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Deterministic assembly and anthropogenic extinctions drive convergence of island bird communities

Short running title: Community convergence in island avifaunas

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ABSTRACT

Aim: Whether entire communities of organisms converge toward predictable structural properties under similar environmental conditions remains controversial. We tested for community convergence in birds by comparing the structure of oceanic archipelago assemblages to their respective regional species pools.

Location: Eighteen major oceanic archipelagos of volcanic origin with global distribution

Major taxa studied: Terrestrial birds

Methods: We compiled a comprehensive database of morphological trait and phylogenetic data for 6,579 bird species, including species known to have become extinct due to human activities. We quantified morphological and phylogenetic dissimilarity among species between pairs of archipelagos, using a modified version of the mean nearest taxon distance. We tested for convergence by estimating whether overall mean turnover among archipelagos and pairwise turnover between archipelagos was lower than expected by chance.

Results: For all land-birds, we found that turnover in body plan, body mass and phylogeny among archipelagos was significantly lower than expected. Seventeen (of 18) archipelagos showed significant body plan and phylogenetic similarity with at least one other archipelago. Similar convergent patterns of community assembly were detected in different subsamples of the data (extant species, endemics, native non-endemics, and Passeriformes only). Convergence was more pronounced for extant species than for extant and extinct species combined.

Main conclusions: Consistent convergence in phylogenetic and morphological structure among archipelagic communities arises through a combination of non-random colonization and *in situ* adaptation. In addition, by including data from extinct taxa, we show that community convergence both precedes and is accentuated by the anthropogenic extinction of endemic lineages. Our results highlight the potential role of non-random extinction in generating patterns of community convergence and also show that convergence existed even prior to anthropogenic extinctions as a result of deterministic community assembly in similar environmental settings at the global scale.

Keywords: birds, community assembly, convergence, determinism, extinct species, historical contingency, island biogeography, morphological traits, oceanic archipelagos.

INTRODUCTION

Whether spatially isolated ecological communities tend to converge under similar environmental conditions towards predictable structural properties, such as traits or functional space occupied, has remained a controversial question for half a century (MacArthur, 1972; Cody & Mooney, 1978; Ricklefs & Travis, 1980; Blondel et al., 1984; Samuels & Drake, 1997; Fukami et al., 2005; Melville et al., 2006; Winemiller et al. 2015; Moen et al., 2016; Santos et al. 2016; Mazel et al., 2018). Although evolutionary convergence – the emergence of similar species traits or syndromes from divergent evolutionary starting points in

geographically distant but environmentally similar locations – is a well-established phenomenon (e.g. Losos *et al.*, 1998; Schluter, 2000; Gillespie, 2004; Muschick *et al.*, 2012; Mahler *et al.*, 2013), the question of whether convergence applies to entire communities remains open to debate. For example, historical contingencies (legacies from previous system states) vary across regions and typically generate unpredictable outcomes in the structural properties of local communities (Gould, 1989; see also discussion in Losos & Ricklefs, 2009).

A major challenge for the study of community convergence is posed by extinct taxa. In particular, if anthropogenic extinctions are non-random (e.g. Steadman, 2006; Sayol *et al.*, 2020) and biased towards outliers, such as the largest and smallest species in an assemblage (e.g. Ripple *et al.* 2017), then apparent evidence of community convergence may be explained by non-random or clustered extinctions rather than any deterministic process based on environmental filtering or evolutionary adaptation (Tobias *et al.*, 2020). Robust tests of community convergence therefore need to account for extinct taxa, particularly in island systems where anthropogenic extinctions have often altered native communities (e.g., Steadman, 2006; Boyer & Jetz, 2014; Sobral *et al.*, 2016; Sayol *et al.* 2021). However, previous studies of community convergence – most of which have focused on islands – have rarely (if ever) accounted for extinctions.

To date, community level convergence has primarily been tested, and in some cases detected, at the level of individual islands (e.g. Gillespie, 2004; Losos, 2011; Mahler *et al.*, 2013), but has never been evaluated at the archipelago level. Yet several filtering processes operate at the scale of archipelagos (Fig. 1), with convergence generated via two primary pathways:

(a) the non-random selection of colonists reaching the archipelago from the regional species pool, resulting in greater phylogenetic or morphological similarity than expected by chance, and (b) *in situ* evolutionary change, including lineage diversification, leading to greater trait similarity among archipelagos than expected by chance (Wiens & Graham, 2005; Emerson & Gillespie, 2008; Grant & Grant, 2008; Losos & Ricklefs, 2009; Barnagaud *et al.*, 2014; Weigelt *et al.*, 2015). The relative contribution of these alternative pathways to community convergence is unclear, although they should leave different signatures in the community structure of native non-endemic and endemic lineages, respectively.

To test for community convergence in the phylogenetic and morphological structure of oceanic archipelago bird assemblages, in relation to their respective regional species pools, we compiled comprehensive data on species composition, phylogenetic history and

morphological traits for birds occurring on volcanic archipelagos across the Pacific, Atlantic and Indian oceans. Since faunal assembly is mostly sourced from larger, older and more complex continental pools, we also collected equivalent data for a far larger number of bird species occurring in the continental source pools for each archipelago (see also Graves & Gotelli, 1983; Cardillo et al. 2008; Santos et al. 2016 for previous approaches). We focused on all extant land-bird species, as well as lineages driven to extinction by anthropogenic causes. The focal archipelagos share five key features: limited land area, persistent geographical isolation, volcanic origin, tropical/sub-tropical latitude, and oceanic climate (Whittaker & Fernández-Palacios, 2007; Gillespie & Clague, 2009; Weigelt et al., 2013; Triantis et al., 2015).

Volcanic oceanic archipelagos have long been considered ideal systems for exploring the processes structuring ecological communities inasmuch as they represent replicated natural experiments in faunal assembly (e.g. Whittaker & Fernández-Palacios, 2007; Grant & Grant, 2008; Losos & Ricklefs, 2009). At the archipelagic level, island communities respond to the insular geography on evolutionary time scales, with species undergoing ‘taxon cycles’, i.e., sequential phases of expansion and contraction across an archipelago (Wilson, 1959; Ricklefs & Bermingham, 2002), and with the divergence of populations in allopatry being arguably the main driving force of diversification (Grant & Grant, 2008; Losos & Ricklefs, 2009). Thus, oceanic archipelagos can be seen as macroevolutionary metacommunities, i.e., sets of interacting island communities linked by dispersal. They therefore represent a higher level of hierarchical organization than individual islands and are amenable to framing analyses of large-scale patterns such as community-level convergence (see also Triantis et al., 2015; Whittaker et al. 2017; Valente et al. 2020).

We developed a novel framework to test for community convergence in both morphological and phylogenetic structure of archipelagic land-bird faunas relative to their respective regional species pools (Fig. 2A). To assess the influence of different assembly or disassembly mechanisms, we re-ran our analyses on five subsamples: (i) native non-endemic species, (ii) endemic species (including extinct species), (iii) a subsample with all extinct species removed, and (iv) a monophyletic group (i.e. Passeriformes) that is also the largest order of birds. Our results show that multiple dimensions of archipelagic bird communities are more similar than expected by chance, even accounting for the influence of extinction, providing strong support that community convergence arises through deterministic community assembly.

MATERIAL AND METHODS

Species lists and regional pools

Contemporary biogeographical patterns on islands have been strongly influenced by historic and pre-historic anthropogenic extinctions (Steadman, 2006; Hume, 2017; Valente et al., 2020). Thus, to understand how species' arrivals and subsequent evolutionary dynamics interact to establish patterns of trait diversity, it is important to include species known to have become extinct due to human activities. We collected data on composition and species-level traits for the avifaunas of 18 volcanic oceanic archipelagos: Austral islands, Azores, Canaries, Comoros, Cook Islands, Fernando de Noronha, Galápagos, Gulf of Guinea, Hawaii, Juan Fernández, Madeira, Marquesas, Mascarenes, Pitcairn, Revillagigedo, Samoa, Society, and Tristan da Cunha (Tables 1 & S1; Fig. 2). For each archipelago, we collated lists of the endemic and native non-endemic species, including all known species extinctions since human colonization (e.g. Steadman, 2006; BirdLife International, 2017; Hume, 2017; Sayol et al., 2020; Valente et al., 2020). A list of the data sources is found in Appendix 1 (see also Supporting Information, Data S1). Roughly one-third (157) of the species are extinct (Table S2 & Data S1). To focus our analyses on species strictly relying on terrestrial habitats, we restricted our sample to land-birds, excluding marine and aquatic species. Of 495 species in our sample, 348 (70%) are archipelagic endemics, highlighting the evolutionary independence of many archipelagic avifaunas. However, there are cases of non-endemic archipelagic species that are inferred to have colonized the archipelago in question from a nearby archipelago, such as *Anthus berthelotii* and *Serinus canarius*, both endemic to Madeira and the Canary Islands (see Valente et al., 2020). However, only 41 (8%) native non-endemic species are present on more than two archipelagos.

To generate regional pools of species as sources for the assembly of each archipelago, we identified the avifaunal regions to which they belong, based on Holt et al. (2013) (Table S3 and Fig. 2A). These 10 regions contain 6,231 land-bird species (Data S2). To validate and improve our approach, we compared the zoogeographical region assigned to each archipelago from Holt et al. (2013) with source region reconstructions based on phylogenetic relationships between island and mainland species found in the literature, when available. Despite some discrepancies, including a few cases where the species pool was a nearby archipelago rather than the mainland, we found that the zoogeographical regions in Holt et al. (2013) were closely aligned with the source region reconstructions (see Supporting Information). We also tested the sensitivity of our approach to a more spatially restricted definition of species pools

by defining a buffer of 100 km width from the nearest coast to each archipelago and only sampling bird species with a geographical distribution overlapping with the buffer. Additionally, to remove any biases arising from the way source pools are delimited, we conducted a further set of analyses restricted to archipelagos in the same zoogeographical region, i.e. with a common source pool. This was possible for Macaronesia (Azores, Madeira and Canary Islands archipelagos) and the South Pacific (Austral Islands, Cook Islands, Marquesas, Samoa, Pitcairn and Society), the only two regions with more than two archipelagos (see Supporting Information).

Defining an appropriate species pool for archipelagos poses substantial challenges (e.g. Si et al. 2022). The sensitivity analyses described above provide an assessment of species pool selection, but some limitations to our approach should be highlighted: (1) zoogeographical regions were defined using current species distributions, and thus might not accurately represent species distributions at the time of colonization; (2) all species in a given pool have the same probability of colonizing and establishing on the focal archipelago, and thus the approach does not account for differences in dispersal ability and niche compatibility (e.g. climate, resource use) between species; and (3) source pools defined at the species level potentially misrepresent the available pool of colonizers, and at least one recent study advocates focusing on higher taxa (genera or families) with geographic distributions overlapping with the focal assemblage (see Si et al. 2022). An additional factor is that extinct species were included in the archipelago species lists, but not for the regional pools, primarily due to the lack of accurate distributional data for extinct continental species. However, this inconsistency seems unlikely to bias our results because recent extinctions have been far more prevalent in island communities than continental source regions. Of all known bird extinctions globally, island endemics comprise 81% (468 of 581 species) of extinctions during the last 125,000 years, and 93% of extinctions since 1500 AD (Sayol et al. 2020).

Morphological and phylogenetic data

We collated a range of morphometric data for our combined sample of 6,579 species (Data S1, S2). For each extant study species ($n = 6,423$), we used a global dataset derived from linear measurements of wild birds and museum specimens (Pigot et al. 2020; Tobias et al., 2022) to compile estimates of wing length, tail length, tarsus length, and beak length (mm). These traits were selected because they reflect the overall body plan (bauplan), and correlate with important dimensions of the avian niche, such as habitat use, dispersal and foraging strategy (Pigot et al., 2020). We also compiled body mass (g) from Wilman et al. (2014). For

36 (23%) of 175 extinct species, measurements were extracted from specialist literature. A list of the data sources is found in Appendix 1, see also Data S1 for sources, including Rothschild, 1907; Amadon, 1950). For a further 121 (77%) extinct species with missing data, we inferred morphological and body mass measurements from the most morphologically similar extant species available, selecting congeners where possible (Tobias et al., 2022). Extant surrogate species were selected based on key skeletal measurements, including the mandible for beak length, humerus for flight capabilities or flightlessness, and the ratio of femur/tibiotarsus/tarsometatarsus to highlight arboreal or terrestrial modifications (Steadman, 2006). As flightless species tend to be relatively heavy, we estimated the body mass of extinct flightless taxa known only from fossil remains with reference to similar-sized extant flightless species, e.g., flightless rails (J. P. Hume, unpublished data). Since all trait data were calculated as species averages, we do not account for intra-specific variation, although previous analyses have shown this to be negligible compared to inter-specific variation in the same avian traits at global scales (Tobias et al., 2022).

All morphological traits were \log_{10} -transformed prior to analyses to avoid the influence of extreme trait values and to linearize data distributions for regressions. To quantify body plan differences between species, we measured morphological dissimilarity using \log_{10} -transformed lengths of tail, tarsus, beak, and wing after accounting for differences in body mass. We obtained these size-corrected traits using the residuals from a linear regression of trait size against body mass; i.e., the \log_{10} -transformed lengths of tail, tarsus, beak, and wing were regressed separately against \log_{10} -transformed body mass to calculate the residuals (e.g. Ingram & Kai, 2014; Supporting Information, Fig. S1).

We based our analyses on the phylogenetic tree from Jetz et al. (2012), using the Ericson backbone with 9,993 species. We selected this backbone topology because it represents a reasonably well-supported hypothesis of the relationships among extant taxa and has been used in many recent studies of avian macroevolution. From a posterior distribution of 1,000 trees obtained from www.birdtree.org, we generated a single maximum clade credibility tree using TreeAnnotator (Drummond et al., 2012). We grafted all extinct species (157) on to this tree using taxonomic constraints and information from the literature (see Supporting Information).

Colonization events

We estimated the number of colonization events for each archipelago according to the following rules. When explicit phylogenetic hypotheses were available (e.g., Valente et al.,

2020), we examined whether congeneric endemic species from a particular archipelago formed a monophyletic group, and assumed that such cases were the product of a single colonization event (Cornuault et al., 2013). Thus, for a particular archipelago, the number of colonization events generating the current endemic avifauna is equal to the number of clades present (mostly genera). Each native non-endemic species was counted as one colonization event.

Molecular data are lacking for most archipelagic extinct species, which can lead to phylogenetic uncertainty, so we estimated the minimum and maximum number of colonization events for these species. The minimum number of events was calculated by assuming congeneric extinct endemics of an archipelago were monophyletic, thus representing a single colonization; the maximum number of events was calculated by assuming that extinct genera were non-monophyletic, with each species representing a different colonization event (see sections B3 and C3 in Supporting Information). Subsequent analyses were implemented in two ways, first using the minimum number of colonization events, and then by randomly selecting a number of colonization events between the minimum and the maximum.

Measuring morphological and phylogenetic convergence

We quantified differences in body mass, body plan (using body mass-corrected wing, tail, tarsus, and beak length; Supporting Information, Fig. S1), and phylogenetic dissimilarity among species, between pairs of archipelagos, using a modified version of the mean nearest taxon distance (MNTD). This metric was designed to focus solely on morphological or phylogenetic turnover (replacement of species traits or phylogenetic lineages across archipelagos) and herein we refer to it as $MNTD_{TURN}$ (Webb et al., 2008, Holt et al., 2018). For a pair of archipelagos, A and B, $MNTD_{TURN}$ is computed as follows:

$$MNTD_{(TURN) A,B} = \min \left[\left(\frac{1}{n} \sum_{i=1}^n \min(d_{iB}) \right), \left(\frac{1}{m} \sum_{j=1}^m \min(d_{jA}) \right) \right]$$

where n and m are the species richness of the archipelagos A and B, respectively, $\min d_{iB}$ is the distance (either morphological or phylogenetic) between each species i of archipelago A and the nearest (in terms of either morphological or phylogenetic distance) species of archipelago B while $\min d_{jA}$ is the distance between each species j of archipelago B and the

nearest species of archipelago A. So, if the least diverse archipelago has no unique species, then $MNTD_{TURN}$ is zero. Moreover, if both archipelagos have completely different species and their species richness is equal, then, $MNTD_{TURN}$ equals $MNTD$ (see Supporting Information). Morphological distances (for both body mass and body plan) between species across archipelagos were measured using Euclidean distances, while pairwise phylogenetic distances between species were quantified using a cophenetic distance matrix (i.e. the phylogenetic branch length distance between species).

Null model

We tested for a pattern of convergent community structure by estimating whether overall mean turnover ($MNTD_{TURN}$) among archipelagos, and each pairwise $MNTD_{TURN}$ value between archipelagos, was lower than expected by chance. To do so, we compared observed turnover values to those simulated under a null model with random phylogenetic and morphological differentiation. For each archipelago, we simulated a null morphospace and phylogeny, constraining our model to the same number of species, endemic species, and colonization events as those observed for the archipelago (Tables 1, S2 and S5). To simulate a null morphospace and phylogeny for a given archipelago, we first started by randomly sampling colonizers from the respective regional pool (see above). Once sampled, each colonizer was randomly assigned to a specific trajectory: either it stays unchanged (native non-endemic), or speciates (becomes endemic) via anagenesis or cladogenesis (Fig. S2), with the number of native non-endemic and endemic species being constrained to the current totals observed in the archipelago (see Supporting Information and Fig. S2). For instance, if two colonization events have generated current totals of one native non-endemic and five endemic species, respectively, in a particular archipelago, then, in our simulation, one colonizer fails to speciate or evolve new traits, while the other gives birth to a monophyletic clade of five endemic species.

