non-passerine island endemics have entered the Holocene with low genetic diversity (Figure 1). A loss of genetic diversity predisposes species to extinction (Mays et al., 2018; Spielman et al., 2004), with a potentially causal relationship for birds (Evans and Sheldon, 2008). Many of these species are Southeast Asian single-island endemics where rapid habitat loss is ongoing (Sodhi et al., 2004). Available models estimate large amounts of exposed landbridge habitat available to our panel's Papuan species to range from lowland evergreen to seasonal rainforest, with an expansion of upland habitats of evergreen to seasonal rainforest. Transitional hill forest formed an ecotone between these two (Cannon et al., 2009). Our results show that large amounts of this intermittently exposed landbridge habitat remained uninhabited by our species. This is supported by the fact that most of our species are dense forest inhabitants (Supplementary table S9).

A strong, passerine association might be driven by their rapid diversification

Passerines are a hyperdiverse clade with over 6000 species representing over 60% of extant avian diversity. The most recent, fossil-calibrated passerine phylogeny (Oliveros et al., 2019) shows that passerines began diversifying in the Middle (47 mya) to Late Eocene (38–39 mya) with increasing diversification rates suggested as we move towards the present. Estimates based on currently available fossil data show that crown passerines originated in the Australo-Pacific region (Oliveros et al., 2019), although fine-grained understanding is unclear. (Moyle et al., 2016). This places the many Papuan and Australian species in our panel close to the passerine diversification centre which is known to have rapid diversification rates (McCullough et al.,

2022). Because bird lineages are known to have arisen on tropical islands in the Pleistocene (Andersen et al., 2015; Irestedt et al., 2013; Moyle et al., 2009), it is likelier that the Southeast Asian species in our panel represent newly arisen lineages over refugia. This is supported by the fact that several of these species belong to small, often oligotypic families such as Oreoicidae (*Aleadryas rufinucha*), Ptilonorhynchidae (*Amblyornis subalaris*), Cnemophilidae (*Cnemophilus loriae)*, Eulacestomatidae (*Eulacestoma nigropectus*), Ifritidae (*Ifrita kowaldi*), Machaerirhynchidae (*Machaerirhynchus nigripectus*), and Rhagologidae (*Rhagologus leucostigma*). Moreover, our panel includes two Zosteropidae members including one *Zosterops* species. *Zosterops* is a well-studied passerine clade that has undergone explosive radiation on Southeast Asian islands (Engler et al., 2021; Gwee et al., 2020; Manthey et al., 2020; Vinciguerra et al., 2023), and the Zosteropidae members in our panel likely represent newly-arisen lineages as well. Many of these species belong to poorly studied tropical genera for which species level divergence times are unavailable. Our species likely represent newly-arisen lineages, possibly belonging to currently rapidly-diversifying clades. The strong association between change in Ne and available habitat area (Cramer's V = 0.96; figure 3, $\beta = 9.45$) within our panel of species reveals that the demographic history of these island birds are strongly plastic to the environment, most possibly as a consequence of their ability to rapidly diversify.

Non-passerines representing a paraphyletic outgroup do not show this trend (Cramer's V = –0.15). The seven non-passerine species for which both ENM and PSMC analyses were possible belong to six different families (Supplement), representing a diverse sample across the avian phylogeny and precluding any non-passerine phylogenetic insight. Notably, habitat area is positively correlated with genomic diversity in a clade non-specific manner for birds in general (Brüniche-Olsen et al., 2021, 2019).

Species traits influenced historic fluctuations in Ne during the LGP

The interplay of species traits and habitat availability determine how Ne fluctuate with time in non-endemic birds (Brüniche-Olsen et al., 2021), and our results confirm this for tropical island endemics as well. Habitat change in the LGP was positively associated with Ne fluctuations (Figure 3, $\beta = 9.45$), that is, species which showed an increase in habitat in the LGP also showed a concurrent increase in Ne. While diet generalists like omnivores showed no significant correlation with Ne fluctuations, specialists like frugivores (Figure 3, $\beta = -11.89$) and invertivores (Figure 3, $\beta = -11.7$) showed significant negative association with fluctuation in Ne, implying that specialist species tended to show decreases in Ne in the LGP. Previous work has shown that large-bodied species have lower values of standing genetic diversity at a given time point (Brüniche-Olsen et al., 2021, 2019; Eo et al., 2011). We find large-bodied species to show a negative association with Ne fluctuations (Figure 3, $\beta = -8.63$) as well. This implies that Ne for large-bodied species have decreased in the LGP. Traits like body size and diet determine extinction risk (Ripple et al., 2017; Willis et al., 2004), and our results add to the understanding of how traits modulate Ne changes through time.

