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Supplementary Data	Supplementary Data	SUPPLEMENTARY_DATA_ALL.xlsx	Supplementary Data Tables 1-5

Title: The consequences of craniofacial integration on the adaptive radiations of Darwin's Finches and Hawaiian Honeycreepers

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The diversification of Darwin's finches and Hawaiian honeycreepers are two textbook examples of adaptive radiation in birds. Why these two bird groups radiated while the remaining endemic birds in these two archipelagos exhibit relatively low diversity and disparity remains unexplained. Ecological factors have failed to provide a convincing answer to this phenomenon, and some intrinsic causes connected to craniofacial evolution have been hypothesized. Tight coevolution of the beak and the remainder of the skull in diurnal raptors and parrots suggests that integration may be the prevalent condition in landbirds (Inopinaves). This is in contrast with the archetypal relationship between beak shape and ecology in Darwin's finches and Hawaiian honeycreepers, which suggests the beak can adapt as a distinct module in these birds. Modularity has therefore been proposed to underpin the adaptive radiation of these birds, allowing the beak to evolve more rapidly and 'freely' in response to ecological opportunity. Here, using geometric morphometrics and phylogenetic comparative methods in a broad sample of skulls of landbirds, we show that craniofacial evolution in Darwin's finches and Hawaiian honeycreepers appears to be characterized by a tighter coevolution of the beak and the rest of the skull (cranial integration) than in most landbird lineages, with rapid and extreme morphological evolution of both skull regions along constrained directions of phenotypic space. These patterns are unique among landbirds, including other sympatric island radiations, and therefore counter previous hypotheses by

showing that tighter cranial integration, not only modularity, can facilitate evolution along adaptive directions.

Why some lineages diversify more or less than others is a central topic in evolutionary biology. Among birds, the adaptive island radiations of Darwin's finches and Hawaiian honeycreepers are notable for their rapid and disparate evolution[1,2]. These clades quickly evolved to become taxonomically and morphologically more diverse than other avian lineages that colonized the same oceanic archipelagos[3-7]. Since these phenomena were first recognized[8,9], many different causal hypotheses have been proposed to explain such rapid island radiations. Extrinsic causes, such as differences in colonization age, have been largely dismissed because other slower evolving lineages of birds colonized the archipelagos at similar times[3-5,10]. Alternatively, intrinsic explanations may offer more insight[4,5,11,12]. *In silico* simulations and empirical studies show that the covariation structure of sets of characters (produced by genetic, developmental, functional, or evolutionary causes) have important influences in phenotypic evolution (Fig.1) (e.g.,[13-15]). For example, simulations show that if an anatomical structure is integrated (its component parts co-evolve, *sensu*[16]), its phenotypic evolution will be constrained along specific lines within trait space. Modularity (weaker integration between component parts), in turn, allows a less constrained exploration of trait space[13,17](Fig. 1a). Therefore, a more modular organization is traditionally believed to facilitate, or even to be a precondition[18] for evolvability[19] by allowing component parts to evolve and adapt more independently from each other[20,21]. An alternative view is that integration may enhance evolvability, by providing an adaptive line of least resistance, along which species may rapidly evolve, albeit within a constrained region of trait space [13,17,22-24] (Fig. 1c). Although the degree to which integration and modularity affect evolution seems to be controlled by selection, some empirical discrepancies still exist[13,17,22-24].It might be expected that birds, a speciose vertebrate group with extremely divergent beak shapes, demonstrate little covariation between the beak and the remainder of the skull. At a broad macroevolutionary level this holds true and the beak evolved as a semi-independent structure displaying weak integration with the rest of the skull, arguably explaining its evolutionary plasticity[25]. Yet, when integration is quantified at the family/subfamily level, studies have shown strong integration between the beak and skull morphology in diurnal raptors and parrots[11,26]. Raptors and parrots occupy key phylogenetic positions at the base and within the landbird (Inopinaves) radiation, respectively[27-29](which also includes Darwin's finches and Hawaiian honeycreepers) suggesting that strong cranial integration might be ancestral to and prevalent in landbirds[11,26]. While there is no inherent reason to preclude that selection on the shape of the beak would not also lead to adaptive changes in the shape of cranium, strong cranial integration within these clades has been suggested to reflect pleiotropic interactions among cranial regions hampering a fine adaptation of beak shape to feeding ecology[11,26]. This is in contrast to the paradigmatic relationship between feeding ecology and beak size and shape evolution in Darwin's finches [30,31] and Hawaiian honeycreepers [5,32] which suggests the beak in these clades is able to respond effectively and more or less independently to feeding selective pressures in their island ecosystems (an observation that was crucial to developing the theory of natural selection[8,33]). A key question therefore is whether relaxation of cranial integration represents an evolutionary innovation in these landbird clades whereby the beak is

able to evolve more 'freely', thereby facilitating rapid evolutionary radiation[11,12], or if integration facilitates rapid evolution along constrained adaptive directions. The recent surge of interest in the implications of integration and modularity for evolvability in evolutionary theory [11,13,15,25,34] makes testing these ideas in an iconic example of adaptive radiation particularly relevant. Therefore, using geometric morphometrics and phylogenetic comparative methods we here quantify whether relaxed integration (modularity) between the beak and skull is linked to rapid and disparate evolutionary radiation in landbirds as per classic interpretations, or whether tighter integration may be key to rapid and large evolutionary change.

Results & Discussion

We found that each of the major clades of landbirds diverged to unique cranial morphologies (Fig. 2, Extended Data. Figs. 3-5). Parrots (Psittaciformes) are characterised by a single ancestral shift towards very high rates of skull shape evolution, resulting in a characteristic cranial anatomy with short, curved beaks and expanded braincases (Fig. 2). Conversely, hoopoes and hornbills (Bucerotiformes) and toucans (Ramphastidae, Piciformes) show similar skull shapes to parrots but have higher aspect ratio, less curved beaks (Extended Data. Figs. 3-5). While passerines (Passeriformes) have radiated to explore a large proportion of landbird morphological variation, they have not achieved the levels of morphological variation seen in non-passerines (Fig. 2). Although most passerines display similar skull morphologies and there is a slowdown in rates of skull shape evolution in the branch leading to the songbirds (Passeri), a few songbird lineages diverge substantially to explore morphologies approaching those of parrots or hoopoes (Fig. 2, Extended Data. 3-5). Darwin's finches and Hawaiian honeycreepers show the highest rates of beak and skull shape evolution in our sample, and experienced multiple positive rate shifts within each clade. This result is similar to that of other recent studies[2,25], suggesting that the rapidity of evolution in these species is not simply a result of their relatively recent divergence relative to the other species in our data. These birds also show considerable craniofacial shape disparity, including some of the most extreme shapes within Passeriformes (Fig. 2).

We found that the beak and the skull are integrated to an extent in all landbird clades (Fig. 3a, Fig. 4a). When considered as separate groups, Passeriformes have more integrated skulls than non-passerines (Fig. 4a, Table 1). This is driven by high integration in the songbirds (Passeri), moderately high integration in the suboscine passerines (Tyranni) within the Passeriformes, and high integration in the parrots (Psittaciformes) within the non-passerines (Fig. 3a, Fig. 4a, Table 1, Extended Data Fig. 10). All other clades show lower and similar levels of cranial integration (Fig. 3a, 4a; Table 1). Within songbirds (Fig. 4b), Passerida, the clade containing Darwin's finches and Hawaiian honeycreepers, exhibits higher levels of integration than all other passerine clades and this likely underscores the high integration displayed by songbirds as a whole group. Interestingly, the Muscicapida, the other passerine clade that radiated in Galapagos and Hawaii (but to a lesser extent than Darwin's finches and Hawaiian honeycreepers), display the lowest levels of integration in our sample (Fig. 3b, 4b, Table 1). High levels of integration and the same pattern of covariation persist in Passerida even when Darwin's finches and Hawaiian honeycreepers are removed from the

analysis (Fig. 3b, 4b; for congruence of these results with other analytical conditions see SI. Figs. 5 & 6, Extended Data Fig. 10, Supplementary Data 1 & 2), suggesting that craniofacial covariation in these clades matches the general covariation pattern of Passerida, indicating high cranial integration may be more widespread in this clade. Therefore, contrary to previous suggestions, our results show that cranial evolution in the classic adaptive radiations of Darwin's finches and Hawaiian honeycreepers was most likely characterised by a pattern of strong integration between of the beak with the rest of the skull.