For each colonizer that undergoes speciation, morphological features of the resulting endemic species were simulated through a Brownian motion model of evolution (BM) (Freckleton et al., 2002). Under a BM model, a trait value changes as a function of time (t) and rate (σ^2), so that the simulated value is normally distributed with the mean equal to its initial value (x_0) and the variance equal to the product of rate and time. For body mass, simulations were performed using a univariate BM model while for body plan, a multivariate BM framework was used to fit the BM model simultaneously to the four size-corrected traits together, while assuming that traits are correlated (Clavel et al., 2015). The BM model was

implemented on a birth-death (BD) tree (Fig. S2), with the number of branches corresponding to the number of species in the endemic clade (see details in Supporting information). The time since the most recent common ancestor was fixed for the stem node at the geological age of the archipelago (using the oldest island currently present; Valente et al., 2020; Table S1).

To simulate the BD tree, we identified the family to which each speciating island-colonizer belongs, and then estimated speciation rate (λ) and extinction rate (μ) for that family using the phylogeny retrieved from 6,231 land-bird species of the 10 avifaunal regions included in our study (the 349 endemic species of 18 archipelagos were excluded from this analyses). For families with fewer than 10 species, we sampled species more widely from the order to which the family belongs (see Supporting information). We then applied a BM model to the branches of the BD tree using the estimated trait value of the speciating colonizer (i.e. the ancestral state x_0) as a starting point, while the σ^2 value was retrieved by fitting a BM model (univariate for body mass; multivariate for body plan) to the phylogeny and the traits of the family members as identified above. Therefore, for a given archipelago A, a species S belonging to the family F is randomly selected from the regional pool of potential colonizers, and is allowed to generate an endemic clade containing N species. We used: (1) the geological age of archipelago A, and λ , μ values estimated for the tree of the family F to create the tree of the endemic clade using the BD tree, and (2) the trait value of S as the ancestral state and σ^2 estimated for the tree and traits of family F, to generate trait values for the N species along the BD tree previously generated. It should be noted that, for the colonizers that stayed unchanged (native non-endemic species), the island species was simply assigned the morphological traits of the mainland species.

We constructed a null phylogeny for each simulation by retaining the phylogenetic relationships between colonizers randomly selected from the pool as a backbone tree onto which we grafted the associated simulated BD tree(s) of the endemic clade. For each archipelago, the simulation protocol was independently implemented 1,000 times. Simulated data (body mass, body plan and phylogeny) were used to generate 1,000 random values for each pairwise MNTD_{TURN} value and 1,000 average pairwise MNTD_{TURN} values among all pairs of archipelagos. To test whether archipelagos overall were convergent in morphological and phylogenetic structure in relation to their respective species pools, we tested whether pairwise turnover and average turnover (measured by MNTD_{TURN}) were less than expected under the null model simulation (one-tailed test). To compare the relative roles of potential influences on community convergence, we also calculated how far the observed overall mean MNTD_{TURN} among archipelagos deviated from null expectations using the standardized effect

size (SES). SES was calculated as $(MNTD_{TURN} - \mu_{sim}) / \sigma_{sim}$, where μ_{sim} is the mean index of the simulated values, and σ_{sim} is the associated standard deviation. Negative SES values indicate lower morphological/phylogenetic $MNTD_{TURN}$ than expected by chance, i.e. negative numbers farther from 0 indicate stronger convergence.

Null model approaches that involve sampling from a (larger) species pool may suffer high type I error rates due to differences between the species richness of the focal assemblages and that of the pool (Kraft et al. 2007). To evaluate the type I error of our approach in detecting community convergence, we first designed a set of simulations to test the type I error associated with using the metric $MNTD_{TURN}$ to detect community convergence by using different combinations of community (i.e. archipelago) and pool size (i.e. regional pool). Second, we re-ran our convergence analyses by randomly selecting, for each archipelago, a subset of the species in the pool. Two subset sizes were used, corresponding to the number of species where the species richness of an archipelago represented 30% and 60% of the pool (Kraft et al. 2007, see Supporting Information for further details of our approach).

Assessing mechanisms of convergence

To evaluate the effects of different assembly processes and to exclude the effects of extinction (Fig. 1), we conducted analyses for all land-birds including both extant and extinct species. We separately analyzed archipelagic non-endemic and endemic species to tease apart the roles of colonization and *in situ* adaptation. To assess whether extinction explains patterns of convergence, we excluded extinct species and restricted our dataset to native bird species that have so far survived the filter effect of anthropogenic activities on each archipelago. To reduce the ecological variation in our sample of species, and test if convergence is significant within more homogeneous groups of species, we re-ran all analyses restricted to the monophyletic order of passerines (Passeriformes) (see Supporting Information).

We further tested for patterns of non-random colonization by comparing the taxonomic composition of each archipelago with its respective species pool, at the family level. We used two metrics: (1) a simple count of families in each archipelago, and (2) the dissimilarity in family composition (see Supporting Information) and the proportion of shared species per family between the archipelago and its associated species pool. Both the observed number of families and dissimilarity were compared against 1000 null values generated by randomly selecting from the species pool the same number of species as observed in the respective archipelagos.

Further details of all methods are given in the Supporting Information. All statistical analyses were implemented within the R programming environment (R Development Core Team, 2018).

RESULTS

Simulations showed that our framework for testing community convergence has very low type I error, and convergence detection was not sensitive to community size or pool size (see Supporting Information, Fig. S3 and S4).

When all extant and extinct land-bird species are analyzed together, we found that turnover in body plan, body mass and phylogeny among the 18 archipelagos was significantly lower than expected by chance (i.e. lower $MNTD_{TURN}$ than expected), indicating convergence in community structure (Fig. 2B, C & D; Table S6). The strongest evidence for convergence was detected in phylogenetic structure. Results were similar when we restricted analyses to Passeriformes only, with the exception of body mass, which did not appear to show a pattern of community convergence (Fig. 2E - J; Table S6). All archipelagos (except Juan Fernández) exhibited significant body plan and phylogenetic similarity (i.e. lower pairwise $MNTD_{TURN}$ than expected) with at least one other archipelago (Fig. 3A–C). For body mass, several archipelagos showed no significant similarity with any other archipelago (Fig. 3B, E and H). The lack of significant findings for Juan Fernández was due to the presence of two hummingbird species (*Sephanoides fernandensis* and *S. sephaniodes*, Trochilidae) on the archipelago, the only species in this morphologically distinct family present on any oceanic archipelago included in this study. A reanalysis of the convergence pattern without the two hummingbirds showed convergence of Juan Fernández with at least four archipelagos for body plan and phylogeny, but still no evidence of convergence for body mass (Fig. S5).

Sensitivity analyses (Supporting Information) revealed these findings to be generally robust to (i) assumptions regarding species pool definition, and (ii) the estimated number of colonization events; with the analysis based on the number of colonization events randomly selected between the minimum and maximum numbers retrieved from the literature providing similar results to the main analysis (Tables 1 and S7–S9). Our analyses testing for differences in taxonomic composition between archipelagos and their species pools for all land birds revealed that most of the avifauna in each of the 18 archipelagos was dominated by two main orders, passerines (Passeriformes) and pigeons (Columbiformes), with the latter being overrepresented on islands compared to the respective zoogeographic regions (Table S10). In addition, we found a significantly reduced number and different composition of families

in most archipelagos compared with null expectations (Table S11), for all land birds and also for Passeriformes only.

Significant convergence in body plan, body mass and phylogenetic structure was also found for the native non-endemic species subset, suggesting that non-random patterns of colonization (and persistence) play an important role in establishing overall convergence patterns. Significant convergence in body plan and phylogenetic structure was detected for native non-endemic Passeriformes (Table S6) but these results have to be interpreted with caution as they are based on a smaller sample size (seven archipelagos). We also found significant convergence in body plan and phylogenetic structure (but not body mass) in the endemic species subset of all birds and Passeriformes only, indicating that colonization is only part of the story, and that *in situ* adaptation also contributes to convergence.

Significant convergence in each of body plan, body mass and phylogeny was also detected in the extant species subset (post-extinction datasets). In addition, we found that body plan convergence was more pronounced in the sample of extant species ($SES = -3.415$; $P = 0.001$) than in the dataset containing extant and extinct species sampled together ($SES = -2.364$; $P = 0.006$). This was also true for extant and extinct species: $SES = -3.277$; $P = 0.001$) but was less pronounced for Passeriformes ($SES = -3.337$; $P = 0.001$ and $SES = -3.291$; $P = 0.001$). These findings suggest that community convergence existed prior to human influences on island faunas, and that convergence has been further strengthened by anthropogenic extinctions.

DISCUSSION

Our results reveal clear evidence of convergence in both the phylogenetic structure and morphology of archipelagic avifaunas, despite their assembly from distinct mainland source pools. The pattern of convergence was particularly strong for phylogenetic structure, suggesting that archipelagic assemblages are drawn from a non-random set of clades predisposed to over-sea dispersal and/or successful establishment in insular environments. The concordance of evidence from phylogeny and key aspects of phenotype can be assigned to the fact that morphology is generally phylogenetically conserved in birds and also reflects dispersal propensity (e.g. Ricklefs, 2012; Barnagaud et al., 2014; Jönsson, et al., 2015; Sheard et al., 2020; Tobias et al., 2020; Table S4).

Support for community convergence is further strengthened by two observations from our analyses. First, the composition and number of families observed in each archipelago are consistently different from the adjacent mainland avifauna (see also Whittaker & Fernández-

Palacios, 2007, pp. 50-53). Second, the assemblages of the majority of volcanic archipelagos analyzed here are dominated by two particular clades (pigeons and passerines), which make up a larger proportion of the archipelago land-bird community than predicted as a random draw based on respective continental source pools. The unusual diversity of pigeons on remote islands was noted long ago by Wallace (1876) and highlights the role of clade-specific traits in the assembly of island fauna (Whittaker & Fernández-Palacios, 2007; Emerson & Gillespie, 2008; Warren et al., 2015; Weigelt et al., 2015). Taken together, these aspects of convergent community structure suggest that dispersal and environmental filters strongly constrain which types of species can reach and thrive on oceanic archipelagos (Fig. 1).

Community convergence is clearly promoted by deterministic colonization and establishment in faunal build-up, but this effect may be augmented by *in situ* adaptation and diversification, as the colonization of islands by avian lineages is often followed by predictable evolutionary change (e.g. Grant & Grant, 2008; Losos & Ricklefs, 2009; Warren et al., 2015). For example, island-dwelling species tend to become less mobile, resulting in a loss or reduction of flight ability (Wright et al., 2016), whereas brain size tends to increase (Sayol et al., 2018). Similarly, beak size may evolve to increase or decrease after species colonize islands, depending on niche availability (e.g. Clegg et al., 2002; Grant & Grant, 2008). Although this process can lead to *in situ* morphological divergence when a lineage diversifies during archipelagic radiation, the resultant communities may nonetheless be convergent if the same sets of niches are repeatedly filled across different archipelagos.

Results from analyses based on endemic and non-endemic species separately confirm the general pattern of convergence, with both subsets structurally more similar than expected by chance. Assuming that non-endemic species are generally more recently derived from mainland populations and that endemic species reflect insular speciation events, these findings suggest that non-random patterns of colonization and *in situ* adaptation both contribute to community convergence. Overall, while our analyses show consistent evidence for convergent patterns in body plan and phylogenetic structure, evidence for body mass convergence, although significant for all species, was not detected for passerines, or archipelagic endemics. There are two potential explanations for these findings. First, larger-bodied species may not be able to overcome the dispersal barrier (Fig. 1) and colonize islands. Species belonging to Struthionidae (e.g. *Struthio camelus*), Rheidae (e.g. *Rhea americana*), and Casuariidae (e.g. *Casuarius casuarius*) are missing from island systems, and this may at least partly explain the pattern of body mass convergence when focusing on all species (body mass of archipelago species ranges from 5.17 to 22,500 g, and for mainland species from 1.9

to 111,000 g). For passerines the ranges of body mass are very similar between archipelagos and mainland areas (Fig. S6), and so it follows that there is also less community convergence between archipelagos with regard to their respective species pools. Moreover, *in situ* speciation events within these groups (Figs 2, 3) resulted in the presence of several relatively large species, such as the pigeons *Raphus cucullatus* (12,450 g) and *Pezophaps solitaria* (22,500 g) in the Mascarenes, further diluting community convergence.

To examine the potential effect of anthropogenic extinctions in driving convergence of community structure, we compiled data for pre- and post-human arrival communities, and then compared evidence for convergence with and without extinct species. Our results show that the pattern of convergence existed prior to the impact of humans and was subsequently strengthened as a result of anthropogenic extinctions. This finding suggests that anthropogenic extinctions have selectively removed morphologically distinctive species – including endemic lineages with large body size or unusual wing morphology (Steadman, 2006; Boyer & Jetz, 2014; Hume, 2017; Heinen et al., 2018) – thus accentuating the signal of convergence in extant avifaunas. Therefore, our results (i) highlight the risk of testing for convergence without accounting for extinct taxa, and (ii) provide the best evidence to date that patterns of convergence precede the effects of anthropogenic extinctions. However, it is worth emphasizing that our knowledge of extinct species remains incomplete (e.g. Steadman, 2006; Hume, 2017; Sayol et al., 2020), with the global number of described extinct species no doubt representing only a partial picture of the original avifaunal diversity driven to extinction by humans. Focusing on oceanic island systems reduces the problem somewhat as many archipelagos have now been relatively well studied by paleontologists, yet the inadequate fossil record of some islands suggests that our dataset of extinct taxa may be missing a large number of species that await discovery (e.g. Steadman, 2006; Hume, 2017; Sayol et al., 2020). Nonetheless, community convergence is evident even without the extinct species.

Historical contingencies arising from regional factors and chance events have resulted in the assembly of unique biotas on archipelagos worldwide, often featuring multiple narrowly endemic species (Whittaker & Fernández-Palacios, 2007; Gillespie & Clague, 2009). Hence, traditional comparisons of species or clade composition among oceanic archipelagos are not suitable for assessing convergence at the community level. By focusing on phylogenetic relationships and morphological traits in relation to distinct regional species pools, we have shown that avian community assembly on oceanic archipelagos is shaped by non-random, deterministic and therefore predictable process regimes over large temporal

scales. Crucially, we show that non-random anthropogenic extinctions contribute to this pattern, yet are insufficient to explain its pervasiveness. These findings clarify that historical contingencies are overridden by a combination of biogeographical assembly, *in situ* evolutionary adaptation, and non-random anthropogenic impacts to generate convergent archipelagic bird communities worldwide. Similar approaches should be extended to other vertebrate groups, as well as plants and invertebrates, to assess the generality of our findings across a wider sample of biodiversity.

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AUTHOR CONTRIBUTIONS

K.A.T, J.A.T., C.T., T.J.M., R.J.W., and F.R. developed the conceptual framework and coordinated the study; J.A.T., C.S. and J.P.H. compiled morphological data; K.A.T., D.P. and C.T. compiled species inventories and distributional data; F.R. designed and conducted all analyses. All the authors contributed to the interpretation of the results. K.A.T., R.J.W, F.R., C.T, T.J.M., J.A.T. wrote the final draft, with all authors contributing to reviewing and editing.

BIOSKETCH

The author team consists of biogeographers, ecologists, ornithologists and paleontologists with diverse backgrounds including island biogeography, community ecology, taxonomy, macroecology and evolutionary biology. This work is a collaborative effort to enhance our understanding of the biodiversity patterns across macro-scales of space and time.

DATA AVAILABILITY STATEMENT:

All data are available in Supporting Information. The code for analyses in R can be download from <https://github.com/frigal001/Functions-Birds-Convergence>.

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the Supporting Information section.

TABLE 1 Species richness, numbers of endemic and extinct species and the retrieved minimum and maximum numbers of colonization events for each of the 18 archipelagos, for all land-birds. For the respective numbers of Passeriformes see Supporting Information.