Assessing the relative contribution of species traits and habitat availability in determining Ne requires their quantitative measurements. Our methods generated values for available habitat at various time points (Supplementary table S5). However, Ne values can so far only be reconstructed using coalescent methods like PSMC. These values depend upon the parameter settings used. While we find these to be generally concordant across settings (Kruskal-Wallis, $p = 0.897$, Supplementary table S4), the estimates vary. We therefore chose to cautiously measure only the direction of change (increase or decrease) and not use precise values.

Caveats of PSMC analyses

Coalescent methods for inferring demographic history like PSMC can trace a local population's demographic history rather than the entire species history (Gattepaille et al., 2013; Heller et al., 2013; Ptak and Przeworski, 2002). Population structure is thus a confounding factor. However, this is unlikely to be a problem given that all our species are single-island endemics. Large peaks followed by apparent collapses in Ne have also recently been shown to be an artefact of PSMC analyses (Hilgers et al., 2024). We try three different parameter combinations, and look for consensus amongst them in order to try and mitigate this. Because reconstructed Ne values are inferred based on these parameter settings, we do not use them directly for analyses, instead looking at the direction of population size change (increase/decrease/no change). Lastly, we emphasise that Ne is a scaled value of the real population size (Wang et al., 2016), and is measured to be up to one-tenth of the real population size in wild populations (Frankham, 1995). We emphasise caution in interpreting Ne results as a proxy for real population size.