Although there is not a common relationship between the strength of cranial integration and rates of morphological evolution for all landbirds in our data (Extended Data Fig. 8), this matches expectations as recent *in silico* models and empirical data show that this relationship is also critically dependent on selection impinging upon functional and developmental factors [15,17,23,24,35]. Specifically, evolution along phenotypic lines of least resistance[23] predicts that, by affecting several traits in unison, higher trait covariation can increase evolutionary rates if selection favours evolutionary change along the line of maximum covariation[17,23,24], allowing more extreme morphologies to be explored [13,36]. Therefore, lack of correlation in an older lineage such as parrots (~ 30 MY crown-group Psittaciformes,[29]) may be due to clade age: this lineage has been affected by multidirectional selective pressures during its long evolution, complicating the identification of a straightforward relationship between strong evolutionary integration of the skull and phenotypic evolution (i.e., the 'fly in a tube' model[15]). Conversely, Darwin's finches and Hawaiian honeycreepers (and sympatric contemporaneous radiations) are much younger clades (Fig. 4c), and geographically restricted to their islands, and therefore represent a rare opportunity to make more detailed inferences of phenotypic evolution. Relaxed selection in island ecosystems is often invoked as resulting from the availability of empty niche space and scarcity of predators, particularly in newly colonized islands (i.e. 'the island rule' [37,38]). Although this selection regime is often linked to divergent evolution[37], it may also facilitate evolution along lines of least resistance by raising the probability of selection favouring change along adaptive phenotypic pathways. Although adaptive peaks could potentially arise in more areas of trait space if selection is more flexible (therefore allowing more directions of evolution), the most likely change will by definition be the one using the line of least resistance (Fig. 1). For example, evolution along an allometric line of least resistance rather than divergent evolution may have facilitated the repeated evolution of phyletic dwarfism in island elephants[39]. In a similar way, the constrained evolution of extreme morphologies along the maximum covariation line in Darwin's finches and Hawaiian honeycreepers might have favoured both rapid allopatric speciation and rapid niche separation by character displacement within each of the families because selection facilitating change in one cranial trait affected a cascade of other cranial regions[37]. This, in turn, might underlie the comparatively higher rates of morphological evolution for the whole skull, and for both the beak and skull individually (Fig. 2 & SI. Tables 1-3; and see also [2,25]). In agreement with this model, we show that at the family level (or sub-family for Darwin's finches and Hawaiian honeycreepers), Darwin's finches and Hawaiian honeycreepers exhibit some of the most extreme shape differences along the axis of maximum covariation between the beak and the skull shapes (the purported phenotypic line of least resistance; see Methods) for the

passeroid songbirds (Passerida) (Extended Data. Fig. 7) and for all songbirds (Fig 4c). This coordinated phenotypic evolution (Extended Data. Fig. 6) might also be biomechanically significant, as the jaw adductor muscles attach exclusively to the braincase block, yet act to power the beak during forceful biting. Increased integration between the beak and braincase may therefore facilitate improved feeding performance in both the beak and the rest of the skull in Hawaiian honeycreepers and in Darwin's finches, for whom a demonstrated link between beak morphology and feeding exists[40]. This directional evolution may also have produced some of the highest values of total craniofacial disparity at the family/subfamily level for both clades (Fig. 4b), which is particularly striking considering that Darwin's finches and Hawaiian honeycreepers are substantially younger than most of the other considered families (Fig.4c). Therefore, the constrained (Figs. 3, 4b & 4d, Table 1, Extended Data. Fig. 7), but morphologically extreme (Figs. 2 & 4c) and rapid (Fig. 2), craniofacial evolution in Darwin finches and Hawaiian honeycreepers meets the expectations of rapid evolution along lines of phenotypic least resistance[17,23], where high integration, rather than high modularity, facilitates evolution along a particular adaptive morphocline.

Rapid evolution along lines of phenotypic least resistance may also explain the apparent contradiction between large phenotypic divergence despite little change in genetic divergence between species in Darwin's finches and in Hawaiian honeycreepers [3,5]. It may also shed some light on why other passerine lineages that colonized both archipelagos at similar times failed to undergo the same explosive adaptive radiation. In Hawaii, the two endemic lineages of passerine birds that colonized the archipelago at similar times to Hawaiian honeycreepers are the Hawaiian thrushes (5 species, Turdidae)[5], and the extinct Hawaiian honeyeaters (5 species, Mohoidae)[10]. Both families belong to the parvorder Muscicapida, the passerine lineage exhibiting the lowest integration in our data (Fig. 4a). Similarly, the other endemic radiation in the Galapagos archipelago, the Galapagos mockingbirds (4 species, Mimidae, also in the Muscicapida), colonised the islands at a similar time but did not undergo a rapid diversification[4]. While multiple ecologically relevant traits of the colonizer species may have contributed to the diversification patterns of passerines in Galapagos and Hawaii, we suggest that their lower craniofacial integration may have been an important factor preventing them exploiting adaptive lines of least resistance that likely produced the rapid and large evolutionary change in cranial morphology that we showed in Darwin's finches and Hawaiian honeycreepers. Nonetheless, our study demonstrates that adaptive radiations are possible under tighter cranial integration.

In summary, we propose that a stronger craniofacial integration was a key factor shaping the extreme craniofacial evolution of two classic radiations of island passeroids. While an intrinsic evolutionary lability of the beak has been proposed for several families of passeroid songbirds [5,31,32,40], other studies have shown that beak shape among the group is constrained to a small series of shape transformations arising from a constrained morphogenetic program[41]. Our hypothesis reconciles both views by showing that although high cranial integration constrains the shapes of the beak and skull, it may also facilitate evolutionary lability along specific phenotypic clines in particular ecological scenarios.

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Author's contributions

The focus and design of this research was developed by GN, JM-L, JAB and ERJ. CRC conducted the Variable Rates Model Analyses. GN conducted the remaining of the analyses. GN JM-L, JAB, CRC and ERJ co-wrote the manuscript.

Competing interests

The authors declare no competing financial interests.

METHODS

Database and phylogenetic hypothesis

Our study includes 128 families of landbirds (i.e: Inopinaves, defined as Telluraves (Yuri et al. 2013) + *Opisthocomus hoazin*, Prum et al. 2015) giving a total of 436 species (Supplementary Data 5. List of specimens). All but five families within the landbird radiation are represented in our sample (Philepittidae, Sapayoaidae, Dasyornithidae, Urocynchramidae and Aegithinidae). These families are either monotypic or have an extremely reduced diversity, and often regarded as belonging within other passerine families [44]. Sampling was non-random and aimed to capture the maximum beak morphological disparity within each family, with a special focus on the subfamilies of Darwin's finches (Geospizinae) and Hawaiian honeycreepers (Drepanidinae) (represented in our sample by ~70% and ~ 60 % of their extant diversity, respectively). A time-calibrated maximum clade credibility (MCC) phylogeny of the 436 species was generated using TreeAnnotator[45] from a population of 10,000 'Hackett's backbone stage 2 trees'. Trees were generated using the in-built tools from www.birdtree.org (for full details regarding tree construction methods, see[1]), and branch lengths were set equal to 'Common ancestor' node heights. The resulting MCC phylogeny is largely congruent with the last genomic phylogenies for the interrelationships of landbirds (Figs. 2, 4a & 4b,[28,29]).

Geometric morphometrics

A set of 17 landmarks and 2 curves (three evenly separated semilandmarks along the dorsal and ventral rims of the beak) was digitized using the software tpsDig.2[46] in lateral views of the skull of each specimen (Extended Data Fig. 1, Landmark position/ Extended Data. Fig. 2, Landmark definition). The Minimum Bending Energy criterion was applied to slide the semilandmarks in tpsRelw[47], as this is more appropriate than the Minimum Procrustes Distance criterion when dealing with data with high morphological variation in the software used here[48]. Landmarks and semilandmarks were then classified as belonging to the 'beak block' (block 1) or 'skull block' (block 2) (Extended Data Figs. 1 & 2). Shape data (Procrustes coordinates) was extracted using three different full Generalized Procrustes Analyses (GPAs) for: 1) the whole landmark configuration; 2) the 'beak block'; and 3) the 'skull block'. An additional Generalized Resistant Procrustes Superimposition (GRPS,[49]) was conducted in the raw coordinates from the whole landmark configuration to identify possible trait-correlation artefacts in our shape data (see Methods. Evolutionary covariation & SI). GPA aligned Procrustes coordinates were thereafter imported to MorphoJ[50] and the R statistical environment[51] for all downstream analyses.

Principal Component Analyses (PCA) and Variable Rates Model Analyses (VRMA)

To explore the main patterns of skull shape variation in landbirds, we conducted Principal Component Analyses (PCAs) for: 1) the whole configuration; 2) the 'beak block'; and 3) the 'skull block'. The time-calibrated MCC phylogeny was mapped over the PCAs by weighted (i.e., including branch length information) square-change parsimony in order to visualize evolutionary changes over the morphospace. Principal Components Analyses (including mapping time calibrated trees) were conducted in MorphoJ.