Archipelago	Species richness	Endemic species	Extinct species	Colonization events (min–max)
Austral	7	6	4	5–7
Azores	20	7	5	17–20
Canary	61	16	4	58–59
Comoros	52	22	0	46
Cook Islands	21	12	9	17–20
Fernando de Noronha	4	3	1	4
Galápagos	30	26	1	13
Gulf of Guinea	60	28	0	53
Hawaii	100	99	68	13–17
Juan Fernández	9	3	0	8
Madeira	32	10	7	29–32
Marquesas	26	22	14	16–20
Mascarenes	49	47	29	32–45
Pitcairn	8	8	3	7
Revillagigedo	16	5	1	15
Samoa	30	12	2	30
Society	24	15	14	21–24
Tristan da Cunha	7	7	0	5

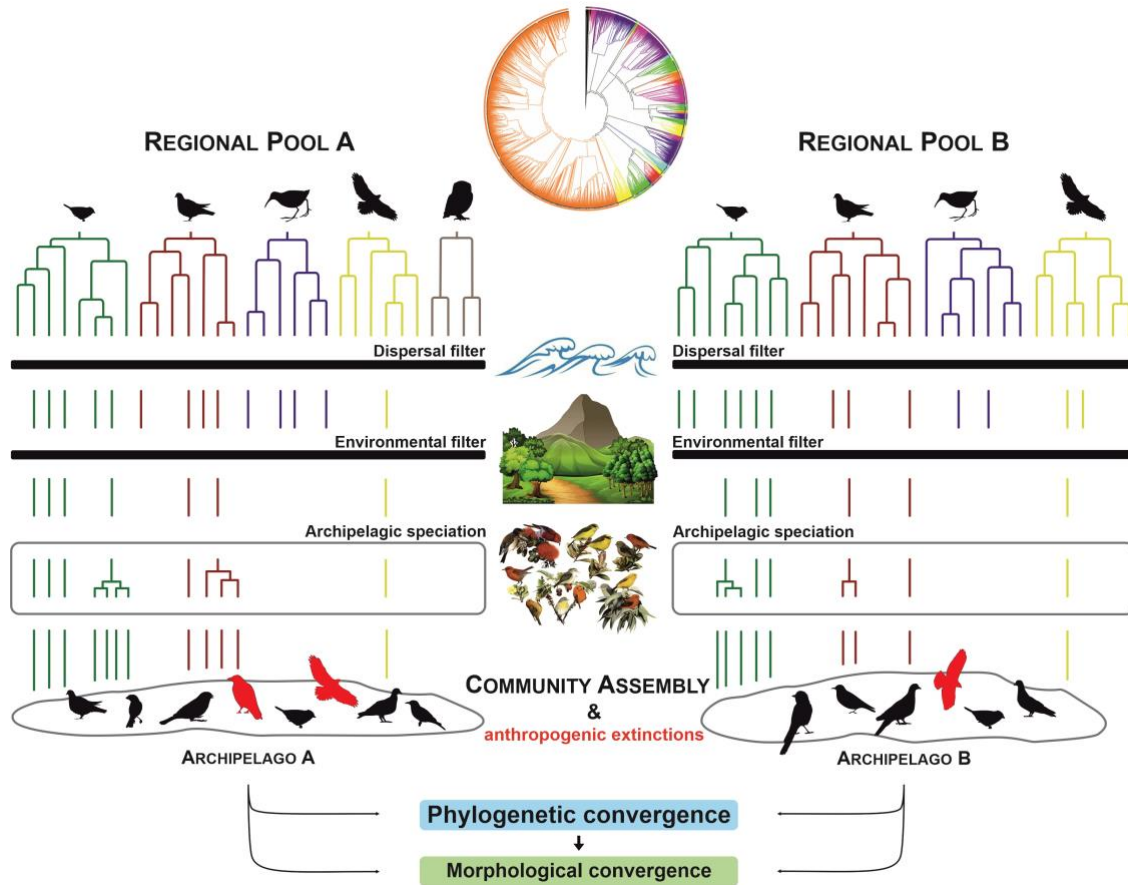


FIGURE 1 Quantifying convergent properties of archipelagic communities. If subsets of bird species from distinctive regional pools reach archipelagos A and B, the constraints of dispersal and environmental filters potentially select species with similar traits from the same regions of the evolutionary tree. *In situ* cladogenesis (archipelagic speciation) generates endemic lineages, further modifying the morphological and phylogenetic profile of archipelagic communities, theoretically increasing the number of species with combinations of traits adapted to insular environments. Thus, morphological or functional similarity between archipelagos may reflect a combination of a) non-random characteristics of colonizing lineages, and b) subsequent convergent evolution. Species highlighted in red are anthropogenic extinctions, which, if also non-random, can generate or strengthen patterns of convergence. Robust analyses of community convergence therefore need to account for the role of extinctions. Pictograms are courtesy of PhyloPic (www.phylopic.org) and the image of Hawaiian honeycreepers is reproduced, with permission, from Pratt (2005).

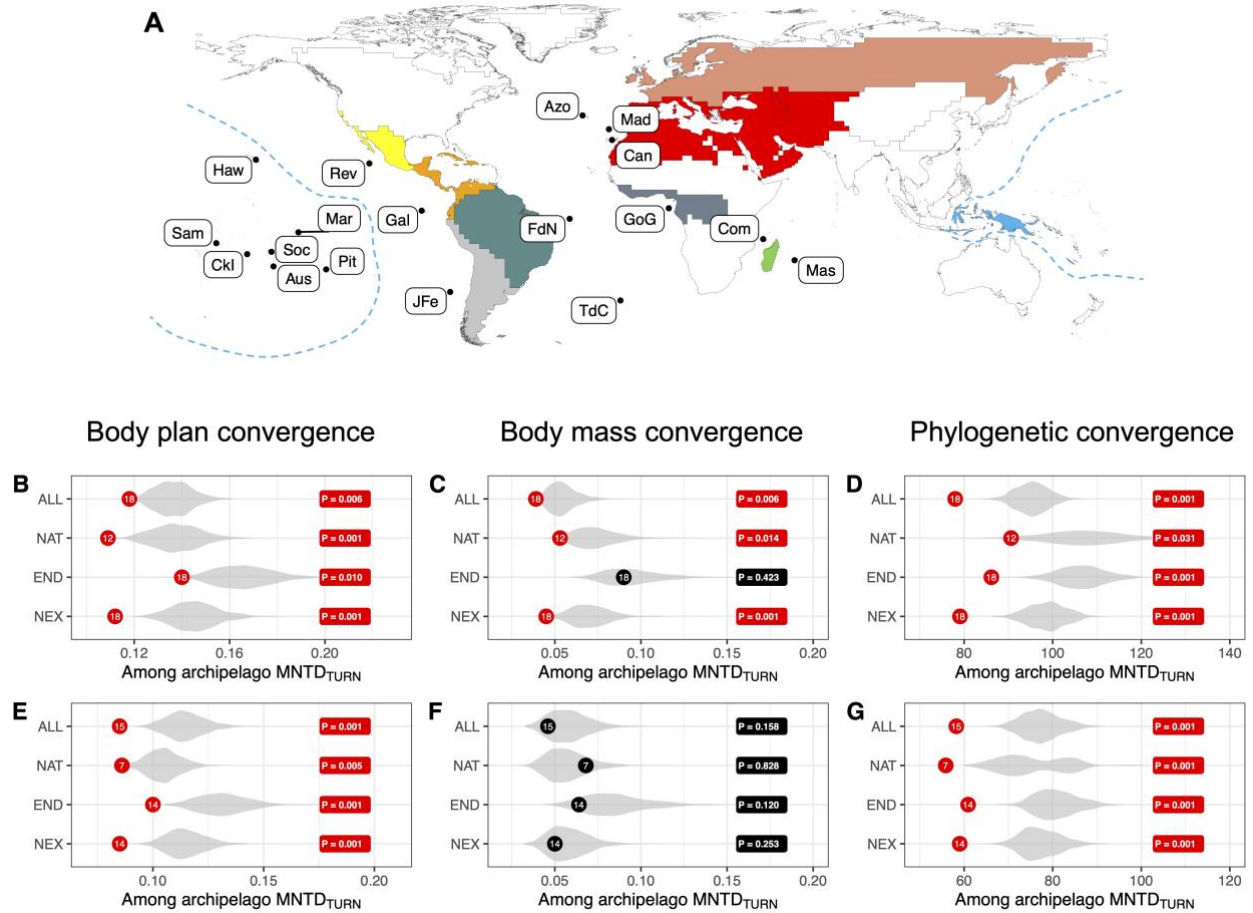


FIGURE 2 Island avifaunas converge on repeated patterns of morphological and phylogenetic structure. (A) Assignment of 18 archipelagos to nine biogeographical regions (Tables S1-S3). Regions are indicated by colour and archipelagos by abbreviations: Aus = Austral islands; Azo = Azores; Can = Canaries; Com = Comoros; CKI = Cook Islands; FdN = Fernando de Noronha; Gal = Galápagos; GoG = Gulf of Guinea; Haw = Hawaii; JFe = Juan Fernández; Mad = Madeira; Mar = Marquesas; Mas = Mascarenes; Pit = Pitcairn; Rev = Revillagigedo; Sam = Samoa; Soc = Society; TdC = Tristan da Cunha. (B–G) Similarity analyses for body plan, body mass, and phylogeny for all land-birds (B–D; $n=496$ species), and Passeriformes (E–G; $n=284$ species). Panels provide results for all (ALL), native-non-endemic (NAT) and endemic (END) species, including extinct species, as well as a comparison with extant species (NEX), i.e. with all extinct species removed. Dots indicate average turnover between pairs of archipelagos (among archipelago turnover); numbers on dots are sample sizes (number of archipelagos). $MNTD_{TURN}$ for body plan (unitless) and body mass ($\log_{10}[g]$) were calculated using Euclidean distances between species and $MNTD_{TURN}$ for phylogeny was calculated using cophenetic distances (million years) between species. Violin plots show the distribution of average $MNTD_{TURN}$ calculated from 1,000 simulations using a null model with random morphological and phylogenetic structure. Boxes show P -values of one-tailed tests (red = significant; black = non-significant).

Deterministic assembly and anthropogenic extinctions drive convergence of island bird communities

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Study system

A1. Oceanic archipelagos

Oceanic islands are discrete biogeographical and environmental settings. Island climates are buffered by surrounding oceans, often differing from nearby areas of continent at the same latitude because of their location in the path of major ocean and/or atmospheric current systems (Whittaker & Fernández-Palacios, 2007; Weigelt et al., 2013). In addition, montane islands tend to generate heavy orographic rainfall, creating a broad range of environments within a relatively small area (Whittaker & Fernández-Palacios, 2007). Islands are often home to relatively few species because of low overall area and reduced rates of colonization (Whittaker & Fernández-Palacios, 2007; Gillespie & Clague, 2009; Losos & Ricklefs, 2009). The increased ecological opportunity presented by species-poor island communities, coupled with unique environmental features, means that islands are often hotbeds for evolutionary diversification (Whittaker & Fernández-Palacios, 2007; Gillespie & Clague, 2009; Losos & Ricklefs, 2009; Whittaker et al., 2017).

Each oceanic archipelago included in the analyses varies in terms of geological history, age, isolation, area, and overall topography, although all are of volcanic origin. To characterize each archipelago, we assembled data on geological age (specifically the maximum age of the oldest surviving island), isolation (as the distance to the closest possible source, either mainland or larger archipelago; Triantis et al., 2015; Valente et al., 2020), total area (sum of the areas of all islands of an archipelago), number of islands, maximum elevation (highest point in the archipelago) and geographical coordinates (Triantis et al., 2015; Valente et al., 2020). We also collected data on annual mean temperature and annual precipitation from the WorldClim database (<http://worldclim.org>; Fick & Hijmans, 2017) (see Table S1). The geological age of the oldest extant island for each archipelago ranges from less than 1 Ma to more than 30 Ma. However, most of our archipelagos are older than the oldest extant island. For example, the maximum geological age for the Madeiran volcanic province is estimated at 68 Ma, whereas the oldest current island in the archipelago, Porto Santo, originated around 14 Ma. For the Canary Islands, with a broadly similar maximum geological age to the Madeiran archipelago, the oldest island, Fuerteventura originated 20 Ma. Similarly, the Hawaiian-Emperor island chain has a geological history dating back to 83 Ma (Meiji Seamount) but there was a period between at least 33 and 29 Ma in which no islands existed and thus distant colonization had to repopulate the younger portion of the Hawaiian chain (Clague et al., 2010); the oldest of the large extant islands, Niihau, is dated to just 5.1 Ma and Kauai to 4.7 Ma (Price & Clague, 2002). There are, however, a few clades that colonized the archipelago before the emergence of the extant high islands (Givnish et al., 2009; Hembry et al. 2021). In the case of the Azores, the oldest island appears to set the time frame of the existence of the archipelago and biologically the Azores is around 3 million years younger than its maximum surface geological age due to a complex history of submergence/emergence (Ramalho et al., 2017). Thus, the maximum geological age of each archipelago provides only a relatively crude estimate of the time available for colonization (Triantis et al., 2016; Valente et al., 2020).

Table S1. Characteristics of 18 archipelagos considered in our study. Mean annual temperature and annual precipitation were collated from the WorldClim at a resolution of 30 arc-seconds (<http://worldclim.org>). For each archipelago, climatic values were calculated as the mean values of all WorldClim cells within relevant island-containing polygons. Elevation is the maximum elevation.

Archipelago	Area (km ²)	Elevation (m)	Age (My)	Isolation (Km)	Mean annual temperature (°C)	Annual precipitation (mm)
Austral	153	650	14.80	500	23.27	1987.52
Azores	2324	2351	6.3	1343	16.20	1169.03
Canary	7496	3711	20	95	17.80	245.53
Comoros	2097	2361	10.58	400	24.59	2068.18
Cook Islands	218	169	18.50	1800	25.25	2220.97
Fernando de Noronha	26	323	12.50	354	26.64	1525.49
Galápagos	7808	1676	4	926	22.11	813.75
Gulf of Guinea	998	2024	31	225	24.56	1189.35
Hawaii	16570	4205	5.2	3200	19.59	1627.08
Juan Fernández	98	1380	4.23	610	14.92	1071.86
Madeira	810	1850	18.8	450	16.06	1908.61
Marquesas	1031	1230	5.5	1300	25.40	1689.81
Mascarene	4481	3069	15	740	21.30	2273.90
Pitcairn	43	349	1.1	4300	22.76	1646.75
Revillagigedo	166	1130	4.46	390	23.68	685.69
Samoa	3045.10	1860	5.21	750	25.19	3493.71
Society	1553	2241	4.3	1442	24.92	2864.98
Tristan da Cunha	198	2010	18	2816	12.43	1819.60

A2. Species list

For each archipelago, we collated species lists of land-birds, which we define as strictly terrestrial indigenous (endemic and non-endemic), resident, breeding birds, including birds of prey, but excluding marine species and those dependent on inland waters, based on data by BirdLife International (2017) for species' main habitat. A complete species list was compiled for each of the 18 oceanic archipelagos based on recent checklists from Avibase (<http://avibase.bsc-eoc.org>) along with the lists provided by Steadman (2006) for various Pacific archipelagos, Hume (2011, 2017; 2019) for Mascarenes, Boyer (2008) for Hawaii, Alcover et al. (2015) and Illera et al. (2016) for the Canary Islands, Azores and Madeira, and Fuller (2000) and Hume (2017) for all archipelagos. The lists were further updated based on the recent paper by Valente et al. (2020). Contemporary biogeographical patterns on islands (as elsewhere) are strongly influenced by historic and pre-historic extinctions (Steadman, 2006; van der Geer et al., 2016). Thus, in order to understand how species' arrivals and subsequent evolutionary dynamics interact to establish species diversity, species that are known to have become extinct due to human activities have also to be considered. However, for many islands, the inadequate fossil record suggests that considerable numbers of now extinct taxa await discovery (Steadman, 2006; Hume, 2017). In the present study, we therefore focused on 18 major oceanic archipelagos of volcanic origin (Table S2; Fig. 2 in main text) that are among the better-studied in regard to extinct avifauna (Steadman, 2006; Hume, 2017). For the extant species we followed the taxonomy provided by the International Ornithological Congress' (IOC) World Bird List, Version 5.3 (July 23, 2015) and downloaded on September 17, 2015 from <http://www.worldbirdnames.org/ioc-lists/master-list-2/> (Gill, & Donsker, 2015). For the taxonomy of extinct species, we considered the same version of the IOC list, along with the species listed in (Steadman, 2006; Boyer, 2008; Hume, 2011, 2017, 2019; Alcover et al., 2015; Illera et al. 2016; see Data S1). Overall, our dataset contains 495 land-bird species occurring across the 18 archipelagos (Data S1); 348 of them (70%) are endemic to a single archipelago and approximately one-third (157) of all species are currently considered extinct (Table S2). To test

the generality of results for all species we re-ran all the above analyses using Passeriformes, which is a well identified monophyletic group and also well-represented in oceanic archipelagos. Passeriformes represent at least 50% of the bird species in 10 out of the 18 archipelagos considered in our study (Table S2). In total, they represent 284 species out of the 495 (Data S1).

Table S2. Species richness, number of extinct and extant species and number of endemic and non-endemic species for each of the 18 archipelagos, first considering all land-bird species together, and Passeriformes.