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Figures

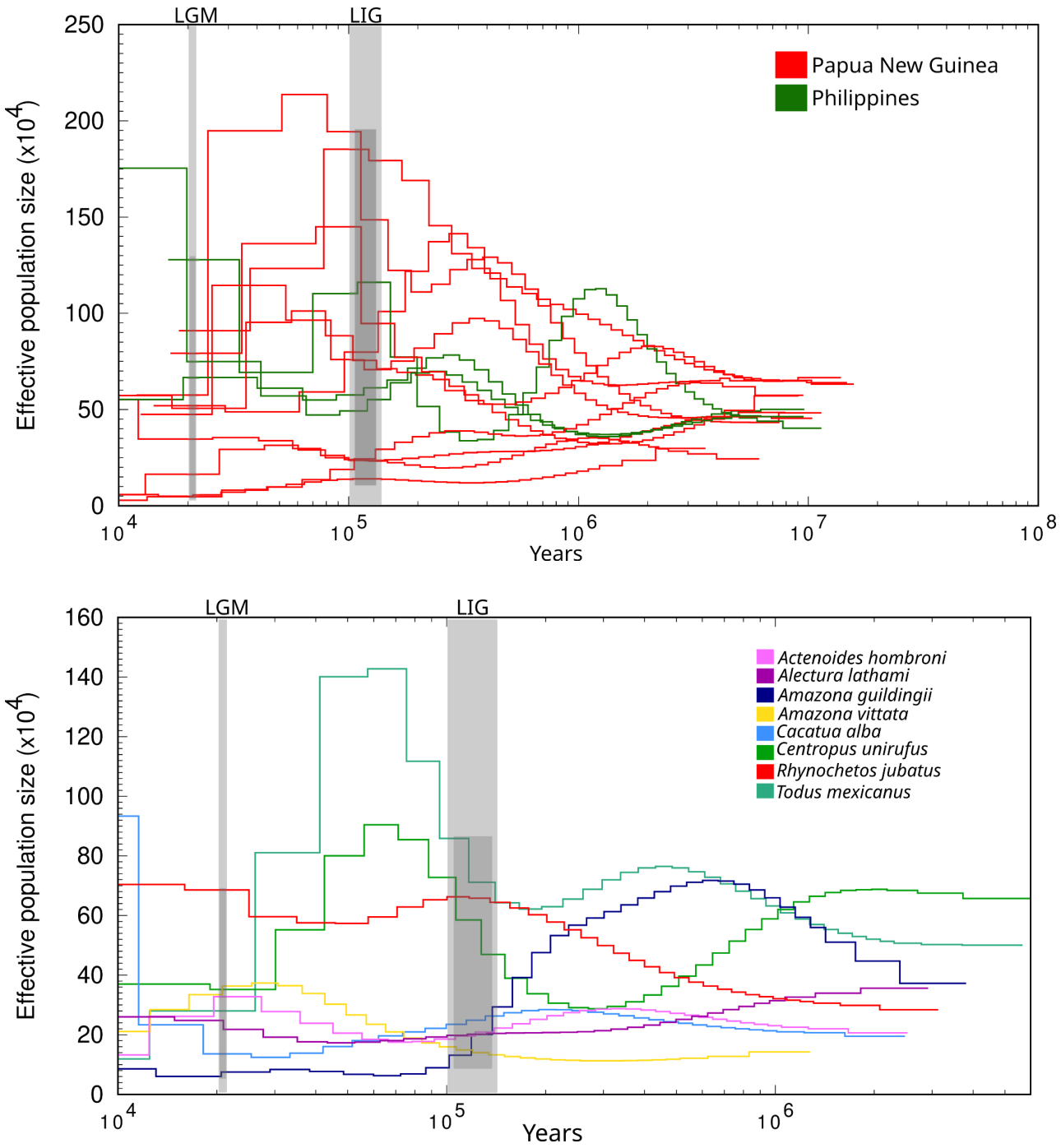

Figure 1:

PSMC plots for passerines (above) and non-passerines (below) using the setting –p "2 + 2 + 30 *

2 + 4 + 6 + 10”. *Zosterops hypoxanthus* displayed exceptionally high Ne values and was not plotted. LGM = Last Glacial Maximum. LIG = Last InterGlacial. The grey bands indicate approximate durations of the LGM and the LIG. Darker insets within the grey bands indicate the approximate spread of Ne at the LGM and the LIG.