To explore the tempo of craniofacial evolution in landbirds, we used the scores derived from the previous PCAs to conduct Variable Rates Model Analyses (VRMAs) using the software BayesTraits V2.0.2[52] (available from http://www.evolution.rdg.ac.uk/). This method uses a reversible jump Markov chain Monte Carlo (MCMC) approach to estimate the location, probability, and magnitude of rate shifts in continuous traits across branches of a phylogenetic tree (see[53]). We used PC scores for: 1) the whole skull (13 PCs); 2) the 'beak block' (6 PCs); and 3) the 'skull block' (10 PCs). We used the number of principal components that account for 95% of shape variance, except for the whole configuration where we used the number that account for 90% to avoid poor performance due to a high number of variables[54]. We ran two replicate chains for each model using default priors and assuming uncorrelated trait axes[2]. Each chain was run for 200,000,000 iterations (sampled every 10,000 iterations), with the first 100,000,000 iterations removed as burn in. We confirmed that replicate runs had converged and combined the output of both runs for further analysis. We summarized the results of each run by calculating (1) the mean rate, and (2) the probability of a rate shift (branch or clade) over all posterior samples for each node in the tree. In the main text, we focus on rate shifts that are inferred with higher posterior probability (PP) than 0.70. To account for rate heterogeneity in downstream analyses of evolutionary covariation (see Methods. Evolutionary covariation and SI), a rate-scaled phylogeny (non-ultrametric) was generated by using the branch lengths predicted by the model of the VRMA conducted with the whole skull configurations.

288 **Evolutionary covariation**

289 Evolutionary covariation between the 'beak block' (block 1) and the 'skull block'
290 (block 2) was examined for each of the clades of landbirds by means of Phylogenetic Partial
291 Least Squares analysis (P-PLS,[55,56]) in three different situations: two blocks using the
292 calibrated time tree (separate GPA for the 'beak block' and the 'skull block') (situation 1);
293 two blocks using the rate-scaled phylogeny (situation 2); and within one configuration (one
294 single GPA for the whole configuration) using the rate-scaled tree (situation 3). Phylogenetic
295 Partial Least Squares (P-PLS) is a multivariate analysis that quantifies the evolutionary
296 covariation between two different sets of data by searching for vectors of correlated variables
297 without implying predictability of one set of variables upon the other.

298 Although least-squares GPA[57] provides a universal criterion for defining shape data,
299 and convenient statistical properties for downstream multivariate analyses that other
300 superimposition methods do not[58], it has some widely recognised limitations when shape
301 differences between landmarks are highly heterogeneous [49,59-61]. This is because GPA
302 assumes that variation among landmarks is homogeneous and that all landmarks vary
303 isotropically[57] (they are equally distributed in all directions). Therefore, if a great deal of the
304 total shape difference is concentrated in just a few landmarks, and/or its variation is skewed
305 towards one or more directions, GPA tends to spread this localized shape variance across the
306 whole configuration, generating artefactual shape differences[49,61-63](i.e., the 'Pinocchio
307 effect'[62]). This issue can be particularly misleading when evaluating covariation patterns (i.e.
308 integration and modularity) as it tends to overestimate integration. There is still debate as to
309 whether this is a critical concern in real biological data or not[49,61,64], however, in an
310 exploratory study Cardini[61], showed that GPA can generate artefactual patterns of covariation
311 even if the original shape data exhibits no covariation at all. The fact that landbirds
312 demonstrate high beak shape variation relative to other skull regions[25,34] led us to
313 contemplate this possibility. Therefore, to identify whether the aforementioned might be a
314 problem in our sample, we carried out a Generalized Resistant Procrustes Superimposition
315 (GRPS[49,60]) in the raw coordinates (unaligned) for the whole configurations for all landbirds
316 and compared them with a GPA superimposition using Resistant Procrustes Software (RPS[49],
317 available online at: https://sites.google.com/site/resistantprocrustes/) (SI. 4). GPRS differs
318 from GPA in that the set of criteria for eliminating rotational information from shape data are
319 estimated through a repeated-medians calculation for each dataset, rather than minimizing the
320 squared sum of Euclidean distances between the landmark coordinates[60]. This criterion is
321 therefore robust to larger variation in a few landmarks with respect to the whole
322 configuration, and thus better portrays localized variation across coordinates[49,60].
323 Additionally, we tested evolutionary shape covariation between blocks 1 and 2 within one
324 configuration (situation 3, single GPA) to gain insight on how localized variation might affect
325 integration results in our sample (SI. Expanded Results, SI. Figs. 5 & 6; SI. Table 2).

326 Because GPRS and other resistant-based procedures are not based in Procrustes
327 distances, concerns have been expressed regarding their ability to generate shape tangent
328 spaces appropriate for Euclidean multivariate statistics (e.g.,[65]). Although there are
329 specifically implemented multivariate methods for dealing with data extracted from a GPRS,

330 the standard usage of GPA in modern geometric morphometrics[66,67] means that most
331 available methods are based on Procrustes distances. These Procrustes-based analyses need
332 the consistency with the Procrustes projection that defines shape variables in geometric
333 morphometrics[58]. To our knowledge, there is not currently an appropriate method able to
334 overcome both trait correlation artefacts yet retain an equivalence with Euclidean
335 multivariate statistics. Consequently, we are forced to quantify covariation using two blocks
336 (situations 1 and 2) in an attempt to mitigate any artefactual spread of variance across the
337 whole configuration (see SI. Expanded Results for further details). This approach is better at
338 portraying the original patterns of local variation in geometric morphometrics and generally
339 eliminate artefactual trait covariation, at least as far as integration is concerned[61]. However,
340 covariation in situations 1 and 2 only reflects evolutionary shape covariation, as information
341 regarding relative size and arrangement between blocks is lost (eliminated in each block's
342 separate GPA) and can only be accessed indirectly (e.g., because the shape data is a 2-
343 dimensional projection of a 3D object, certain shape changes might be indicative of
344 differences in arrangement angle).

345 Several studies have shown that landbirds exhibit extreme heterogeneity of rates of
346 craniofacial evolution [2,25], which we also quantified here (Fig 2; SI. Tables 1-3). Computation
347 of Phylogenetic Partial Least Squares in *geomorph*[68] assumes a single-rate Brownian Motion
348 model of evolution which is unlikely to conform to shape data that evolved with highly
349 heterogeneous rates. When shape data does not conform to a single-rate BM model, previous
350 approaches rescaled the branch lengths of the phylogeny using the parameters estimated by
351 the model that best fits the data from a selection of *a priori* models, namely: single-rate BM,
352 Ornstein–Uhlenbeck, and Early-Burst (e.g,[69]). This approach coerces the phylogenetic
353 covariation matrix to approximate a BM model, therefore meeting the expectations of the
354 analysis. However, recent research has shown that current model-fitting methods based on
355 maximum-likelihood tend to exhibit ill-conditioned covariation matrices, leading to
356 misidentifications of the model of evolution[54], even when the data is generated under a
357 particular model like BM [70]. Here, we chose a different approach: we used the branch lengths
358 estimated by the VRMA for the whole skull configuration. In this way, we rescaled the
359 branch lengths in our tree to account for the actual rates of phenotypic evolution rather than
360 using parameters estimated by the fit to a particular set of *a priori* single-process models.
361 Although this solution is not ideal, it allows for the inclusion of branch lengths estimated by
362 more complex models than previous approaches, which have also been shown to exhibit best
363 fits for other cases of trait evolution like body mass[71]. The methodological endeavour needed
364 to implement more complex evolutionary models in phylogenetic comparative methods for
365 high dimensional data[72] goes well beyond the scope of this study. Here, comparisons between
366 situations 1 (two blocks using the calibrated time tree) and 2 (two blocks using the rate-scaled
367 tree) aimed to gain insight on the effects of accounting for variable rates in evolutionary
368 covariation in measures of evolutionary integration (SI. Figs. 2 & 3; Supplementary Data 3).

369 The strength of evolutionary covariation in each of the three scenarios was compared
370 and tested between major radiations of landbirds and between the major radiations of
371 passerines following a recently developed statistical procedure[73]. The major non-passerine

radiations were compared to the major subdivisions of the Passeriformes (Passeri and Tyranni) based on the high support in all the latest phylogenetic hypotheses of these clades and similar node age estimations[29]. The more recently-branching passerine parvorders were compared between each other. As P-PLS correlation values (*rpls*) have been shown to be influenced by sample size[74], comparing or testing for differences in integration levels between two different sample sizes using this statistic is problematic. Adams & Collyer[73] recently proposed the use of *rpls* effects sizes (z-scores). Z-scores were therefore calculated as the standard deviates of the *rpls* values from the permutation procedure for the P-PLS analyses of each clade, and confidence intervals were calculated for each value. Pairwise differences in z-scores were then compared and statistically tested in order to discriminate between levels of integration between clades. Z-score values were used directly to elucidate which clades exhibited higher integration when differences were found. To explore the differences in the pattern of cranial integration between clades, pairwise angles and correlations of PLS1 vectors (the pair of vectors that covary most for each P-PLS) were calculated for all the clades in situation 2 (Extended Data Fig. 6; Extended Data Fig. 10; SI. Fig. 1; Supplementary Data 1 & 2). Histograms of frequency of binned angles and shape differences across each vector were plotted for visual comparisons (Extended Data Fig. 6; SI. Fig. 1).