Archipelago	All land-birds					Passeriformes				
	Species	Extinct	Extant	Endemic	Non-endemic	Species	Extinct	Extant	Endemic	Non-endemic
	richness	species	species	species	species	richness	species	species	species	species
Austral*	7	4	3	6	1	1	0	1	1	0
Azores	20	5	15	7	13	10	1	9	3	7
Canary	61	4	57	16	45	36	3	33	13	23
Comoros	52	0	52	22	30	27	0	27	16	11
Cook Islands	21	9	12	12	9	4	1	3	4	0
Fernando de Noronha*	4	1	3	3	1	2	0	2	2	0
Galápagos	30	1	29	26	4	23	1	22	23	0
Gulf of Guinea	60	0	60	28	32	38	0	38	23	15
Hawaii	100	69	31	99	1	81	52	29	81	0
Juan Fernández	9	0	9	3	6	4	0	4	2	2
Madeira	32	7	25	10	22	15	2	13	4	11
Marquesas	26	14	12	22	4	8	2	6	8	0
Mascarenes	49	29	20	47	2	19	5	14	18	1
Pitcairn*	8	3	5	8	0	2	0	2	2	0
Revillagigedo	16	1	15	5	11	8	0	8	3	5
Samoa	30	2	28	12	18	15	0	15	8	7
Society	24	14	10	15	9	6	4	2	6	0
Tristan da Cunha	7	0	7	7	0	5	0	5	5	0

A3. Rationale for assignment to regions and development of null expectations

As colonization events are comparatively frequent within oceanic archipelagos but rare between them, we treat archipelagos as independent units for the purposes of our analysis. Remote archipelagos are stocked by chance long-distance over-water dispersal, so the probability of any particular lineage colonizing is extremely small, with a bias towards more dispersive phenotypes. This may contribute to phylogenetic and morphological similarity among archipelagic faunas at the point of establishment. However, typically, archipelagic faunas are assembled from a dominant regional species pool, so an unconstrained comparison of pairs of archipelagos located within one region would theoretically generate higher degrees of similarity than pairs located within different regions/ocean basins simply as a consequence of random colonization from the respective source pools (Figure 1). To correct for autocorrelation within regions, we therefore considered the potential species pool for each archipelago to be defined by its respective zoogeographical region.

We generate these regional species pools using the regional boundaries defined solely on bird species distributions, based on Holt et al. (2013), provided here, <https://macroecology.ku.dk/resources/wallace> and corresponding to their Figure S4B. We extracted species lists of all land-birds for each zoogeographical region from BirdLife International (2017). Overall, the 18 archipelagos were assigned to 10 different zoogeographical regions (see details below). The total number of land-bird species in the ten zoogeographical regions is 6,231 species (Table S3; Data S2).

To validate and improve our approach, we compared the zoogeographical region assigned to each archipelago from Holt et al. (2013) with source region reconstructions based on phylogenetic relationships between islands and mainland species found in the literature, when available. Despite some discrepancies, we found that overall the zoogeographical regions in Holt et al. (2013) showed strong agreement with source region reconstructions. For example, most phylogenetic analyses have confirmed the close relationships between Macaronesian avifauna (Azores, Madeira and Canary Islands) and the closest western Palaearctic mainland areas [Europe and west-Africa corresponding mainly, in Holt et al. (2013), to the zoogeographical region 9 for the Iberian Peninsula and west-Africa, and to a lesser extent to region 11 for North-Europe] (Illera et al., 2012). In Holt et al. (2013), the Canary Islands and Madeira were assigned to zoogeographical region 9, and the Azores to region 11. Following Illera et al. (2012), we did not modify the assignment of the Canary Islands and Madeira since they are both mainly connected to the Iberian Peninsula and North-West-Africa. For the Azores, we merged both regions 9 and 11 to create a larger and more realistic pool. For the Galápagos, most studies suggest a Caribbean and central America origin of the avifauna, which is congruent with region 3 in Holt et al. (2013), to which the Galápagos is assigned (Sato et al., 2001; Arbogast et al., 2006; Chaves et al., 2012). The assignment of Juan Fernández and Tristan da Cunha to South-American (Amazonian region excluded) in Holt et al. (2013) (region 4), is also in accordance with the literature (Roy et al., 1998; Ryan et al., 2013). For the Gulf of Guinea islands, at least for Zosteropidae, Melo et al. (2011) have suggested an origin from southwestern Africa (Cameroon), corresponding to region 7 in Holt et al. (2013). Comoros and the Mascarene were both assigned to Madagascar (region 10) and South Asia – India (region 12) in Holt et al. (2013). However, the literature mainly suggests a close affinity with the Madagascan avifauna (Warren et al., 2006; Thébaud, 2009) even if, unexpectedly, some groups might be related to more remote regions, notably Asia and the Indo-Pacific region (Thébaud, 2009; Warren et al., 2011). Nevertheless, and since most experts advocate Madagascar as the main species pool for both Comoros and the Mascarenes, we only selected Madagascar (region 10) for our analysis. In Holt et al. (2013), most of the South Pacific archipelagos (Cook Islands, Marquesas, Samoa, Pitcairn and Society) were assigned to a Pacific region [region 19 in Holt et al.], which consists of insular areas only. Therefore, region 19 should not be seen as a species pool *sensu stricto* from which the avifauna of Pacific islands might have originated, but as a cluster of islands sharing some specific phylogenetic bird lineages, most notably those that have extensively colonized and radiated throughout the South Pacific (Filardi & Moyle, 2005). Among the South-Pacific archipelagos considered in our study, the Austral islands was the only one not assigned to region 19, but instead connected to the Papua-Melanesian region [region 17 in Holt et al. (2013)]. Overall, in the literature,

the origin of many South Pacific island birds is not clear and few studies have addressed the issue (Filardi & Moyle, 2005; Cibois et al., 2014). For example, recent studies have documented a probable New Guinea origin for the Pacific fruit doves and imperial pigeons (Columbidae) (Cibois et al., 2017). Kirchman (2012) suggests also that rails (Rallidae) of the Pacific islands originated from Australia – New Zealand. In our analysis, we decided to merge both the Pacific and Papua-Melanesian region (region 19 and 17) to create a large and more realistic species pool, which is analogous to the Oceanian realm delimited by Holt et al. (2013) in a global classification of vertebrate zoogeographic units (i.e. combining amphibians, non-pelagic birds and non-marine mammals).

Table S3. Zoogeographical regions to which the 18 archipelagos were assigned. For each region, the number of species for all land-birds, and Passeriformes are given. Regions were extracted from Holt *et al.* (2013). Note that, for Pacific islands (Austral, Cook Islands, Hawaii, Marquesas Islands, Samoa, Pitcairn Islands and Society islands), regions 19 and 17 were merged. For the Azores, analyses were performed with regions 9 and 11 merged. The number of bird species retrieved by restricting our pools to a buffer of 100 km width from the coast is given in brackets (See Supplementary Analyses in section C for more details).

Archipelago	Bioregion	Species richness in bioregions	Passeriformes
Revillagigedo	1	97 (65)	50 (32)
Galápagos	3	2071 (1283)	1260 (784)
Juan Fernández	4	1715 (491)	1147 (325)
Tristan da Cunha	4	1715 (491)	1147 (325)
Fernando de Noronha	5	2292 (1130)	1497 (716)
Gulf of Guinea	7	885 (642)	575 (404)
Canary Islands, Madeira	9	811 (244)	508 (145)
Comoros, Mascarenes	10	139 (24*)	73 (2*)
Azores	11+9	922 (244)	604 (145)
Austral, Cook Islands, Hawaii, Marquesas, Samoa, Pitcairn, Society	17+19	1280 (1273)	768 (764)

*For Madagascar (zoogeographical region 10), the number of species in the pool retrieved by restricting the species pool to a buffer of 100 km width from the coast was lower than the species richness of its associated archipelago (N=50, and N= 19 for Mascarenes, and N = 52, and N=27 for Comoros, for all land-birds, and Passeriformes, respectively). Consequently, we kept the whole species pool for Madagascar with 139 land-bird species and 73 Passeriformes in the analysis of convergence performed with the restricted species pools (see further details below in the section C.2 Uncertainty in the definition of the species pool)

A4. Phylogeny

We based our analyses on the phylogenetic tree from Jetz et al. (2012) using the Ericson backbone tree with 9,993 species. A posterior distribution of 1,000 trees was obtained from <http://www.birdtree.org>. A single maximum clade credibility tree was then generated using TreeAnnotator (Drummond et al., 2012). We selected this backbone topology as it has been used in many recent studies of avian macroevolution and because it represents a well-supported hypothesis of the relationships among extant taxa (Jetz et al., 2012). We grafted all extinct species (157) on to this tree using taxonomic constraints and information from the literature. However, for some extinct species, accurate taxonomic information is missing at species or genus levels, and therefore we grafted species randomly within the lowest known taxonomic ranks. For instance, a species is randomly grafted within its genus when the genus is known but no information is available for the position of the species within the genus. A species would be randomly grafted within its family if its genus was also unknown. Subsequently, we pruned the trees to keep only the 6,579 species we considered in the following analysis. For extinct species, branch lengths were set at random. To test the validity of this decision, we generated 100 trees and tested if the phylogenetic turnover between pairs of archipelagos (see below in section B1 for the computation of phylogenetic turnover) were sensitive to random placement of extinct species on the tree. We found that the average correlation between 100 pairwise phylogenetic turnover matrices was 0.985, with a standard deviation of 0.007, suggesting that tree uncertainty was negligible. The results presented in the main text were obtained using a randomly selected tree from the set generated.

B. Metrics and models

B1. Morphological and phylogenetic turnover

We measured morphological dissimilarity between archipelagos separately for body mass and body plan. All morphological traits were \log_{10} -transformed prior to the analyses to avoid the influence of extreme trait values in our analyses and to linearize data distributions for the following regressions. For body plan, we quantified dissimilarity between archipelagos by combining \log_{10} -transformed lengths of tail, tarsus, beak and wing after having adjusted these four traits for differences in body mass. Indeed, and as expected, our four morphological traits increase with body mass (Fig. S1) and it was then necessary to separate differences in body plan from differences in body mass. We then used a very common method of size-correction in ecological / evolutionary research studies whereby residuals were obtained from a linear regression of the size-dependent trait against body mass (Krasnov et al., 2003; Hulsey et al., 2007; Ingram & Kai, 2014). Thus, the \log_{10} -transformed lengths of tail, tarsus, beak and wing were regressed separately against \log_{10} -transformed body mass to obtain the size-corrected traits (i.e. residuals). This procedure was applied to all 6,579 bird species and, separately, for the restricted datasets of Passeriformes, 4,236 species.

A single morphological space for all species, regardless of the archipelago/species pool to which they belong to was used (Villeger et al. 2017; but see Sobral et al. 2016 and Cianciaruso et al 2017 for alternative views). Since, our analyses aimed to compare assemblages (archipelagos) between each other across the globe, we processed our morphological traits at the global scale, i.e. considering all species from different pools and archipelagos. Therefore, the Euclidean distance between a pair of species, wherever that pair is located, remains the same. For example, the Euclidean distance of body shape between *Tyto alba* and *Milvus migrans* is the same (0.336) for the Canary Islands, the Comoros and the Gulf of Guinea islands.

We used Pagel's λ to estimate the degree to which morphological traits show phylogenetic signal according to the prediction of a simple Brownian model of trait evolution (Pagel, 1999). Pagel's λ measures the extent to which a trait evolves by random drift from its ancestral value; λ takes values between zero and one, with $\lambda = 0$ implying that there is no phylogenetic signal and $\lambda = 1$ indicating a strong phylogenetic signal. We calculated confidence intervals (CI) for λ , and assumed that CI excluding 0 is indicative of a significant phylogenetic signal. Phylogenetic signal was estimated for all archipelagic land-bird species (N=495), for Passeriformes (N=284), as well as for all land-birds (N=6,579), and all Passeriformes (N=4,236); results are shown in Table S4. As expected, a significant phylogenetic signal was found for all cases with, overall, a stronger phylogenetic signal detected for body mass.

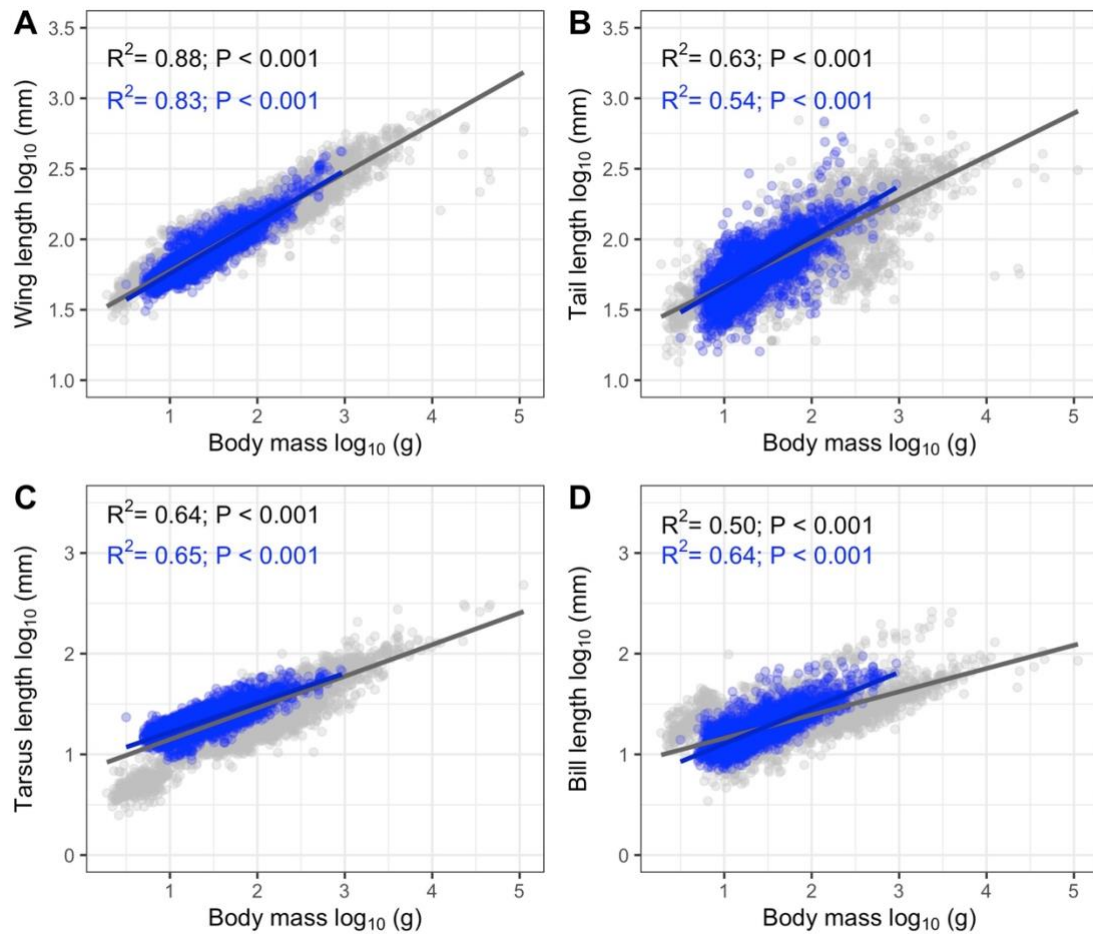


Figure S1. Relationship between \log_{10} body mass and (A) \log_{10} wing length, (B) \log_{10} tail length, (C) \log_{10} tarsus length and (D) \log_{10} beak length for all 6,579 land-bird species (grey dots) and for the 4236 Passeriformes (blue dots). The four \log_{10} traits were regressed separately against \log_{10} body mass using a linear model to obtain size-corrected traits (i.e. residuals) which were subsequently used to quantify dissimilarity in body plan between archipelagos. Regression lines are indicated by solid grey, blue and red lines for all land-birds, and Passeriformes respectively. R^2 and its associated P -values are indicated on the top left of each panel.

Table S4. Results of the phylogenetic signal analyses performed on size-corrected wing, tail, tarsus and beak lengths, and on body mass. Values of λ and associated confidence interval are given. Analyses were performed on six different samples: the global dataset for all land-birds, for and Passeriformes only; archipelagic birds for all land-birds, and for Passeriformes only. Numbers of species included in each dataset are given in parenthesis.

	All land-bird species		Passeriformes	
	λ	CI	λ	CI
Archipelagic species (495, 284, 368)				
Size-corrected wing length	0.96	[0.95,0.98]	0.97	[0.96,0.97]
Size-corrected tail length	0.82	[0.77,0.88]	0.87	[0.85,0.88]
Size-corrected tarsus length	0.85	[0.8,0.91]	0.92	[0.91,0.93]
Size-corrected beak length	0.86	[0.81,0.91]	0.92	[0.91,0.93]
Body mass	0.85	[0.79,0.91]	0.91	[0.9,0.93]
All species pool (6,579, 4,236, 5098)				
Size-corrected wing length	0.97	[0.96,0.97]	0.98	[0.96,0.99]
Size-corrected tail length	0.86	[0.85,0.88]	0.82	[0.71,0.94]
Size-corrected tarsus length	0.92	[0.91,0.93]	0.93	[0.89,0.98]
Size-corrected beak length	0.9	[0.89,0.91]	0.93	[0.89,0.97]
Body mass	0.93	[0.92,0.94]	0.93	[0.89,0.98]

Morphological and phylogenetic convergence between archipelagos was quantified using a metric of dissimilarity. Herein, we used an approach based on pairwise distances among species, since it can be applied to both trait and phylogenetic data. We used a modified version of the mean nearest taxon distance (MNTD) metric (Webb et al., 2008). This nearest neighbour approach is appropriate for testing convergence either within clades between regions or between clades within the same region (Rutschmann et al., 2011; Holt et al., 2018), and it has been commonly used in the context of community convergence analyses (Kozak et al., 2009; Mahler et al., 2013; Ingram & Kai, 2014).