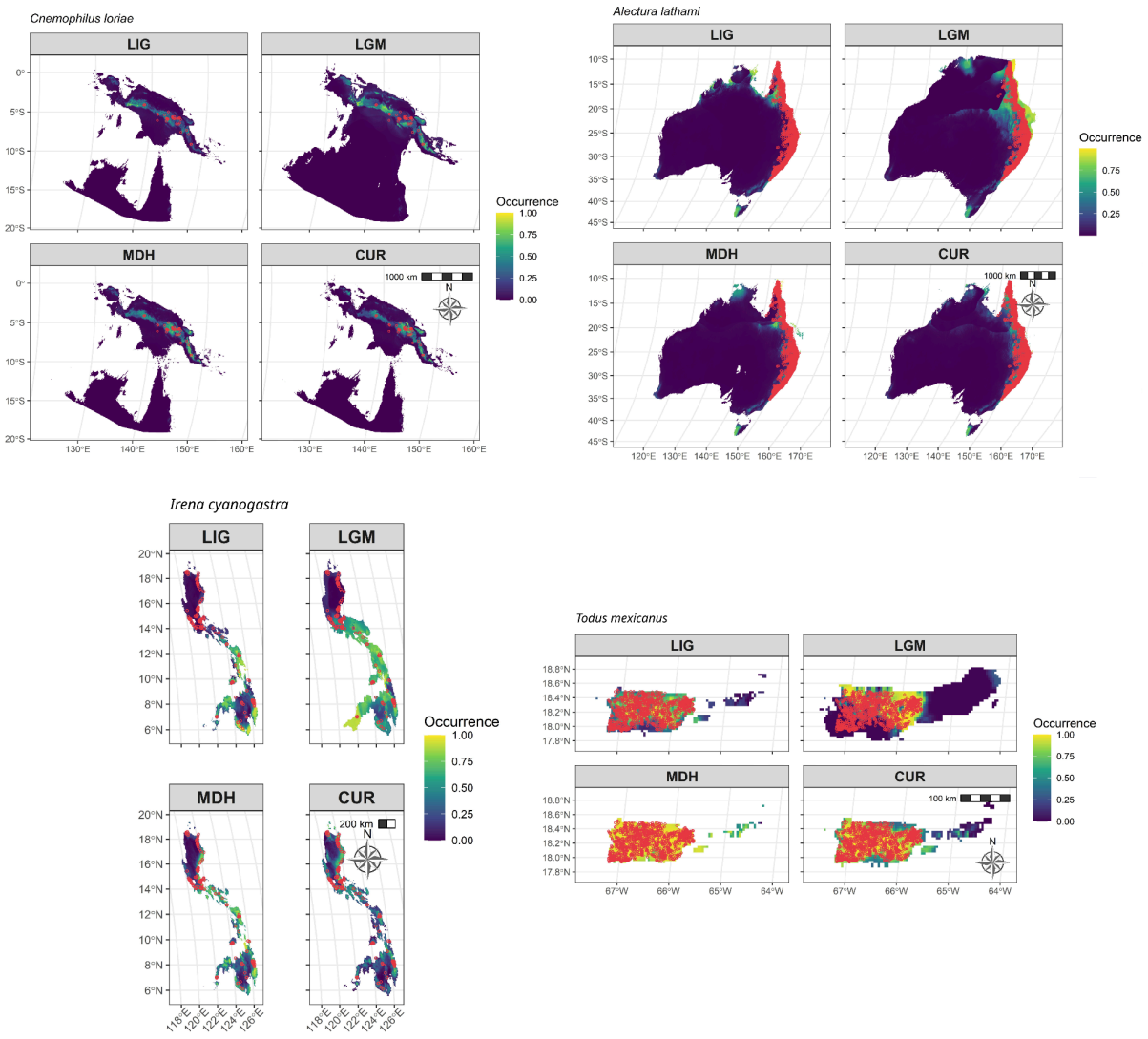

Figure 2:

Example ENM plots for species from Papua (*Cnemophilus loriae)*, Australia (*Alectura lathami*), the Philippines (*Irena cyanogastra*), and the Caribbean (Puerto Rico, *Todus mexicanus*). LIG = Last Interglacial. LGM = Last Glacial Maximum. MDH = Mid Holocene. CUR = Current. The continuous heatmap represents the probability of occurrence of the species and red points are known occurrences from GBIF.