Finally, we addressed whether stronger cranial integration generated greater morphological change along the evolutionary line of least resistance in Darwin's finches and Hawaiian honeycreepers than in other landbird families. To do so, we computed maximum distances within each family (or subfamily for Geospizinae and Drepanidinae) of landbirds for the PLS1 scores of the beak and skull blocks as a proxy of the degree of spread along the line of least resistance. We did this for the PLS1 axes defined for each order (and Passeri and Tyranni for the Passeriformes) and compared PLS1 distances for the beak and skull block between all the families. Furthermore, we repeated this for the parvorder Passerida and compared PLS1 distances for the beak and skull block between passeroid families alone. To ascertain whether a larger spread across the lines of least resistance also corresponds to more extreme cranial morphologies, we computed maximum Procrustes distances within each family/subfamily using the Procrustes coordinates (both from the whole configuration and beak and skull blocks separately).

Data availability

All relevant data is available via the University of Bristol's DataBris repository at https://data.bris.ac.uk/data/dataset/3kpwgpnqewcy2tvak6uzzdztt.

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Figures legends:

Figure 1. How integration and selection direct phenotypic evolution. a) Approximate areas of simulated phenotypic evolution for high (dark grey ellipse) and zero (light grey circle) trait-covariation (modified from [13]). Higher integration entails exploration of more extreme trait values (following [17]); b) A complete modular organization between beak and skull shape (i.e. zero covariation) representing the extreme scenario of the condition proposed for the classic passerine adaptive radiations whereby the beak can evolve more freely [7,11,12]. This scenario permits the initial theoretical phenotype (small dark grey ellipse) reaching all three theoretical adaptive peaks (white ellipses), allowing greater evolutionary flexibility (e.g. [13,42]); c) The alternative scenario, an integrated organization between beak and skull shape (i.e. stronger covariation) strongly facilitates reaching the theoretical adaptive peak that is aligned with the axis of maximum phenotypic covariation (i.e. phenotypic line of least resistance, *sensu* [23]) to the detriment of the adaptive peaks that are not aligned with this axis [17,23,24]. Boundary lines are dashed to reflect that phenotypic evolution is more likely to happen within the area described by the covariation structure (yellow area) but can occur beyond those limits (greenish blue background), for instance if directional selection is strong enough (e.g. [43]).

Figure 2. Pattern and tempo of craniofacial evolution in landbirds. Phylomorphospaces of the first three principal components of shape (left), shape changes associated with these shape axes (centre), and rates of morphological evolution (right) for a) the whole skull; (b) 'beak'; and (c) 'skull' blocks. Light grey convex hull encloses Passeriformes, dark grey convex hull encloses Psittaciformes; purple dots represent Darwin's finches and pink dots represent Hawaiian honeycreepers (see Extended Data Figs 3-5 for the main landbird orders labelled in the phylomorphospaces). Branch colours in the phylogenies indicate relative rate of evolution. Inferred rate shifts with higher posterior probability than 0.7 are plotted in corresponding branches (circles) or nodes (triangles) in the phylogeny (see SI. Tables 1-3 for the full list of rate shifts). Posterior probability of each inferred rate shift is indicated by the size of said circle or triangle. Clade labels as in Figs. 3,4 and Table 1.

Figure 3. Evolutionary integration between the beak and the skull in landbirds. PLS1 plots for the Two Blocks-Phylogenetic Partial Least Squares Analyses using the rate-scaled phylogeny (situation 2, see Methods) in each clade (numbers correspond to clades as detailed in Table 1). Y axes show PLS1 scores beak block; X axes show PLS1 scores skull block. a) Major landbird lineages, b) major lineages of passerines. Purple dots represent Darwin's finches and pink dots represent Hawaiian honeycreepers.

Figure 4. Strength of cranial integration across landbirds and maximum phenotypic distances per family/subfamily. a) Z-scores and corresponding intervals of confidence for each major lineage of landbirds and (b) passerine parvorder. Z-scores are effect sizes from the randomized distribution of *rpls* values from the phylogenetic PLS for each clade (situation 2, two blocks, using the rate-scaled phylogeny; see Methods). Cladograms portray the simplified phylogenetic relationships of the main landbird lineages in our phylogeny (solid colours) as compared to other recently published phylogenetic hypothesis[29](transparent colour). (b) Brighter silhouettes represent the island passeroids Darwin's finches (purple) and Hawaiian honeycreepers (pink), whereas less contrasted silhouettes represent the island muscicapoids that radiated in Galapagos (greyish purple) and Hawaii (greyish pink). Our phylogeny is exactly coincident with Prum et al.'s[29] for the interrelationship of major passerine lineages. c) Maximum total Procrustes distances per family/subfamily for the 'beak' and the 'skull' blocks. d) Maximum PLS1 distances per family/subfamily for the 'beak' and 'skull' block. Labels in c and d correspond to families as detailed in Extended Data Fig. 9. Dot colours in c and d

correspond to the ages of the most common recent ancestor (MRCA) for each of the focal families in our MCC

Main landbird lineages

tree.