For a pair of archipelagos A and B, $MNTD_{A,B}$ is computed as follows:

$$MNTD_{A,B} = \frac{1}{2} \left[\left(\frac{1}{n} \sum_{i=1}^n \min(d_{iB}) \right) + \left(\frac{1}{m} \sum_{j=1}^m \min(d_{jA}) \right) \right] \quad \text{eq. 1}$$

where n and m are the species richness of the archipelagos A and B, respectively, $\min d_{iB}$ is the distance (either morphologic or phylogenetic) between each species i of the archipelago A and the nearest species of the archipelago B while $\min d_{jA}$ is the distance between each species j of the archipelago B and the nearest species of the archipelago A.

As is the case for many measures of dissimilarity, MNTD is sensitive to differences in species richness between assemblages. Let us consider an archipelago A with four species S1, S2, S3, and S4, and an archipelago B with 3 species, with B having no species that are not also in A (i.e. S1, S2 and S3). Below we show a hypothetical matrix of the pairwise distances between the four species; these distances that could either be morphological or phylogenetic:

	S1	S2	S3	S4
S1	0			
S2	0.4	0		
S3	0.2	0.5	0	
S4	0.7	0.5	0.6	0

If we calculate $MNTD_{A,B}$ (eq. 1), we will obtain a non-zero dissimilarity value of 0.083 for this comparison and this value will be driven only by the fact that B has fewer species than A, since B has no unique species at all. This is not desirable for our analysis and we therefore used a modified form of MNTD, recently proposed by Holt *et al.* (2018) to focus solely on turnover patterns (i.e. replacement of species traits or phylogenetic lineages across archipelagos). The turnover expression of MNTD (called hereafter $MNTD_{TURN}$) is expressed as:

$$MNTD_{(TURN) A,B} = \min \left[\left(\frac{1}{n} \sum_{i=1}^n \min(d_{iB}) \right), \left(\frac{1}{m} \sum_{j=1}^m \min(d_{jA}) \right) \right] \quad \text{eq.2}$$

so that only the archipelago with the lowest richness in the pairwise comparison influences the result. If the least diverse archipelago has no unique species, then turnover is zero. Moreover, if both archipelagos have completely different species and their species richness is equal, then, $MNTD_{TURN}$ equals $MNTD$. For $MNTD_{TURN}$ calculated using body mass and morphological shape, we used the Euclidian distance matrix while for $MNTD_{TURN}$ based on phylogeny, we used the cophenetic distance matrix. To quantify average among-archipelago dissimilarity with a single metric, we calculated the mean of all among-archipelago $MNTD_{TURN}$ values for each of body plan, body mass and phylogeny (Mahler et al., 2013; Ingram & Kai, 2014).

B2. Null models

To test whether mean among-archipelago turnover and pairwise turnover (measured using $MNTD_{TURN}$) between archipelagos were lower than expected by chance, we compared them to the same measures simulated under a null model with random phylogenetic and morphological differentiation. Recent work on convergence has typically used one or more evolutionary model(s) [e.g., Brownian motion (BM) or Ornstein-Uhlenbeck (OU)] to generate null trait dissimilarities against which observed trait dissimilarities are compared (Muschick et al., 2012; Mahler et al., 2013; Ingram & Kai, 2014; Mazel et al., 2018). However, these studies focused on specific monophyletic groups [an entire group, e.g. mammals- (Mazel et al., 2018); or specific clades, e.g. Anolis- (Mahler et al., 2013)], that have diversified *in situ*, i.e. within the spatial unit considered, either continental scales or islands. Given that we want to study the convergence between different spatial units (archipelagos) that enclose only some representatives of many different clades, these approaches cannot be directly applied to our data. Indeed, on oceanic archipelagos, bird communities emerge from the interplay between colonization, *in-situ* speciation and extinction (MacArthur, 1963, 1967; Whittaker & Fernández-Palacios, 2007; Valente et al., 2020), leading species from distant clades to coexist in the same spatial units. As an example, the Canary Islands have 61 land bird species, including extinct species, belonging to 25 different families. Moreover, in most of the archipelagos, native non-endemic species, for which morphological evolution has taken place in the source areas, and endemic species, for which morphological evolution has taken place on the archipelago, coexist; realistic null models have then to simulate morphological diversity that has originated from both colonization from the species pool and *in-situ* speciation after establishment on the islands.

Here, we decided to construct null morphospaces for each archipelago, under the null hypothesis that archipelagic morphospaces neither converge nor diverge between archipelagos. In other words, our null model assumes that the morphospace of an archipelago results from random colonization and *in-situ* speciation processes. Our approach relies on our current knowledge of colonization events and *in-situ* diversification patterns on the studied archipelagos. We construct random morphospaces by:

- (1) selecting colonizers at random from the potential species pool,
- (2) allowing colonizers, once established in an archipelago, to speciate or not.

Two types of speciation were considered: anagenesis, where an island population diverges through time and becomes reproductively isolated from the mainland source population without an increase in

island species richness, and cladogenesis, where one colonizer splits into two or more island endemic species (Triantis et al., 2015; Valente et al., 2020).

The first step of the simulation procedure aims to simulate colonization for each archipelago by randomly selecting species from their respective regional species pool. It is noteworthy to mention that the regional pool does not contain the endemic species of the focal archipelago(s). The number of colonization events was retrieved from existing data (see Table S5 and section ‘Estimation of Colonization Events’, below). The number of colonization events was based on, a) existing molecular phylogenies, and b) the taxonomic position of each species. Given that no molecular data exist for most extinct archipelagic endemic species (extinct species were randomly grafted in the tree within their respective genera or family), we tested two primary hypotheses to estimate the minimum and maximum number of colonization events with regard to those species. Congeneric endemics of an archipelago are considered as monophyletic, thus representing a single colonization event (minimum number of colonisations) or are treated as polyphyletic, whereby each species represents a different colonization event (maximum number). Additionally, if a genus has n archipelagic species and molecular phylogenies exist for $n-1$ species, the remaining species is considered as either a sister clade to all the rest (minimum number) or as an independent colonization event (maximum number).

This approach might over-estimate colonization events where there are multiple genera with endemic species in an archipelago, all of which are extinct, because genera are treated a priori as independent colonisations notwithstanding that they might also represent monophyletic groups (i.e., lineages that have radiated *in situ* following colonization by a common ancestor). Therefore, our main analyses were performed using the minimum number of colonization events retrieved (but see Section C.3 and C.5 below). After having randomly selected a given number of colonizers from the pool, morphological data and the phylogenetic position of each newly established colonizer were recorded.

The second step aimed to simulate *in-situ* speciation, keeping constant (1) the total number of species in each archipelago, and (2) the number of endemic species. We did not keep constant the number of anagenetic and cladogenetic species (Fig. S2) and once a species has colonized the archipelago, it was permitted either to stay unchanged (native non-endemic), speciate via anagenesis, or radiate through cladogenesis (Fig. S2). The numbers of anagenetic and cladogenetic events were constrained therefore by both the number of colonization events and the total number of endemic species.

To illustrate the approach, let us consider an archipelago that has had three colonization events, and contains one native non-endemic species and five endemic species. One of the colonization events will have led to the one native non-endemic, and the two other colonization events could have resulted in two possible scenarios generating the five endemic species: (1) either one anagenetic species and a monophyletic endemic clade of four species (cladogenesis), (2) or two monophyletic endemic clades of two and three species, respectively. One of these two possibilities (in this example) is then randomly chosen. Therefore, at each run, our simulation procedure randomly selects a possible scenario determining the number of anagenetic and cladogenetic species, given the number of colonizations, number of species and number of endemic species of the archipelago considered.

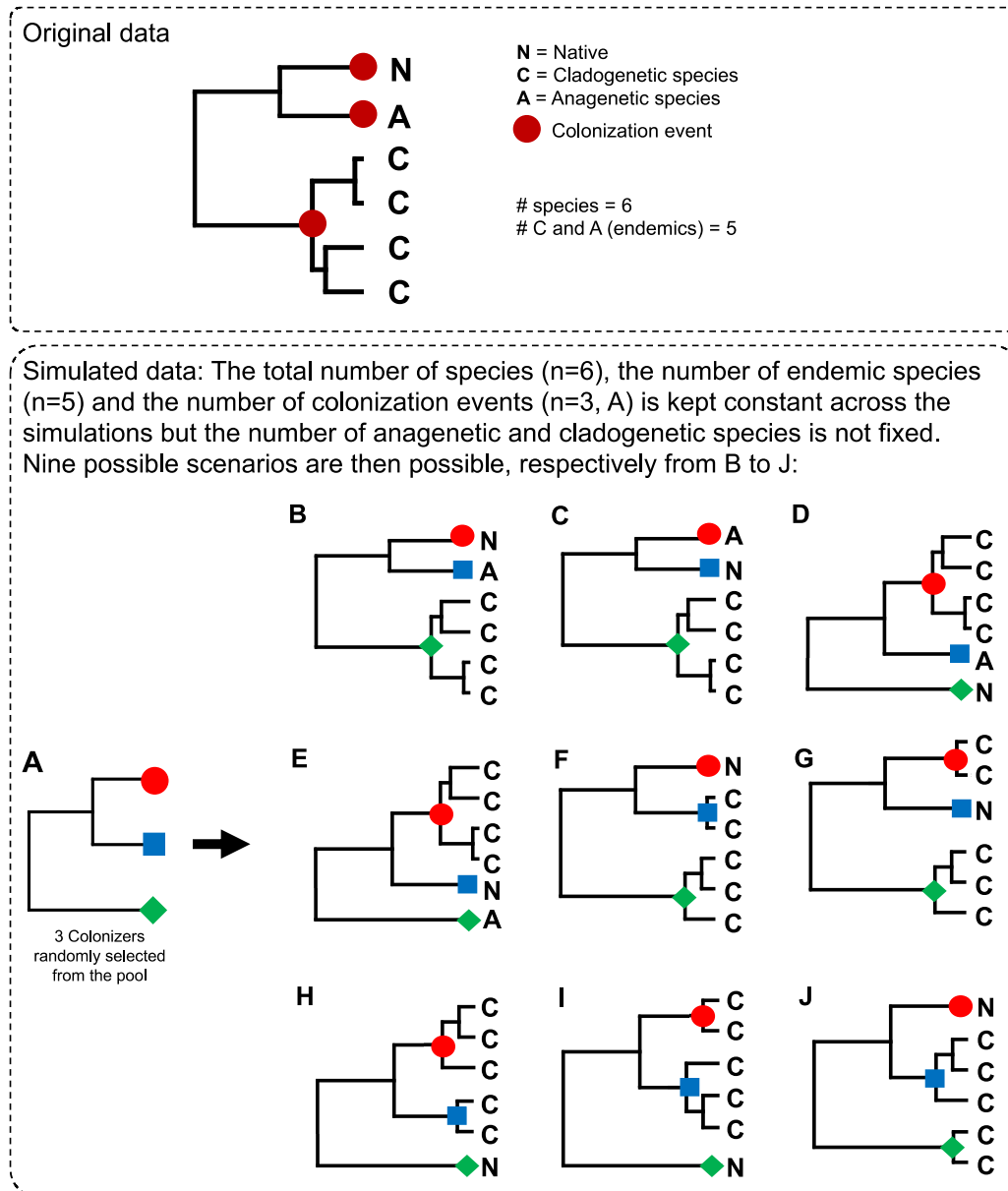


Figure S2. The figure represents how the null model implemented in the study deals with uncertainty in the status of the endemic species. The top panel illustrates the case of a hypothetical archipelago with a total of six species, among which one is a native non-endemic, one results from anagenetic speciation, while four belong to the same monophyletic endemic clade. In total, this archipelagic assemblage originated from three colonization events. Since our model keeps constant only the number of species, the number of endemics per archipelago, and the number of colonization events, it may lead to nine distinct species arrangements for this given archipelago. Note that for the cases B, C, D and E, another arrangement exists between the four species C of the endemic clade that is not shown for simplicity.

New morphological features of anagenetic species and *in-situ* radiations were simulated through a Brownian motion model of evolution (BM). Under a Brownian model of evolution, a trait value changes as a function of elapsed time (t) and rate (σ^2), so that the simulated value is normally distributed with the mean equal to its initial value (x_0) and the variance equal to the product of rate and time:

$$x_t \sim \mathcal{N}(x_0, \sigma^2 t).$$

We modelled the evolution of body plan and body mass with a BM model. For body mass, simulations were performed using an univariate BM model while, for body plan, a multivariate BM framework was used to fit the BM model simultaneously to the four size-corrected traits together while assuming that traits are correlated (Armbruster et al., 2014; Clavel et al., 2015). To simulate morphological traits of endemic species resulting from cladogenetic events, a birth-death (BD) tree was first generated with a fixed number of extant species, corresponding to the number established in scenario B or C in Fig. S1 (e.g. the BD tree for a monophyletic clade of four endemics in scenario B). The time since the most recent common ancestor was fixed for the stem node at the age of the oldest currently occurring island (Valente et al., 2015; 2017; 2020; Table S1). For both anagenetic species and endemic clades, the BM model was applied on the branches of the tree using as starting values (i.e. ancestral states) the trait values of the colonizers.

One critical aspect of our approach was to properly select a rate of birth (speciation rate λ) and death (extinction rate μ) to generate the BD phylogeny, as well as the rate of morphological evolution, σ^2 , for body mass and morphological shape separately, to create null trait values for the new anagenetic and cladogenetic species. Here, we used the rates estimated for the family to which the colonizers belong. We estimated speciation rate (λ) and extinction rate (μ) of each family of the global dataset by fitting a BD model on the respective phylogeny (island species excluded). We also retrieved the σ^2 value for each family by fitting a BM model to the phylogeny and the traits of each family (island species excluded).

As detailed previously, univariate and multivariate models were used for body mass and morphological shape, respectively. Therefore, in the course of our simulation procedure and for a given archipelago A, if a species S, belonging to the family F, has been randomly selected from the pool to colonize archipelago A, and subsequently to give birth to an endemic clade of four species, we (1) used the geological age of archipelago A, and λ , μ estimated for the tree of the family F to create the tree of the endemic clade, and (2) the trait value of S as the ancestral state and σ^2 estimated for the tree and traits of family F, to generate trait values for the four endemic species along the BD tree previously generated. For families with fewer than 10 species, we used species from the order to which the family belongs, for a better estimation of σ^2 . In total, σ^2 was estimated for 84 families, representing 6,035 species (96% of the species included in the pools) and for 19 orders representing 199 species (4% of the species included in the pools).

It is worth noting that, along with null species traits (see above), a null phylogeny was also reconstructed during each simulation. To do so, we retained as a backbone tree the phylogenetic relationships between colonizers randomly selected from the pool and grafted to the colonizers that gave birth to an endemic clade, the associated simulated BD tree(s) of the clade. The simulation protocol was independently implemented 1000 times for each archipelago. Simulated data (body plan with size-corrected traits, body mass and phylogeny) were used to generate 1000 random values for all pairwise turnover values (the turnover value between a pair of archipelagos) and 1000 average pairwise turnover values among all pairs of archipelagos. To test if archipelagos were convergent in terms of morphology and phylogeny, we tested whether pairwise turnover values and average turnover were less than expected under the null model simulation (one-tailed test). The P-values were

then estimated as the ratio between the number of times the observed turnover was lower than the null values (one-tailed test).

Null model approach using species pool may suffer high Type I error rate due to differences between the species richness in the focal assemblages and the pool (Kraft et al. 2007, Swenson et al. 2006). To evaluate the type I error of our approach in detecting community convergence, we first designed a set of simulations to test the power and particularly the type I error of the metric $MNTD_{TURN}$ in detecting community convergence by using different combinations of community (i.e. archipelago) and pool size (i.e. regional pool) and second we re-ran our convergence analyses by randomly selecting for each archipelago a subset of the pool for which the size of the archipelago corresponds to 30 and 60% of its size (Kraft et al. 2007). Details of the methods and results are presented in section C.6 and C.7.

All statistical analyses were implemented within the R programming environment (R Development Core Team, 2018) using the package *geiger* (Pennell et al., 2014), *Rphylopars* (Goolsby et al., 2016), *mvMORPH* (Clavel et al., 2015), *qgraph* (Epskamp et al., 2012), *TreeSim* (Stadler, 2011), and *phytools* (Revell, 2012). Spatial data analysis was performed using QGIS 3.4.

B3. Estimation of Colonization Events.

We estimated the number of colonization events for each of the 18 archipelagos according to the following rules. When explicit phylogenetic hypotheses were available (Valente et al., 2020), we examined whether congeneric endemic species from a particular archipelago formed a monophyletic group or not, assuming, when this was the case, that they were most likely the product of a single colonization event (Cornuault et al., 2013). Thus, for a particular archipelago, our measure of the number of colonization events that gave rise to the current endemic avifauna was the number of clades (mostly genera) present on this archipelago. For native non-endemic species, each was thus counted as one colonization event. See Table S5 for the minimum and maximum numbers of colonization events for each of the 18 archipelagos. Colonization events for different archipelagos are summarized as follows.