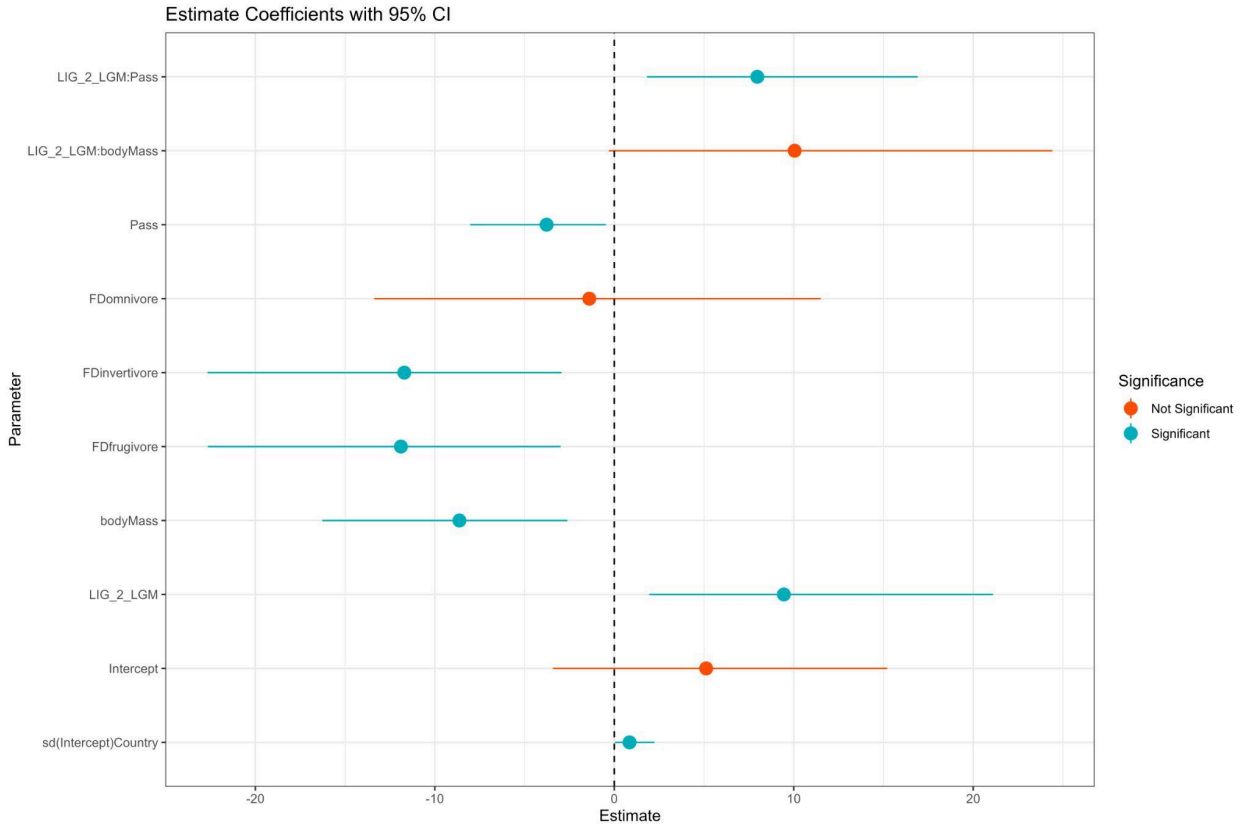

Figure 3:

Results of the best Bayesian multivariate regression model performed. The response variable represents whether or not the Ne increased (=1) or decreased (=0) during the LGP. Circles represent mean values and lines represent 95% confidence intervals. Model parameters and coefficients are in S9.

Tables

Species	PSMC	ENM	Endemic Region	Passerine	Family
Actenoides hombroni	y	y	Philippines	n	Alcedinidae
Aleadryas rufinucha	y	y	Papua New Guinea	y	Oreoicidae
Alectura lathami	y	y	Australia	n	Megapodiidae
Amazona guildingii	y	y	St Vincent	n	Psittacidae
Amazona vittata	y	y	Puerto Rico	n	Psittacidae
Amblyornis subalaris	y	n	Papua New Guinea	y	Ptilonorhynchidae
Cacatua alba	y	n	Indonesia	n	Cacatuidae
Centropus unirufus	y	y	Philippines	n	Cuculidae
Chaetorhynchus papuensis	n	y	Papua New Guinea	y	Rhipiduridae
Cicinnurus regius	y	y	Papua New Guinea	y	Paradisaeidae
Cnemophilus loriae	y	y	Papua New Guinea	y	Cnemophilidae
Dicaeum eximium	y	y	Bismarck Archipelago	y	Dicaeidae
Diphyllodes magnificus	y	y	Papua New Guinea	y	Paradisaeidae
Eulacestoma nigropectus	n	y	Papua New Guinea	y	Eulacestomatidae
Ifrita kowaldii	n	y	Papua New Guinea	y	Ifritidae
Irena cyanogastra	y	y	Philippines	y	Irenidae
Machaerirhynchus nigripectus	y	y	Papua New Guinea	y	Machaerirhynchidae
Myiagra hebetior	y	y	Bismarck Archipelago	y	Monarchidae
Oreocharis arfaki	n	y	Papua New Guinea	y	Paramythiidae
Pachycephala philippinensis	y	y	Philippines	y	Pachycephalidae
Paradisaea raggiana	y	y	Papua New	y	Paradisaeidae

			Guinea		
Paradisaea rubra	n	y	Indonesia	y	Paradisaeidae
Parotia lawesii	n	y	Papua New Guinea	y	Paradisaeidae
Pseudorectes ferrugineus	n	y	Papua New Guinea	y	Pachycephalidae
Ptilorrhoa leucosticta	n	y	Papua New Guinea	y	Cinclosomatidae
Rhagologus leucostigma	y	y	Papua New Guinea	y	Rhagologidae
Rhynochetos jubatus	y	y	New Caledonia	n	Rhynochetidae
Sterrhoptilus dennistouni	y	y	Philippines	y	Zosteropidae
Todus mexicanus	y	y	Puerto Rico	n	Todidae
Zosterops hypoxanthus	y	y	Bismarck Archipelago	y	Zosteropidae

Table 1

The species we analyse, showing whether or not PSMC and ENM analyses were performed, the island/archipelago the species is endemic to, whether or not the species is a paserine, and the taxonomic family it belongs to.. y = yes, n = no.