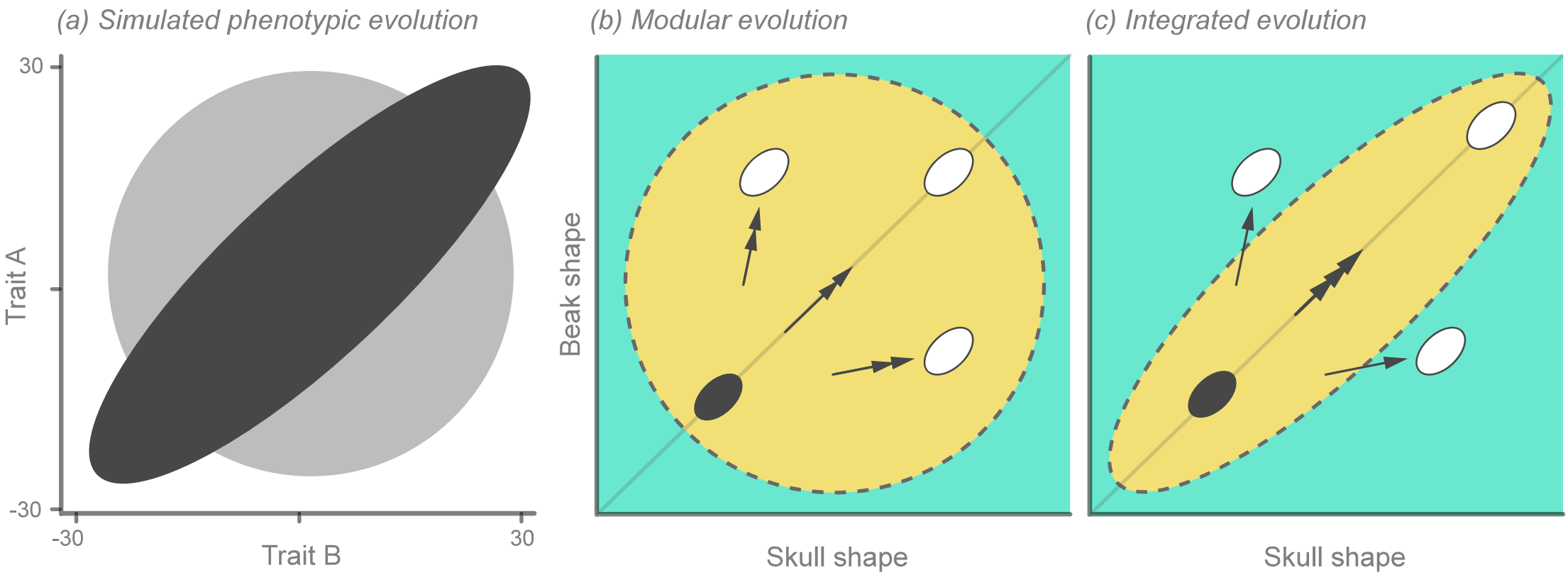
Tables

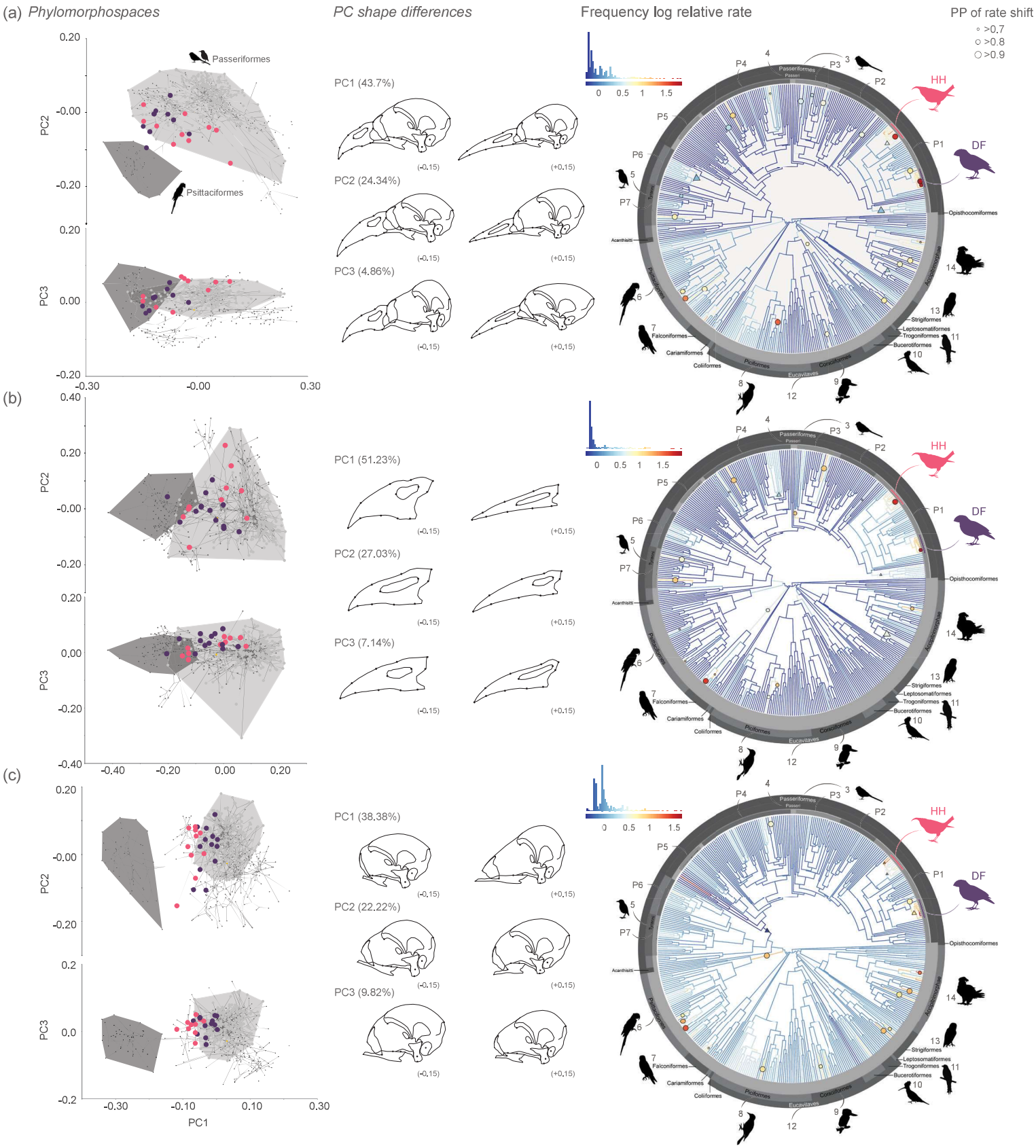
Table 1. Pairwise comparisons of z-scores (strength of evolutionary covariation between beak and skull) between clades and associated *P* values for situation 2 (two blocks, using the rate-scaled phylogeny, see Methods). Bold values are statistically significant ($P < 0.05$). Each clade z-score value is provided. 1*Passerida = Passerida excluding Darwin's finches and Hawaiian honeycreepers.

Z (means)	Clades	1	2	3	4	5	6	7	8	9	10	11	12	13
10.25	**1. All landbirds**													
5.47	**2. Non-Passerines**	***0.0196***												
7.62	**3. Passeriformes**	0.4057	***0.0245***											
5.63	**4. Passeri**	0.2287	0.1715	0.1986										
2.71	**5. Tyranni**	0.0943	0.4649	0.0847	0.2324									
5.03	**6. Psittaciformes**	0.2087	***0.0250***	0.2683	0.1147	0.0532								
0.24	**7. Falconiformes**	***0.0016***	***0.0301***	***0.0017***	***0.0091***	0.0642	***0.0015***							
0.80	**8. Piciformes**	***0.0003***	***0.0237***	***0.0005***	***0.0052***	0.0720	***0.0008***	0.3873						
0.76	**9. Coraciiformes**	***0.0033***	0.0584	***0.0034***	***0.0182***	0.1103	***0.0031***	0.3675	0.4652					
1.38	**10. Bucerotiformes**	***0.0183***	0.1643	***0.0172***	0.0642	0.2292	***0.0125***	0.2224	0.2814	0.3272				
1.36	**11. Trogoniformes**	***0.0083***	0.1189	***0.0083***	***0.0402***	0.1885	***0.0069***	0.2420	0.3087	0.3564	0.4609			
1.21	**12. Eucavitaves**	***0.0001***	***0.0165***	***0.0001***	***0.0029***	0.0719	***0.0004***	0.3380	0.4453	0.4898	0.3074	0.3389		
1.26	**13. Strigiformes**	***0.0071***	0.1066	***0.0071***	***0.0354***	0.1740	***0.0061***	0.2598	0.3318	0.3781	0.4391	0.4769	0.3648	
0.83	**14. Accipitriformes**	***0.0008***	***0.0345***	***0.0010***	***0.0086***	0.0865	***0.0013***	0.3716	0.4775	0.4862	0.3038	0.3326	0.4718	0.3556