Austral islands: There are two undescribed extinct species of *Pampusana* and *Ptilinopus huttoni* and the undescribed *Ptilinopus* sp. (Steadman, 2006), also extinct. In the absence of phylogenetic information on these extinct species, our estimate of the minimum number of colonization events was thus based on considering both *Ptilinopus* as belonging to the same clade, while for estimating the maximum number, we considered that they belong to two separate clades. We treated the two *Pampusana* species similarly.

Azores: *Pyrrhula* is represented by two endemic species, *P.* and *P. crassa*, the latter being extinct. *Rallus* is represented by three archipelagic-endemic and extinct species (Alcover et al., 2015) In the absence of phylogenetic information on these extinct species, our estimate of the minimum number of colonization events was thus based on considering all *Rallus* species as belonging to the same clade, while for estimating the maximum number, we considered that they belong to three separate clades. We treated the two *Pyrrhula* species similarly.

Canary Islands: The *Columba* species clearly arose from separate colonization events (Cornuault et al., 2013). *Fringilla polatzeki* and *F. teydea* are sister species (Dourado et al., 2014; Valente et al., 2020). *Cyanistes* species represent at least three independent colonizations (Suárez et al., 2011; Stervander et al., 2015).

Comoros: *Zosterops* species, belonging to the Indian Ocean *Z. maderaspatanus* clade, seem to be paraphyletic with respect to the Malagasy species (Melo et al., 2011). An additional species (*Z. mouroniensis*) belongs to a different *Zosterops* clade. For the four *Otus* species, evidence supports two

independent colonization events, *Otus moheliensis*/*O. pauliani* and *O. capnodes*/*O. mayottensis* (Fuchs et al., 2008). *Nesillas brevicaudata* and *N. mariae* are sister species (Fuchs et al., 2016). The *Hypsipetes* species (Warren et al., 2005) are paraphyletic relative to a number of taxa from diverse regions, suggesting a minimum of two separate colonizations, and the *Cinnyris* species (Warren et al., 2003) possibly arose from two colonizations of the archipelago. The three *Dicrurus* species (two are archipelagic endemics) are non-monophyletic and likely represent three independent colonization events (Pasquet et al., 2007).

Cook: *Ducula pacifica* and *D. aurorae* are sister species but the relationships with *D. galeata* are unresolved. While the first two species are present on other archipelagos too, they are considered as endemic to Cook Islands for the estimation of the minimum number of colonizations (Cibois et al., 2014). *Aerodramus manuoi* (extinct) and *A. sawtelli* are considered sister species for the minimum number of colonizations, and as non-sisters for the maximum number. The same rule was applied for *Aplonis cinerascens* and *A. mavornata*.

Fernando de Noronha: All species belong to different genera and no molecular data indicate monophyly between any of them.

Galápagos: Darwin's finches (*Camarhynchus* spp., *Certhidea* spp. *Geospiza* spp. and *Platyspiza crassirostris*) and Galápagos mockingbirds (*Mimus* spp.) each form monophyletic groups (Valente et al., 2015). *Pyrocephalus dubius* and *P. nanus* are also sister-species and may represent a single colonization event (Carmi et al., 2016).

Gulf of Guinea: All *Zosterops* species endemic to the archipelago form a monophyletic group (Ryan et al., 2013). *Turdus olivaceofuscus* and *T. xanthorhynchus* are sister species (Fabre et al., 2012). *Terpsiphone atrochalybeia* and *T. smithii* are not sister species and represent two independent colonization events (Fabre et al., 2012).

Hawaii: The number of colonizations for Passeriformes is estimated to be six (Ricklefs & Bermingham, 2007), with Hawaiian honeycreepers being monophyletic (Lerner et al., 2011). *Zapornia* species are inferred to be the result of two independent colonization events (Slikas et al., 2002).

Juan Fernández: The relationship between *Sephanoides fernandensis* as sister species of *S. sephaniodes* is debatable (see Valente et al., 2020). Following Roy et al. (1998) we consider that the species represent two independent colonization events. The rest of the species belong to different genera and no molecular data indicate any monophyletic groupings among them.

Madeira: All but four species belong to different genera and there are no molecular data to indicate monophyly between any of them (Dourado et al., 2014). Two undescribed extinct species of *Coturnix* (Cibois et al., 2004) are considered as being sister species for the minimum estimate of the number of colonization event and non-sister and polyphyletic for the maximum estimate, respectively, and the same stands for the extinct species *Rallus adolfocaesaris* and *R. lowei* (Alcover et al., 2015).

Marquesas: *Ptilinopus mercierii* and *P. dupetithouarsii* form a monophyletic group (Cibois et al., 2014) and all *Pomarea* species endemic to the archipelago also belong to a monophyletic group (Cibois et al., 2004). *Acrocephalus mendanae* and *A. percernis* are not sister species and clearly represent two independent colonization events (Cibois et al., 2011). There are three extinct endemic species of *Gallirallus* (Kirchman & Steadman, 2007) and three undescribed species of *Porzana* (Steadman, 2006); in each case, for the minimum number of colonizations, we considered that both *Gallirallus* and *Zapornia* diversified *in situ* following a single colonization event.

Mascarenes: The four *Zosterops* endemic species (*Z. borbonicus*, *Z. chloronothos*, *Z. mauritanus* and *Z. olivaceus*) form a monophyletic clade (Warren et al., 2006). *Lalage newtoni* and *L. typica* are sister species (Jönsson et al., 2010). *Raphus cucullatus* and *Pezophaps solitaria* are also considered to be sister species (Soares et al., 2016). *Hypsipetes borbonicus* and *H. olivaceus* represent independent colonizations (Warren et al., 2005) and we also treat the extinct *Hypsipetes cowlesi* as such (Hume, 2015). Similarly, *Foudia flavicans* and *F. rubra* may represent independent colonizations (Melo et al., 2011), and we treat the extinct *Foudia delloni* as such too (Cheke & Hume, 2008, 2018). The three endemic, extinct species of *Alectroenas* (*A. nitidissimus*, *A. payandeei* and *A. sp.*) (Hume, 2019) are considered to form a monophyletic group for the estimation of the minimum number of colonizations.

The same applies to *Psittacula* spp. (five species, only *P. eques* is extant), *Nesoenas* spp. (five species, only *N. mayeri* is extant), *Necropsittacus* spp. (two species), *Otus* spp. (three species), and *Dryolimnas* spp. (two species).

Pitcairn: All species belong to different genera and there are no molecular data that indicate any monophyly between any of them, apart from *Acrocephalus taiti* and *A. vaghani*, which are sister species (Valente *et al.*, 2020).

Revillagigedo: *Troglodytes tanneri* and *T. sissonii* may prove to be sister species (Gómez *et al.*, 2005; Sosa-López, 2014). Therefore, we considered both scenarios, i.e., either two independent colonization events or one colonization event.

Samoa: Neither *Lalage maculosa* and *L. sharpie* (Jønsson *et al.*, 2010), nor *Todiramphus chloris* and *T. recurvirostris* (Andersen *et al.*, 2015) are considered to be sister species. Therefore, two independent colonizations events were assumed in both cases.

Society Islands: *Acrocephalus longirostris*, *A. musae*, and *A. caffer* are probably unrelated but their relationships are not fully unresolved (Cibois *et al.*, 2008). Therefore, we considered three colonization events, but see Valente *et al.* (2020).

Tristan da Cunha: The three *Neospiza* species form a monophyletic group (Ryan *et al.*, 2007, 2013).

Table S5. Retrieved minimum and maximum numbers of colonization events for each of the 18 archipelagos, first considering all land-bird species, and then Passeriformes, including extinct species and for extant species only. Min. = minimum; Max. = maximum.

	All land-bird species				Passeriformes			
	All species		Extant species		All species		Extant species	
	Min.	Max.	Min.	Max.	Min.	Max.	Min.	Max.
Austral	5	7	3	3	1	1	1	1
Azores	17	20	15	15	9	10	9	9
Canary Islands	58	59	56	56	32	33	30	31
Comoros	46	46	46	46	26	26	26	26
Cook Islands	17	20	11	11	3	4	3	3
Fernando de Noronha	4	4	3	3	2	2	2	2
Galápagos	13	13	13	13	6	6	6	6
Gulf of Guinea	50	50	50	50	29	29	29	29
Hawaii	13	17	8	8	6	6	6	6
Juan Fernández	9	9	9	9	4	4	4	4
Madeira	29	32	25	25	13	15	13	13
Marquesas	16	20	9	9	3	3	3	3
Mascarenes	32	45	17	17	15	15	10	10
Pitcairn	7	7	5	5	1	1	1	1
Revillagigedo	14	15	14	15	7	8	7	8
Samoa	30	30	28	28	15	15	15	15
Society	21	24	10	10	3	6	2	2
Tristan da Cunha	5	5	5	5	3	3	3	3

C. Supplementary analyses and results

C.1 Overview of the supplementary analyses

We first performed a series of sensitivity analyses to assess the Type I error rate in detecting convergence with of the metric $MNTD_{TURN}$ in relation to the pool and community size.

To evaluate how convergence patterns vary with different processes of species accumulation, we restricted our convergence analyses to three different sets of species: non-extinct species, endemics, and native non-endemics. This was done for all land-birds and, separately, for Passeriformes. We also performed analyses to test whether our findings were sensitive to (1) the definition of our species pool and (2) the uncertainty regarding the number of colonization events. For all the aforementioned analyses, we re-implemented our analytical pipeline to test for convergence of body plan, body mass and phylogeny using among archipelago morphological/phylogenetic turnover (See section B). To summarize and simplify the outcomes of these supplementary analyses, we calculated the deviations of the observed among archipelago turnover from null expectation using a standardized effect size (SES). SES was calculated as:

$$SES = \frac{(MNTD_{TURN} - \mu_{null})}{\sigma_{null}}$$

where $MNTD_{TURN}$ is the observed among archipelago turnover value, μ_{null} , the mean of the $MNTD_{TURN}$ of the simulations, and σ_{null} its associated standard deviation. Negative SES values indicate lower morphological/phylogenetic turnover than expected by chance. P-values were also estimated as the ratio between the number of times observed turnover was lower than simulated and the number of simulations (one-tailed test).

We also explored the difference in taxonomic composition, i.e. orders, families, between each archipelago and its respective species pool to test if the convergence patterns reported in our study might be due to the fact that only certain orders/families preferentially colonized oceanic archipelagos globally. Finally, we tested the effect of the removal of the two hummingbird species of Juan Fernández (the only species in this morphologically distinct family present on any of the oceanic archipelagos included in this study) in the convergence patterns between pairs of archipelagos.

Details of the aforementioned analyses are given below and a brief summary of their results and main conclusions is given in section C.7 (below).

C2. Influence of the size pool in detecting convergence with $MNTD_{TURN}$.

Null model approach using species pool may suffer high Type I error rate due to differences between the species richness in the focal assemblages and the pool (Kraft et al. 2007, Swenson et al. 2006). To evaluate the type I error of our approach in detecting community convergence, we first designed a set of simulations to test the power and particularly the type I error of $MNTD_{TURN}$ in detecting community convergence by using different combinations of community (i.e. archipelago) and pool size (i.e. regional pool). Second, we re-ran our convergence analyses by randomly selecting for each archipelago a subset of the pool for which the size of the archipelago corresponds to 30 and 60% of its size (See Kraft et al. 2007).

For the first set of analyses, we first created two trait pools of N species using a normal distribution bounded between 0 and 1 with a mean around 0.5. To simulate convergence, we selected within each pool a community of n species with trait values closest to the mean (0.5), the mean being considered here as the niche optimum i.e. the value to which communities converge. To simulate the absence of convergence (neutral scenario), we simply selected at random from each pool a community of n species without respect to trait values. For each scenario (convergence and neutral), we then calculated the $MNTD_{TURN}$ between the two communities, with these $MNTD_{TURN}$ values considered in the following analyses as our observed values, one representing convergence and the other representing no convergence. The next step was to randomly select n species from each pool 1000 times and to recalculate $MNTD_{TURN}$ between the two communities at each run to generate 1000 values of null expectation for $MNTD_{TURN}$. Our observed $MNTD_{TURN}$ values (both convergence and neutral) were then compared to these 1000 null values by calculating one-tailed p-values under the null hypotheses of no convergence. We then expected the $MNTD_{TURN}$ for the convergence scenario to be lower than expected ($P < 0.05$) while for the neutral scenario to not differ from the null values ($P > 0.05$). If, for the latter, $P < 0.05$, this means that our approach has a type I error, showing convergence (rejected H_0) when it should not.

All these analyses were performed 1000 times and a percentage of correct outcomes was calculated (number of $P < 0.05$ for the convergence scenario and $P > 0.05$ for neutral scenario). We implemented this set of simulations for different combination of pool (N) and community (n) sizes with N being set up at 50, 100, 300, 500, 1000 and 2000 and n at 5, 10, 20, 50, 100. Only the combination $N = n = 50$ was excluded.

To test whether our approach was sensitive to the trait distribution we choose, we also performed the analysis with only half of a normal distribution rescaled to be bound between 0 (max prob) and 1 with 0 being the trait optimum to which communities converge (equivalent to directional filtering).

In Figure S3, we show the results obtained for the test for the neutral scenario. For the convergence scenario, all runs did show significant convergence (100% correct, data not shown). For the neutral scenario with the trait normally distributed (left panel), we found that all combinations of size produced on average 95% of correct outcomes with a minimum of 91 for $N=100$ and $n=5$ and a maximum of 0.99 for $N=500$ and $n=20$. Similar results were obtained for the trait distributed in half of a normal distribution, with on average 94% of correct outcomes (right panel). Therefore, these analyses show that the statistical approach implemented in our study had very low type I error, with around a 5% chance of detecting convergence when it is not present, and this was not sensitive to either the size of the community or the size of the pool.

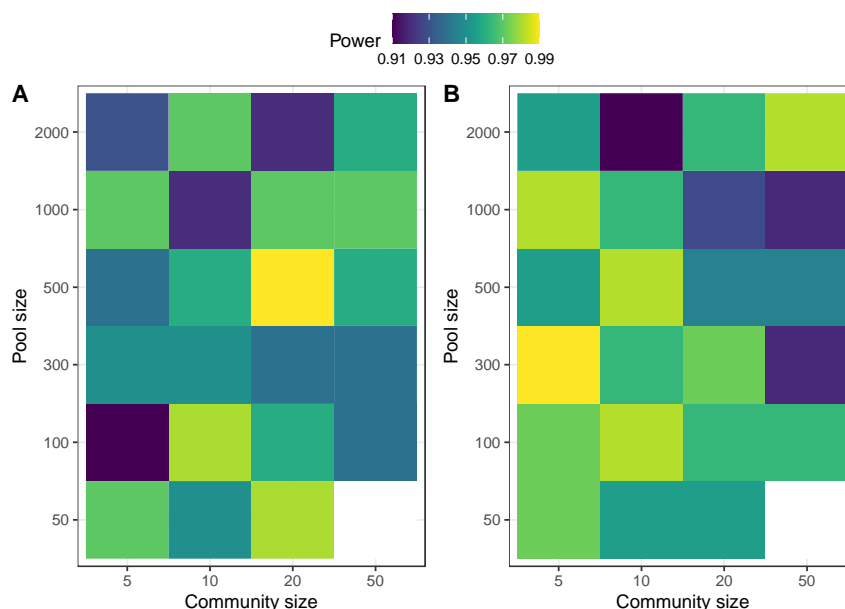


Figure S3. Results from simulations showing the effect of variation in pool and community size on the detection of convergence using one two trait distribution: trait normally distributed (A bounded between 0 and 1 with a mean around 0.5 and a trait distributed in half of a normal distribution (B) rescaled to be bound between 0 (max prob) and 1 with 0 being the trait optimum to which communities converge (equivalent to directional filtering). Only the results of the neutral scenario are shown. The

power of the test is expressed as the percentage of correct outcomes (no convergence) per combination of size.

For the second set of analyses, we performed our convergence analyses by randomly selecting for each archipelago a subset of the pool for which the size of the archipelago corresponds to 30 and 60% of its size. This was done 100 times and the results are shown in Figure S4. Analyses were performed for body shape, size and phylogeny, with each dot representing the P-values of the one-tailed test of whether among archipelago $MNTD_{TURN}$ was lower than expected. We clearly show that, in most cases, we detected significant convergence, as per our original analyses. We only detected an absence of convergence for 5 and 4 runs for shape and size, respectively, at 30% and for 4 and 3 runs for shape and size, respectively, at 60%.