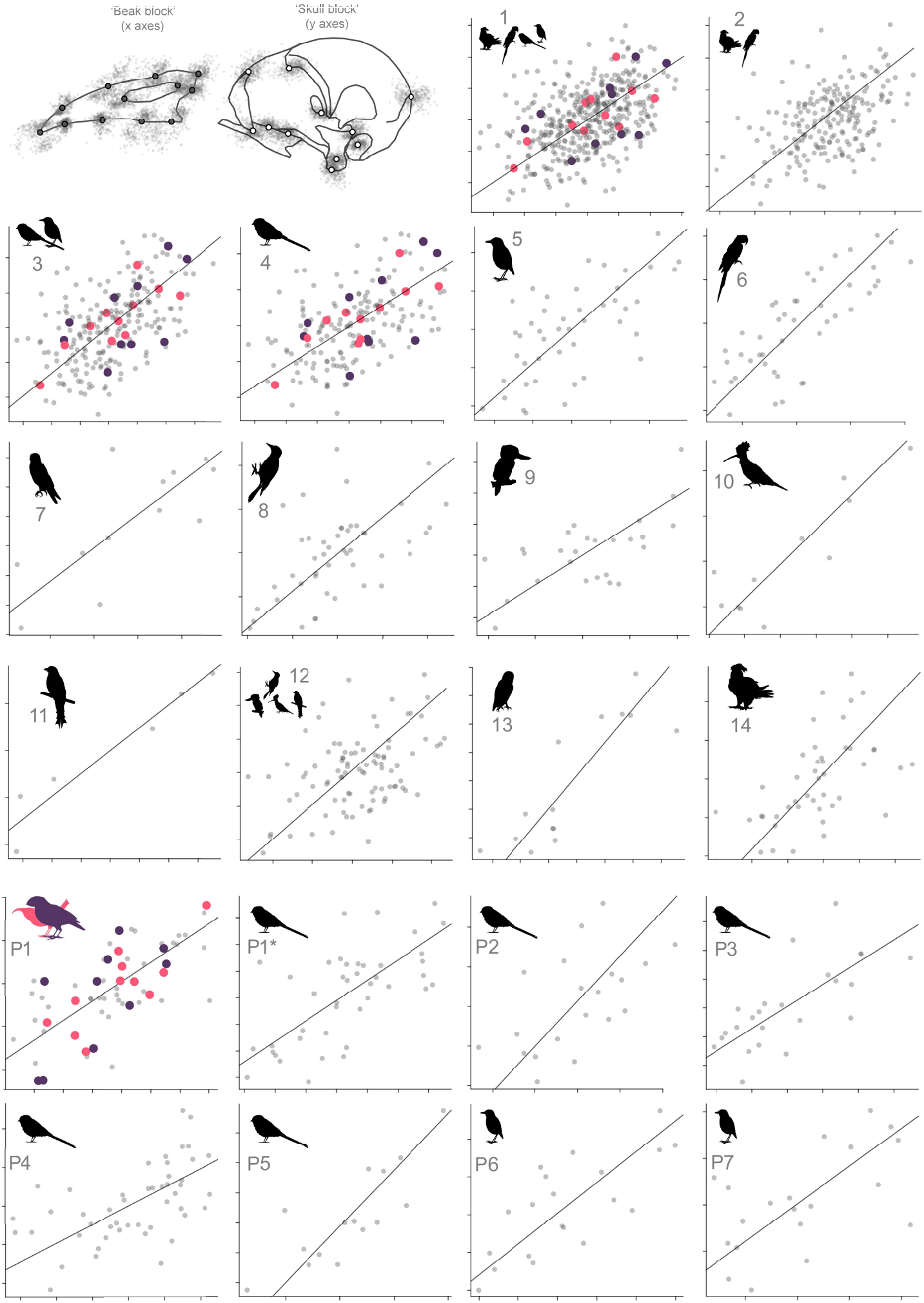
Main passerine lineages

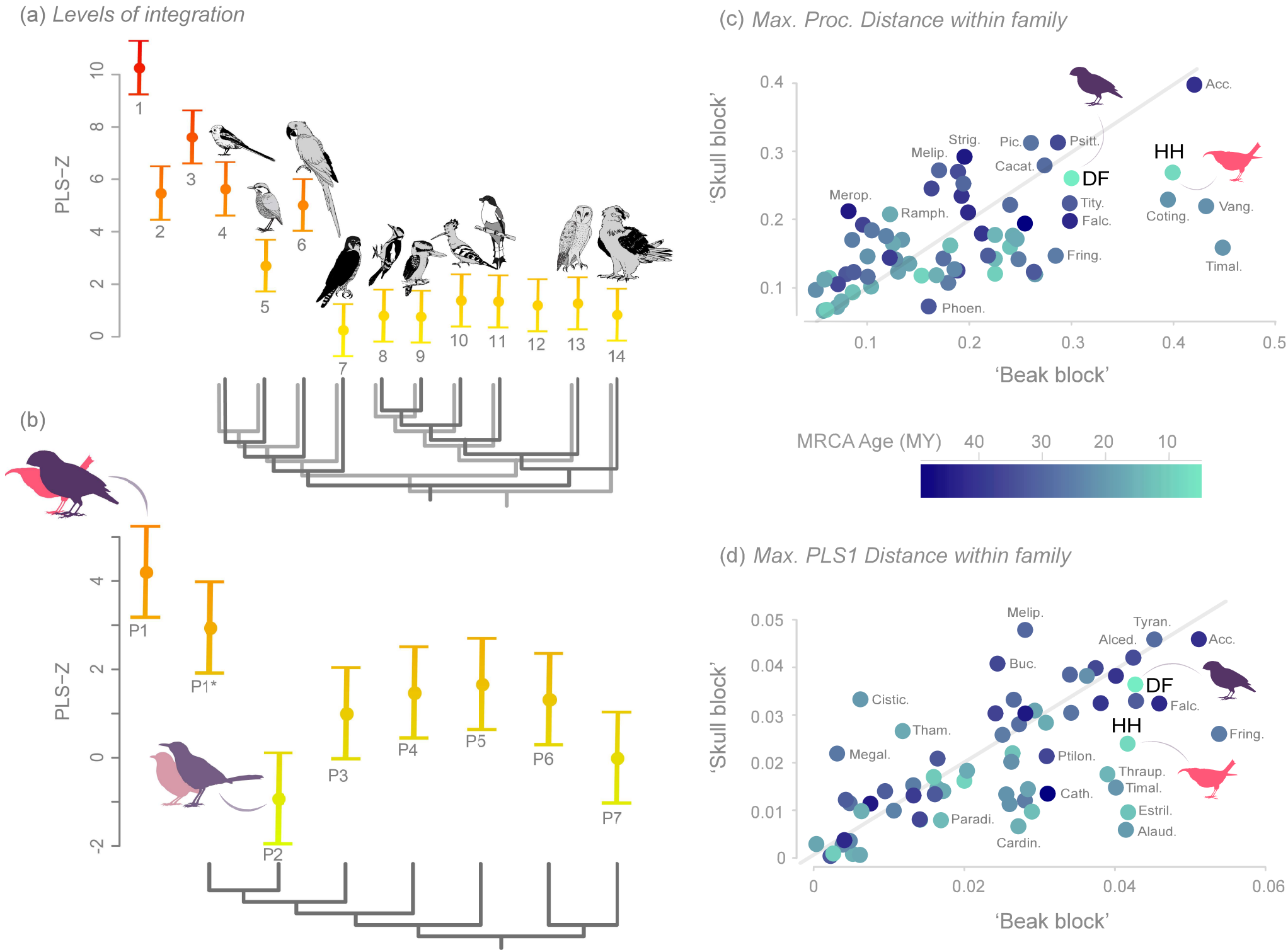
Z (means)	Clades	1	1*	2	3	4	5	6
4.22	**P1.Passerida**							
2.95	**P1*.Passerida***	0.2589						
-0.92	**P2. Muscicapida**	***0.0004***	***0.0042***					
1.01	**P3. Sylviida**	***0.0310***	0.1133	0.0853				
1.48	**P4. Corvides**	***0.0344***	0.1352	***0.0483***	0.4225			
1.66	**P5. Meliphagoidea**	0.1284	0.2916	***0.0321***	0.2881	0.3401		
1.33	**P6. Tyrannida**	0.0635	0.1838	0.0544	0.3956	0.4631	0.3831	
0.00	**P7. Furnariida**	***0.0053***	***0.0287***	0.2609	0.2431	0.1755	0.1143	0.1739

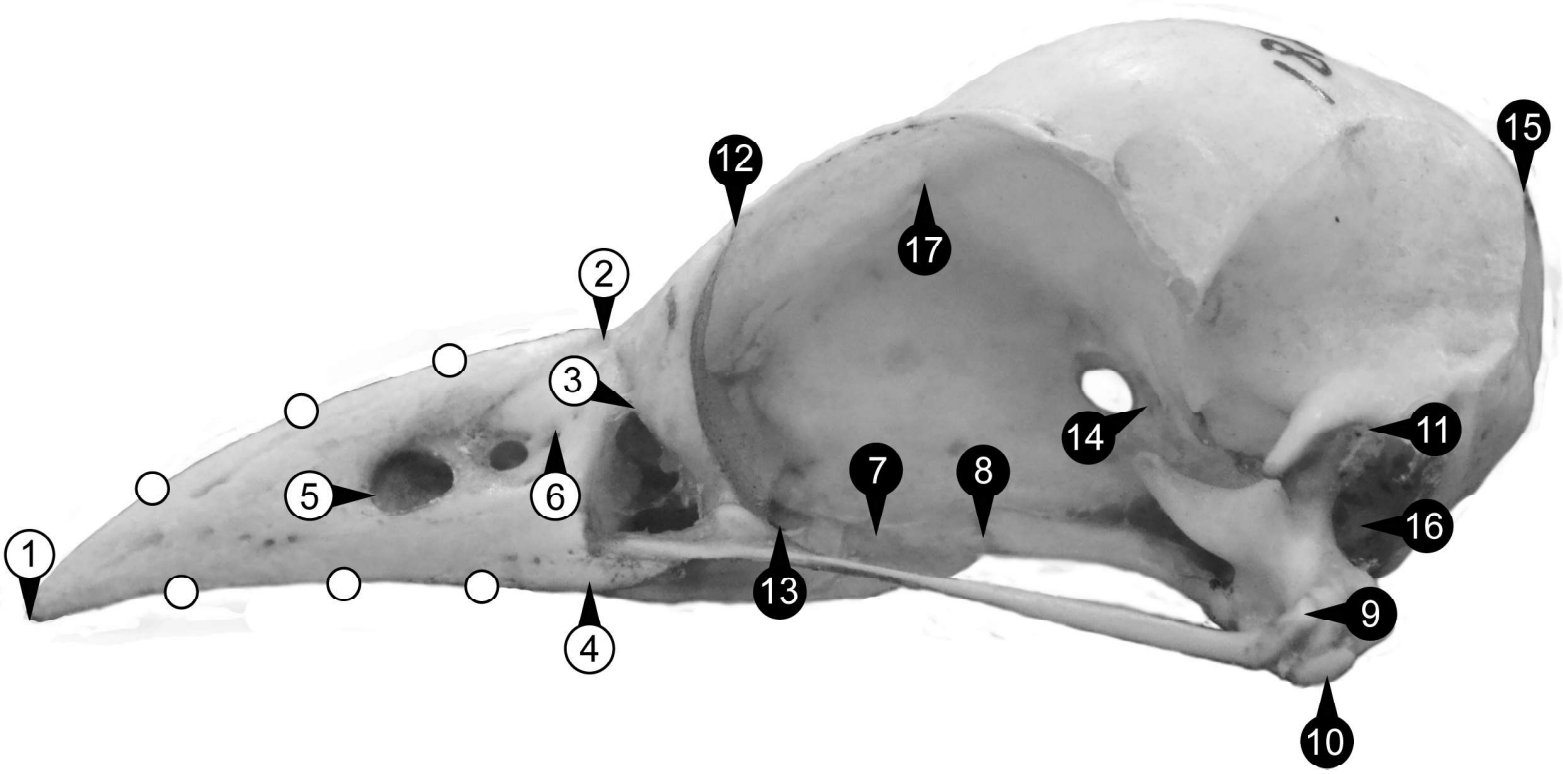

(a) Simulated phenotypic evolution
30
-30
Trait A
-30
30
Trait B
(b) Modular evolution
Beak shape
Skull shape
(c) Integrated evolution
Skull shape