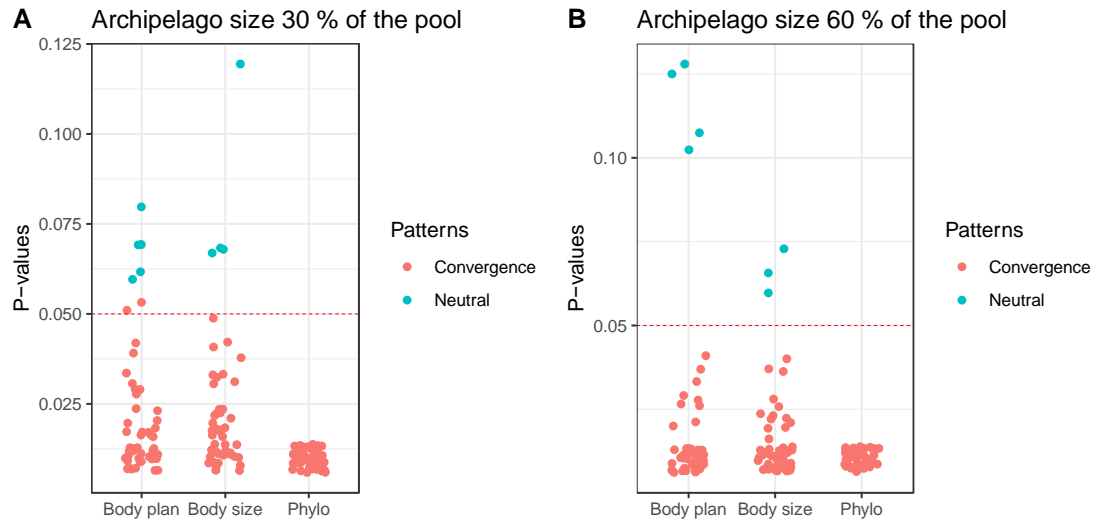


Figure S4. Results from simulations showing the effect of variation in size pool in relation to the community size where convergence analyses for each archipelago were recomputed by randomly selecting as a pool a subset of the original pool for which the size of the archipelago corresponds to (A) 30 and (B) 60% of its size. The analyses were performed 100 times. For each dimension (body plan, body mass and phylogeny), P-values for each run were recorded and plotted, with red dots showing significant convergence and blue dots showing absence of convergence.

C.3 Uncertainty in the definition of the species pool

a) The species pools adopted in our study [i.e. the zoogeographic region the archipelago belongs to, based on Holt et al. (2013)] are approximate. Thus, we also test the sensitivity of our approach to a more spatially restricted definition of species pool by defining a buffer of 100 km width from the nearest coast to the archipelago of interest and considering only the species with a distribution overlapping with the buffer. Through this approach we are restricting the potential species pool to those species close to the coastal regions that will potentially have higher chances of colonizing the relevant archipelago. This approach was applied to all pools except for Madagascar (region 10 in Table S3), for which the number of species in the pool retrieved by our approach ($N=24$ for all land-birds and 2 for Passeriformes) was lower than the species richness of its associated archipelago (i.e. $N=50$, and $N=19$ and for Mascarenes, and $N=52$, and $N=27$ for Comoros, for all land-birds,

and for Passeriformes, respectively). Therefore, we kept the whole species pool for Madagascar in the analysis. The number of species retrieved for each restricted pool is given in Table S3.

b) Analyses were also undertaken when considering only archipelagos belonging to the same zoogeographical region. This was possible only for Macaronesia (Azores, Madeira and Canary Islands archipelagos) and for the South Pacific (Austral Islands, Cook Islands, Marquesas, Samoa, Pitcairn and Society), two regions with more than two archipelagos. This analysis allows us to test the validity of our results without the potential effect of the species pool definition. Within each set, these archipelagos were considered as belonging to the same zoogeographic region and thus in theory having the same species pool. Within these two regions, analyses were also performed for non-extinct, endemic and native non-endemic species, both for all land-birds and for a dataset restricted to Passeriformes, and also by considering uncertainty in the number of colonization events.

C.4 Uncertainty in the number of colonization events.

Our null model for convergence was implemented using the minimum number of colonization events retrieved from our literature search. However, we also implemented a second set of analyses where, in each run, the number of colonization events was randomly chosen to be between the minimum and the maximum (Table S5).

C.5 Difference in taxonomic composition between each archipelago and its respective species pool.

We explored the difference in taxonomic composition between each archipelago and its respective species pool, the goal being to evaluate whether any observed convergent properties may be due to limitations on which orders/families can overcome sea-barriers and establish on oceanic archipelagos globally, leading, thus, to phylogenetic and morphological similarity among oceanic archipelagos.

First, we simply compared the identity of the two most dominant orders (i.e. the orders with the largest number of species) in each of the 18 archipelagos considered in the study, with those of their respective regional pools. To facilitate comparisons between archipelago and regional pool, we ranked the orders based on the species richness of each order. For most archipelagos, the rank is therefore 1 and 2 for the most and the second most dominant orders, except for Society Islands, where Columbiformes and Passeriformes had similar numbers of species (Rank 1 for both).

Second, we tested for any taxonomic differences between each archipelago and its respective regional pool at family level. To do so, we used two metrics: (1) we simply counted the families in each archipelago and (2) we calculated the dissimilarity in family composition and proportion of species per family between the archipelago and its associated species pool. Dissimilarity in family composition was quantified using the *Manly* distance (Manly, 1994), a measure of distance well-suited to percentage values. Both the observed number of families and the dissimilarity were compared against 1000 null values generated by randomly sampling from the species pool the same number of species as observed in the respective archipelagos.

Deviation from null expectation for both number of families and dissimilarity was quantified using the standardized effect size (SES). Deviations were considered significant if the SES value was either lower or higher than -1.96 and 1.96 respectively [two-tailed tests, (Gotelli & McCabe, 2002)]. Regarding the number of families per archipelago, a positive and significant SES value indicates that the number of families occurring in the archipelago is higher than expected by chance, while a negative and significant SES value indicates a lower number of families than expected by chance. For the dissimilarity in family composition, positive and significant SES values indicate that the observed archipelagic family composition is significantly more dissimilar to the family composition of the pool (divergence) while negative and significant SES values indicate that the observed archipelagic family composition is significantly less dissimilar (convergence) to the family composition of the pool. Both analyses were performed for all land birds, and for Passeriformes (See Table S10 and S11).

C.6. Testing the effect of the removal of hummingbird species of Juan Fernández in convergence patterns between pairs of archipelagos.

In the analyses implemented with all land birds, all archipelagos exhibited significant body plan and phylogenetic convergence (i.e. lower pairwise MNTD_{TURN} than expected) with at least one other archipelago with exception of Juan Fernández (Figure 3A and C). For body mass, several archipelagos showed no significant similarity with any other archipelago (Fig. 3B). The lack of significant findings for Juan Fernández could potentially be accounted for by the presence of two hummingbird species (i.e. *Sephanoides fernandensis* and *Sephanoides sephaniodes*; Trochilidae) on the archipelago, the only species in this morphologically distinct family present on any oceanic archipelago.

C.7 Results of the supplementary analyses

We detected convergent properties in body mass, body plan and phylogeny in communities of all land-birds. Similarly, we detected convergent properties in body plan and phylogeny (but not for body mass) for communities restricted to Passeriformes. When we restricted our analysis to extant species only, body plan and phylogenetic convergence was highly significant (Table S6) for all land-birds, and Passeriformes alone presumably because most of the morphologically divergent species were endemic and are now extinct, with extreme examples such as *Raphus cucullatus* and *Pezophaps solitaria*, both highly distinct from any extant Columbiformes. However, significant convergence for body mass was only detected for all land birds. For native non-endemic species, convergence was detected for land-bird species (although convergence was weaker); for Passeriformes, however, convergence was again absent for body mass and phylogeny.

Overall, results obtained for native non-endemic species have to be viewed with caution since only 12, and 7 out of 18 archipelagos were considered in the analyses for land-birds, and Passeriformes, respectively. That is, 6 and 11 archipelagos had fewer than 3 native non-endemic species for land-birds and Passeriformes, respectively, and were excluded from the analyses. Additionally, morphological and phylogenetic convergence was found to be stronger among all groups when extinct species were excluded from the analyses compared to results obtained with all species, suggesting therefore a pattern consistent with a trend towards biotic homogenization due to human-induced extinctions (Sax & Gaines, 2002; Cassey et al., 2007; Rosenblad & Sax, 2017).

Similar patterns were found when we restricted our analysis to archipelagos with the same potential source (the three Macaronesian archipelagos and the South Pacific archipelagos, Table S6), suggesting that our overall results are not an artefact due to the definition of the regional species pools. Convergence appears even when only archipelagos with the same species pool are considered. Similar patterns were also obtained from (1) the analysis with the number of colonization events randomly selected between the minimum and maximum number retrieved from the literature and (2) the analyses performed with the restricted species pool (buffer of 100km width from the coast) (Table S7, S8 and S9), indicating therefore that our main outcomes were robust to the uncertainty regarding the number of colonization events and in respect of species pool definition.

Results of our analyses testing differences in taxonomic composition between archipelagos and their species pools revealed that: (1) most of the avifauna of the 18 archipelagos was dominated by two main orders, Passeriformes and Columbiformes, with Columbiformes being overrepresented compared to the respective zoogeographic regions (Table S10) and; (2) most of the archipelagos displayed a family composition and a number of families significantly different and smaller, respectively, than 1,000 random draws from their respective species pools (Table S11). Together these results provide support for the idea that both dispersal and environmental filtering shape species community structure on these oceanic archipelagos.

Finally, a reanalysis of the convergence pattern without the two hummingbirds showed convergence of Juan Fernández with at least four archipelagos for body plan and phylogeny, but still no evidence of convergence for body mass (Fig. S5). (See Figure S5).

Table S6 Results of the convergence analysis using the minimum number of colonization events retrieved and defining the species pools as the entire zoogeographic regions to which each archipelago belongs. Analyses were performed for all species, non-extinct species, endemic species and native non-endemic species, for all land-birds, and for Passeriformes. Analyses were performed for all archipelagos together and for Macaronesia (Canaries, Azores and Madeira) and the South Pacific (Austral, Cook Islands, Marquesas, Samoa, Pitcairn and Society) separately. For among archipelago turnover in body plan, body mass and phylogeny, standardized effect size (SES) and the P-values of the one-tailed tests are also provided; negative and significant SES indicating community convergence. See further details in section C. In parentheses, the number of archipelagos considered is given, with the first number being for all land-birds and the second number for Passeriformes, considering that an archipelago was included in an analysis of a given group (All, Non-Extinct, Endemic and native non-endemic) only if more than two species were represented. For South Pacific native non-endemic Passeriformes, less than two archipelagos fulfilled the aforementioned criteria and therefore no convergence analyses were performed in these cases. Significant results are marked in bold (see also Fig. 2).

All archipelagos	Grouping	All land-bird species		Passeriformes	
		SES	P	SES	P
	All species (18, 15)				
	Body plan	-2.364	0.006	-3.291	0.0010
	Body mass	-1.868	0.006	-0.970	0.1578
	Phylogenetic	-4.679	<0.001	-4.325	0.0010
	Non-Extinct species (18, 14)				
	Body plan	-3.415	<0.001	-3.337	0.0010
	Body mass	-2.275	<0.001	-0.720	0.2527
	Phylogeny	-4.534	<0.001	-4.038	0.0010
	Endemic species (18, 14)				
	Body plan	-2.130	0.010	-2.770	0.0010
	Body mass	-0.324	0.423	-1.082	0.1099
	Phylogeny	-3.757	<0.001	-4.135	0.0010
	Native non-endemic (12, 7)				
	Body plan	-2.836	<0.001	-2.391	0.0050
	Body mass	-1.633	0.014	0.898	0.8282

	Phylogeny	-1.877	0.031	-2.597	0.0010
Macaronesia		SES	P		
	All species (3, 3)				
	Body plan	-3.556	<0.001	-3.556	0.001
	Body mass	-2.459	<0.001	-2.459	0.001
	Phylogeny	-4.245	<0.001	-4.245	0.001
	Non-Extinct species (3, 3)				
	Body plan	-7.501	<0.001	-7.501	0.001
	Body mass	-2.821	<0.001	-2.821	0.001
	Phylogeny	-6.100	<0.001	-6.100	0.001
	Endemic species (3, 3)				
	Body plan	-0.804	0.219	-0.804	0.219
	Body mass	-0.898	0.169	-0.898	0.169
	Phylogeny	-1.688	0.039	-1.688	0.039
	Native non-endemic (3, 3)				
	Body plan	-7.662	<0.001	-7.662	0.001
	Body mass	-2.344	<0.001	-2.344	0.001
	Phylogeny	-6.048	<0.001	-6.048	0.001
South Pacific		SES	P	SES	P
	All species (6, 5)				
	Body plan	-2.427	0.002	-2.299	0.001
	Body mass	-1.638	0.006	-1.096	0.099
	Phylogeny	-5.714	0.001	-5.057	0.001
	Non-Extinct species (6, 4)				

Body plan	-3.156	0.001	-1.550	0.025
Body mass	-2.165	0.001	-0.442	0.392
Phylogeny	-5.663	0.001	-3.669	0.001
Endemic species (6, 5)				
Body plan	-1.416	0.068	-1.974	0.007
Body mass	-1.449	0.028	-1.253	0.057
Phylogeny	-4.202	0.001	-5.503	0.001
Native non-endemic (4, 1)				
Body plan	-4.412	0.001	-	-
Body mass	-2.274	0.001	-	-
Phylogeny	-6.305	0.001	-	-

Table S7. Results of the convergence analysis considering uncertainty in the number of colonization events and using as species pools the entire zoogeographic regions to which each archipelago belongs. For each run, number of colonization events was randomly selected between the minimum and maximum number of colonization events retrieved from the literature (see Table S5). Analyses were performed for all species, non-extinct species, endemic species and native non-endemic species, both for all land-birds and for Passeriformes. Analyses were performed for all archipelagos together and for Macaronesia and the South Pacific separately. For among archipelago turnover in body plan, body mass and phylogeny, standardized effect size (SES) and the P-values of the one-tailed tests are also provided; negative and significant SES indicating community convergence. See further details in section C. In parentheses, the number of archipelagos considered is given, with the first number being for all land-birds and the second number for Passeriformes, considering that an archipelago was included in an analysis of a given group (All, Non-Extinct, Endemic and native non-endemic) only if more than two species were represented. For South Pacific native non-endemic Passeriformes, less than 2 archipelagos fulfilled the aforementioned criteria and therefore no convergence analyses were performed in these cases. Significant results are marked in bold. Significant results are marked in bold.

All archipelagos	Grouping	All land-bird species		Passeriformes	
		SES	P	SES	P
	All species (18, 15)				
	Body plan	-1.807	0.025	-3.393	0.001
	Body mass	-1.530	0.033	-0.923	0.161
	Phylogenetic	-4.114	0.001	-4.377	0.001
	Non-Extinct species (18, 14)				
	Body plan	-3.137	0.001	-3.297	0.001
	Body mass	-2.045	0.001	-0.756	0.232
	Phylogeny	-4.255	0.001	-4.015	0.001
	Endemic species (18, 14)				
	Body plan	-1.788	0.019	-2.852	0.001
	Body mass	0.013	0.575	-0.998	0.147
	Phylogeny	-3.618	0.001	-4.122	0.001
	Native non-endemic (12, 7)				
	Body plan	-2.473	0.002	-2.306	0.010

	Body mass	-1.501	0.046	0.899	0.831
	Phylogeny	-1.837	0.037	-2.620	0.002
Macaronesia		SES	P	SES	P
	All species (3, 3)				
	Body plan	-3.367	0.001	-3.556	0.001
	Body mass	-2.620	0.001	-2.459	0.001
	Phylogeny	-4.254	0.001	-4.245	0.001
	Non-Extinct species (3, 3)				
	Body plan	-7.849	0.001	-7.501	0.001
	Body mass	-2.704	0.001	-2.821	0.001
	Phylogeny	-6.217	0.001	-6.100	0.001
	Endemic species (3, 3)				
	Body plan	-0.720	0.240	-0.804	0.219
	Body mass	-0.915	0.157	-0.898	0.169
	Phylogeny	-1.863	0.027	-1.688	0.039
	Native non-endemic (3, 3)				
	Body plan	-7.958	0.001	-7.662	0.001
	Body mass	-2.376	0.001	-2.344	0.001
	Phylogeny	-5.898	0.001	-6.048	0.001
South Pacific		SES	P	SES	P
	All species (6, 5)				
	Body plan	-1.712	0.024	-2.408	0.001
	Body mass	-1.258	0.028	-1.036	0.093

Phylogeny	-4.057	0.001	-5.192	0.001
Non-Extinct species (6, 4)				
Body plan	-2.665	0.001	-1.603	0.025
Body mass	-1.743	0.001	-0.396	0.423
Phylogeny	-4.184	0.001	-3.750	0.001
Endemic species (6, 5)				
Body plan	-1.013	0.146	-2.039	0.005
Body mass	-1.058	0.116	-1.205	0.054
Phylogeny	-2.824	0.002	-5.682	0.001
Native non-endemic (4, 1)				
Body plan	-3.867	0.001	-	-
Body mass	-2.304	0.001	-	-
Phylogeny	-4.509	0.001	-	-

Table S8. Results of the convergence analysis using the minimum number of colonization events retrieved and considering our restricted species pools. Our restricted species pools were defined as a buffer of 100 km width from the nearest coast of the original pool, centered on the nearest point to the archipelago of interest (see Table S3). Analyses were performed for all species, non-extinct species, endemic species and native non-endemic species, both for all land-birds and for Passeriformes. Analyses were performed for all archipelagos together and for Macaronesia and the South Pacific separately. For among archipelago turnover in body plan, body mass and phylogeny, standardized effect size (SES) and the P-values of the one-tailed tests are also provided; negative and significant SES indicating community convergence. See further details in section C. In parentheses, the number of archipelagos considered is given, with the first number being for all land-birds and the second number for Passeriformes, considering that an archipelago was included in an analysis of a given group (All, Non-Extinct, Endemic and native non-endemic) only if more than two species were represented. For South Pacific native non-endemic Passeriformes, less than two archipelagos fulfilled the aforementioned criteria and therefore no convergence analyses were performed in these cases. Significant results are marked in bold. Significant results are marked in bold.