(a) Phylomorphospaces
PC shape differences
Frequency log relative rate
PP of rate shift
>0.7
>0.8
>0.9
Passeriformes
Psittaciformes
PC1 (43.7%)
PC2 (24.34%)
PC3 (4.86%)
(b)
PC1 (51.23%)
PC2 (27.03%)
PC3 (7.14%)
(c)
PC1 (38.38%)
PC2 (22.22%)
PC3 (9.82%)
PC1
PC2
PC3
HH
DF
Opisthocomiformes
Strigiformes
Leptosomatiformes
Trogoniformes
Bucerotiformes
Coliformes
Cariamiformes
Falconiformes
Piciformes
Coraciiformes
Eucavitaves
Passeriformes
Psittacifomes
Acanthisitti

(a) *Phylogenetic Partial Least Squares*




(a) Levels of integration
PLS–Z
0
2
4
6
8
10
1
2
3
4
5
6
7
8
9
10
11
12
13
14
(b)
PLS–Z
-2
0
2
4
P1
P1*
P2
P3
P4
P5
P6
P7
(c) Max. Proc. Distance within family
'Skull block'
'Beak block'
0.1
0.2
0.3
0.4
0.5
Acc.
Strig.
Pic.
Psitt.
Melip.
Cacat.
HH
DF
Merop.
Ramph.
Tity.
Falc.
Coting.
Vang.
Fring.
Timal.
Phoen.
MRCA Age (MY)
40
30
20
10
(d) Max. PLS1 Distance within family
'Skull block'
'Beak block'
0
0.01
0.02
0.03
0.04
0.05
0.06
Melip.
Tyran.
Alced.
Acc.
Buc.
DF
Falc.
Cistic.
HH
Tham.
Fring.
Megal.
Ptilon.
Thraup.
Timal.
Cath.
Estril.
Paradi.
Alaud.
Cardin.


1
2
3
4
5
6
7
8
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14
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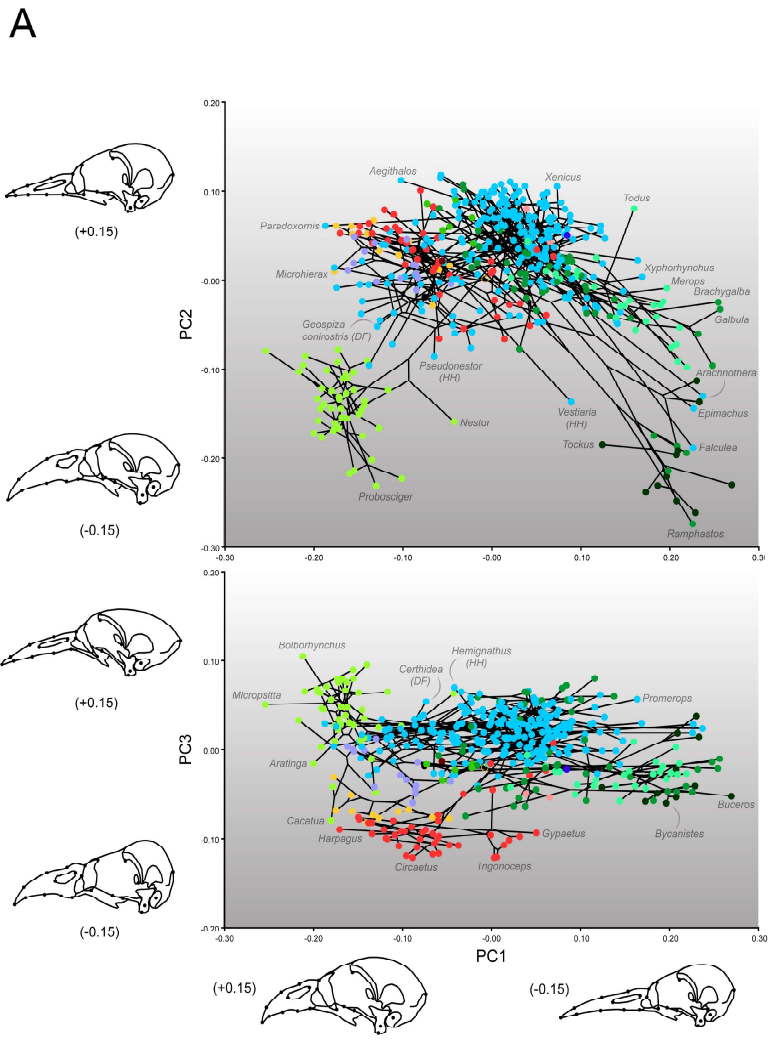
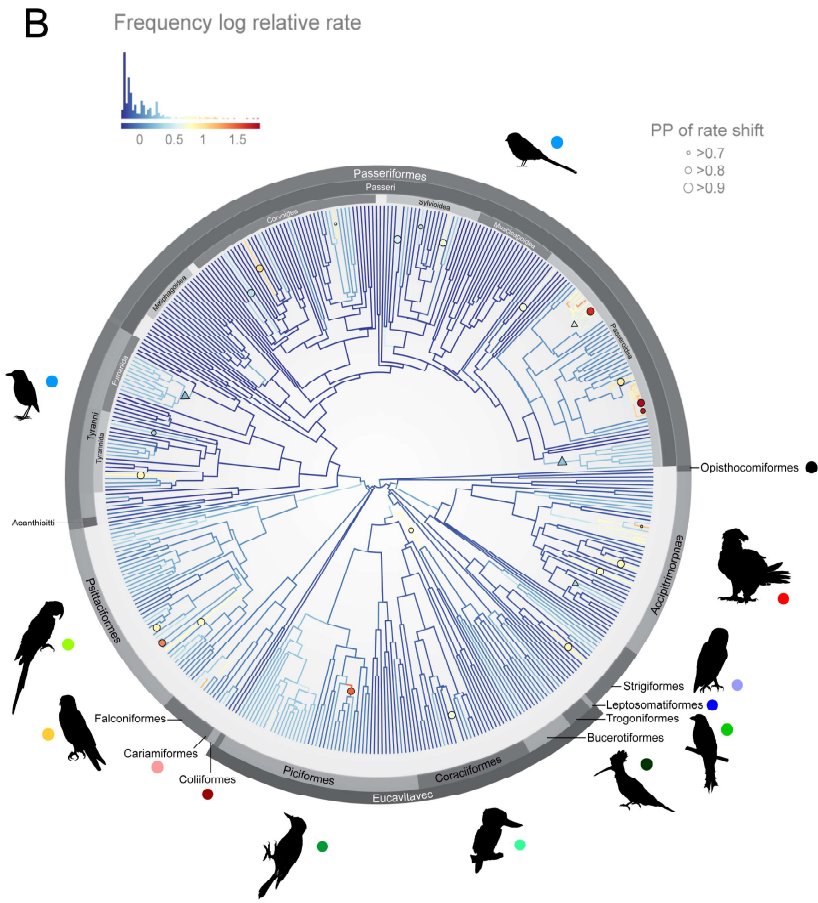
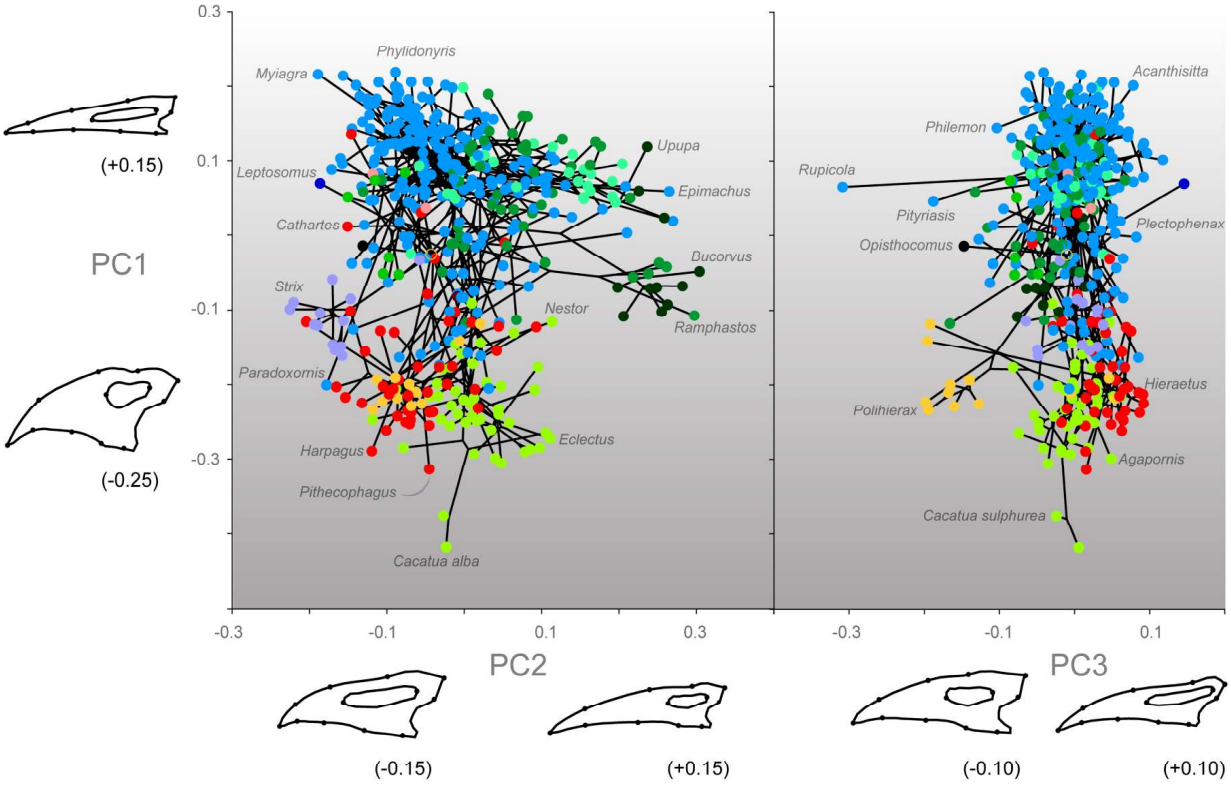
16
17