All archipelagos	Grouping	All land-bird species		Passeriformes	
		SES	P	SES	P
	All species (18, 15)				
	Body plan	-2.276	0.006	-3.318	0.001
	Body mass	-1.899	0.008	-0.981	0.170
	Phylogenetic	-4.682	0.001	-4.366	0.001
	Non-Extinct species (18, 14)				
	Body plan	-3.378	0.001	-3.501	0.001
	Body mass	-2.416	0.001	-0.809	0.209
	Phylogeny	-4.472	0.001	-4.039	0.001
	Endemic species (18, 14)				
	Body plan	-2.213	0.009	-2.688	0.002
	Body mass	-0.493	0.326	-1.054	0.120
	Phylogeny	-4.042	0.001	-4.167	0.001
	Native non-endemic (12, 7)				

	Body plan	-2.717	0.001	-2.311	0.007
	Body mass	-1.704	0.022	0.820	0.820
	Phylogeny	-1.854	0.028	-2.518	0.002
Macaronesia		SES	P	SES	P
	All species (3, 3)				
	Body plan	-2.753	0.001	-3.556	0.001
	Body mass	-2.192	0.001	-2.459	0.001
	Phylogeny	-3.281	0.001	-4.245	0.001
	Non-Extinct species (3, 3)				
	Body plan	-6.704	0.001	-7.501	0.001
	Body mass	-2.280	0.001	-2.821	0.001
	Phylogeny	-4.920	0.001	-6.100	0.001
	Endemic species (3, 3)				
	Body plan	-0.897	0.187	-0.804	0.219
	Body mass	-0.974	0.119	-0.898	0.169
	Phylogeny	-1.712	0.033	-1.688	0.039
	Native non-endemic (3, 3)				
	Body plan	-6.636	0.001	-7.662	0.001
	Body mass	-2.059	0.001	-2.344	0.001
	Phylogeny	-5.286	0.001	-6.048	0.001
South Pacific		SES	P	SES	P
	All species (6, 5)				
	Body plan	-2.294	0.002	-2.339	0.001

Body mass	-1.660	0.009	-1.078	0.116
Phylogeny	-5.692	0.001	-5.094	0.001
Non-Extinct species (6, 4)				
Body plan	-2.953	0.001	-1.638	0.015
Body mass	-2.200	0.001	-0.430	0.388
Phylogeny	-5.478	0.001	-3.584	0.001
Endemic species (6, 5)				
Body plan	-1.392	0.066	-1.996	0.006
Body mass	-1.395	0.046	-1.252	0.072
Phylogeny	-4.253	0.001	-5.386	0.001
Native non-endemic (4, 1)				
Body plan	-4.389	0.001	-	-
Body mass	-2.346	0.001	-	-
Phylogeny	-6.203	0.001	-	-

Table S9. Results of the convergence analysis considering uncertainty in the number of colonization events and using restricted species pools. For each run, number of colonization events was randomly selected between the minimum and maximum number of colonization events retrieved from the literature (see Table S5). Our restricted species pools were defined as a buffer of 100 km width from the nearest coast of the original pool, centred on the nearest point to the archipelago of interest (See Table S3). Analyses were performed for all species, non-extinct species, endemic species and native non-endemic species, both for all land-birds and for Passeriformes. Analyses were performed for all archipelagos together and for Macaronesia and the South Pacific separately. For among archipelago turnover in body plan, body mass and phylogeny, standardized effect size (SES) and the P-values of the one-tailed tests are also provided; negative and significant SES indicating community convergence. See further details in section C. In parentheses, the number of archipelagos considered is given, with the first number being for all land-birds and Passeriformes only, considering that an archipelago was included in an analysis of a given group (All, Non-Extinct, Endemic and native non-endemic) only if more than two species were represented. For South Pacific native non-endemic Passeriformes, less than two archipelagos fulfilled the aforementioned criteria and therefore no convergence analyses were performed in these cases. Significant results are marked in bold. Significant results are marked in bold.

All archipelagos	Grouping	All land-bird species		Passeriformes	
		SES	P	SES	P
	All species (18, 15)				
	Body plan	-2.299	0.006	-3.605	0.001
	Body mass	-1.678	0.010	-0.991	0.144
	Phylogenetic	-4.407	0.001	-4.403	0.001
	Non-Extinct species (18, 14)				
	Body plan	-3.512	0.001	-3.409	0.001
	Body mass	-2.386	0.001	-0.760	0.232
	Phylogeny	-4.574	0.001	-4.073	0.001
	Endemic species (18, 14)				
	Body plan	-2.070	0.010	-2.936	0.001
	Body mass	-0.295	0.420	-1.014	0.139
	Phylogeny	-3.848	0.001	-4.167	0.001
	Native non-endemic (12, 7)				

	Body plan	-2.693	0.002	-2.382	0.008
	Body mass	-1.737	0.022	0.763	0.797
	Phylogeny	-1.819	0.032	-2.574	0.002
Macaronesia		SES	P	SES	P
All species (3, 3)					
	Body plan	-2.992	0.001	-3.556	0.001
	Body mass	-2.276	0.001	-2.459	0.001
	Phylogeny	-3.249	0.001	-4.245	0.001
Non-Extinct species (3, 3)					
	Body plan	-6.811	0.001	-7.501	0.001
	Body mass	-2.394	0.001	-2.821	0.001
	Phylogeny	-5.048	0.001	-6.100	0.001
Endemic species (3, 3)					
	Body plan	-0.880	0.190	-0.804	0.219
	Body mass	-1.041	0.107	-0.898	0.169
	Phylogeny	-1.856	0.028	-1.688	0.039
Native non-endemic (3, 3)					
	Body plan	-6.645	0.001	-7.662	0.001
	Body mass	-2.074	0.001	-2.344	0.001
	Phylogeny	-5.207	0.001	-6.048	0.001
South Pacific		SES	P	SES	P
All species (6, 5)					
	Body plan	-2.435	0.003	-2.565	0.001

Body mass	-1.626	0.001	-1.043	0.108
Phylogeny	-5.897	0.001	-5.232	0.001
Non-Extinct species (6, 4)				
Body plan	-3.144	0.001	-1.640	0.032
Body mass	-2.010	0.001	-0.419	0.392
Phylogeny	-5.500	0.001	-3.673	0.001
Endemic species (6, 5)				
Body plan	-1.408	0.066	-2.187	0.006
Body mass	-1.445	0.030	-1.236	0.069
Phylogeny	-4.532	0.001	-5.661	0.001
Native non-endemic (4, 1)				
Body plan	-4.308	0.001	-	-
Body mass	-2.303	0.001	-	-
Phylogeny	-6.087	0.001	-	-

Table S10. Comparison of dominant orders in each of 18 oceanic archipelagos and their associated regional pool. To facilitate comparisons between archipelago and regional pool, the rank of the proportion is given. For example, in the Austral Islands, *Columbiformes* and *Gruiformes* are the first and the second most represented order, while in the regional pool of Austral Islands, *Columbiformes* are the second most dominant and *Gruiformes* only the sixteenth.

Archipelago	Order	Rank	
		Archipelago	Regional pool
Austral	Columbiformes	1	2
	Gruiformes	2	16
Azores	Passeriformes	1	1
	Columbiformes	2	6
Canary	Passeriformes	1	1
	Accipitriformes	2	2
Comoros	Passeriformes	1	1
	Columbiformes	2	5
Cook Islands	Columbiformes	1	2
	Gruiformes	2	16
Fernando de Noronha	Passeriformes	1	1
	Columbiformes	2	9
Galapagos	Passeriformes	1	1
	Strigiformes	2	8
Gulf of Guinea	Passeriformes	1	1
	Columbiformes	2	8
Hawaii	Passeriformes	1	1
	Gruiformes	2	16
Juan Fernandez	Passeriformes	1	1
	Apodiformes	2	2
Madeira	Passeriformes	1	1
	Columbiformes	2	6
Marquesas	Passeriformes	1	1
	Gruiformes	2	16
Mascarenes	Passeriformes	1	1
	Columbiformes	2	5
Pitcairn	Columbiformes	1	2
	Passeriformes	2	1
Revillagigedo	Passeriformes	1	1
	Columbiformes	2	4
Samoa	Passeriformes	1	1
	Columbiformes	2	2
Society*	Columbiformes	1	2
	Passeriformes	1	1
Tristan da Cunha	Passeriformes	1	1
	Gruiformes	2	15

* For Society, *Columbiformes* and *Passeriformes* were found to display similar proportions and were both ranked first.

Table S11. Taxonomic difference between archipelago and their respective regional pool at family level. Two taxonomic comparisons were made: (1) total number of families in each archipelago, and (2) dissimilarity in family composition and proportion of species per family using *Manly* distance. Both observed number and dissimilarity of families were compared against 1000 null values generated by randomly selecting from the species pool the same number of species as observed in the respective archipelago. Deviation from null expectation was quantified using standardized effect size (SES). Significant SES indicate that the observed number of families and dissimilarity is significantly different from the random expectation. Analyses were performed for all land-birds, and for Passeriformes only. An archipelago was included in an analysis if it had more than two species. For Passeriformes, three archipelagos did not meet this criteria namely Austral islands, Fernando de Noronha and Pitcairn. Significant results are marked in bold. Significant results are marked in bold.

	All land-birds				Passeriformes			
	Number of families		Dissimilarity of families		Family composition		Number of families	
	SES	<i>P</i>	SES	<i>P</i>	SES	<i>P</i>	SES	<i>P</i>
Austral	-4.24	<0.001	2.34	<0.001	-	-	-	-
Azores	-3.25	<0.001	0.77	0.21	-0.61	0.71	-1.79	0.10
Canary	-2.99	<0.001	3.81	<0.001	2.63	0.02	-2.53	0.01
Comoros	-1.64	0.07	9.22	<0.001	10.25	<0.001	0.06	0.61
Cook Islands	-4.59	<0.001	4.68	<0.001	2.11	<0.001	-4.32	0.01
Fernando de Noronha	-1.32	0.28	0.75	0.24	-	-	-	-
Galapagos	-3.19	<0.001	5.30	<0.001	5.75	<0.001	-3.51	<0.001
Gulf of Guinea	-2.45	0.01	6.27	<0.001	5.19	<0.001	-0.36	0.48
Hawaii	-10.37	<0.001	20.22	<0.001	18.69	<0.001	-10.25	<0.001
Juan Fernández	-0.20	0.59	0.17	0.42	-0.87	0.77	-1.45	0.29
Madeira	-3.38	<0.001	2.43	0.01	2.51	0.03	-3.05	<0.001
Marquesas	-5.92	<0.001	6.52	<0.001	3.97	<0.001	-6.77	<0.001
Mascarenes	-3.76	<0.001	14.54	<0.001	9.21	<0.001	-1.81	0.07
Pitcairn	-4.65	<0.001	2.66	<0.001	-	-	-	-
Revillagigedo	-2.71	0.01	4.24	<0.001	3.83	<0.001	-1.34	0.18
Samoa	-1.11	0.19	0.62	0.26	3.09	<0.001	-0.94	0.30
Society	-5.20	<0.001	5.43	<0.001	2.82	<0.001	-4.59	<0.001
Tristan da Cunha	-3.24	0.01	1.99	0.03	1.56	0.05	-1.53	0.20

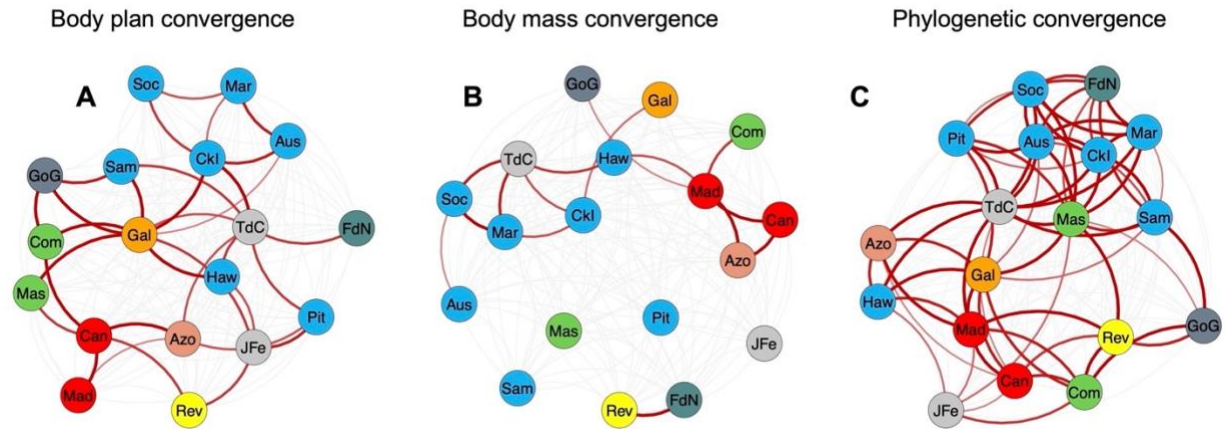


Figure S5. Pairwise convergence in morphological and phylogenetic structure between pairs of archipelagos after having removed the two hummingbird species of Juan Fernández (namely *Sephanoides fernandensis* and *Sephanoides sephaniodes*). The networks show convergence properties in body plan (A), body mass (B) and phylogeny (C) for all land-birds. Nodes correspond to the 18 major oceanic archipelagos. Red and grey connectors depict convergence and non-convergence, respectively. Convergence was estimated by comparing pairwise morphological and phylogenetic turnover between pairs of archipelagos against the distribution of values calculated from 1,000 simulations using a null model with random morphological and phylogenetic differentiation. A pair of archipelagos was considered convergent when the observed dissimilarity was below the lower bound of the 95% of the confidence limits of the null model distribution. Colours indicate the biogeographical region to which each archipelago belongs (see Fig. 2 and Tables S1–S3, for regions and archipelago names). In contrast to the network in Figure 3 (in the main text), these reanalyzes of the convergence pattern without the two hummingbirds showed convergence of Juan Fernández with at least four archipelagoes for body plan and phylogeny, a lack of convergence being still reported for body mass.

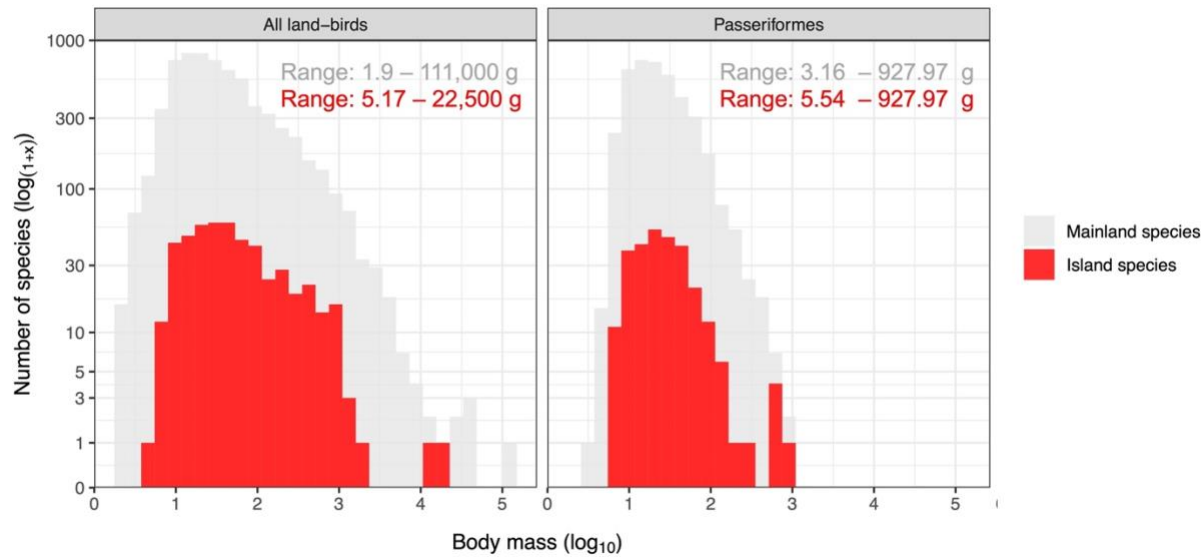


Figure S6. The distribution of log₁₀-transformed body mass values for mainland species and the island species present in the 18 archipelagos considered herein, for all land bird species and for Passeriformes only. For each grouping, the range of non-transformed body mass is given for both mainland and island species in the top right of each panel. For graphical convenience, the y-axis was log(x+1)-transformed to better visualize and compare the body mass distribution between mainland and island species.

D. References

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