N	Block	Anatomical region	Description
1	Beak	Rostrum	Anterior tip of the premaxillary symphysis
2	Beak	Rostrum	Nasofrontal hinge
3	Beak	Rostrum	Ventrolateral end of the contact between nasal and lacrimal (or lacrimal-ectethmoid complex**)
4	Beak	Rostrum	Anteriormost edge of antorbital fossa orthogonally projected to the ventral rim of the maxilla
5	Beak	Rostrum	Anteriormost point of external naris fossa
6	Beak	Rostrum	Posteriormost point of external naris fossa
7	Skull	Palate	Middle point of the medial contact between palatines
8	Skull	Palate	Middle point of the lateral contact of palatine and pterygoid
9	Skull	Quadrate	Medial condyle of quadrate
10	Skull	Quadrate	Contact of jugal bar and quadrate
11	Skull	Quadrate	Lateral contact of ootic process of quadrate and squamosal
12	Skull	Lacrimal-ectethmoid	Posterolateral tip of lacrimal (or lacrimal-ectethmoid complex**)
13	Skull	Lacrimal-ectethmoid	Posterolateral end of the contact between lacrimal (or lacrimal-ectethmoid complex**) and frontal
14	Skull	Neurocranium	Ventralmost point of the foramen of the optic nerve
15	Skull	Neurocranium	Intersection of *crista nuchalis transversus* and *crista nuchalis sagittalis*
16	Skull	Neurocranium	External ear (geometric centre of the auditory meatus)
17	Skull	Neurocranium	Foramen of the olfactory nerve (geometric centre)
18-21	Beak	Rostrum	Curve 1 of three semilandmarks along the beak culmen
21-24	Beak	Rostrum	Curve 2 of three semilandmarks along the right tomial ridge
			** term coined by Cracraft[1] to describe the coordinated evolution of both bones in modern birds which we used for the purposes of landmarking.

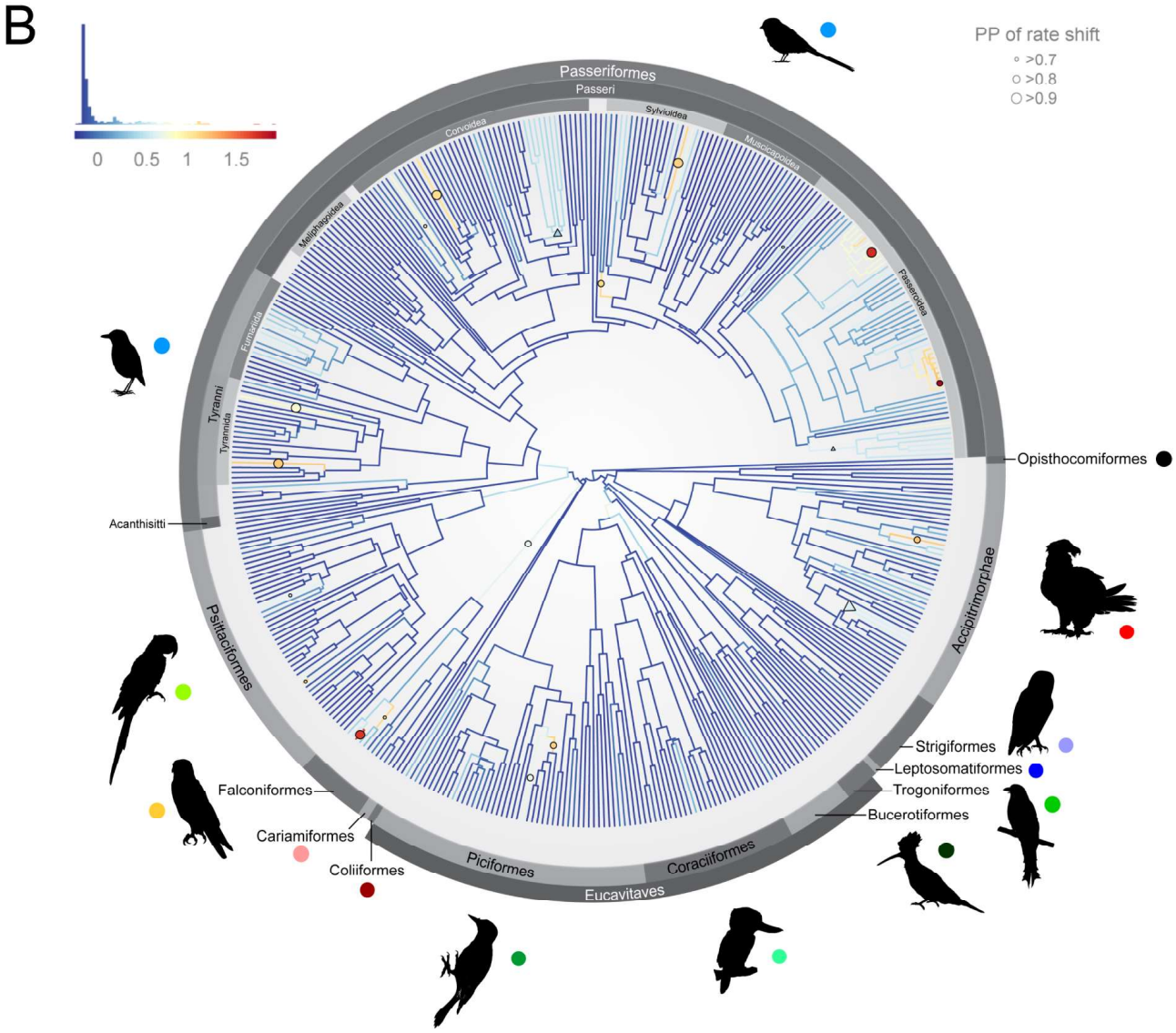

A
(+0.15)
(-0.15)
(+0.15)
(-0.15)
PC2
PC3
PC1
Aegithalos
Xenicus
Todus
Paradoxornis
Microhierax
Xyphorhynchus
Merops
Brachygalba
Galbula
Geospiza conirostris (DF)
Pseudonestor (HH)
Arachnothera
Epimachus
Nestor
Vestiaria (HH)
Tockus
Falculea
Proboscigerr
Ramphastos
Bolborhynchus
Hemignathus (HH)
Certhidea (DF)
Micropsitta
Promerops
Aratinga
Buceros
Cacatua
Harpagus
Gypaetus
Bycanistes
Circaetus
Ingonoceps
(+0.15)
(-0.15)

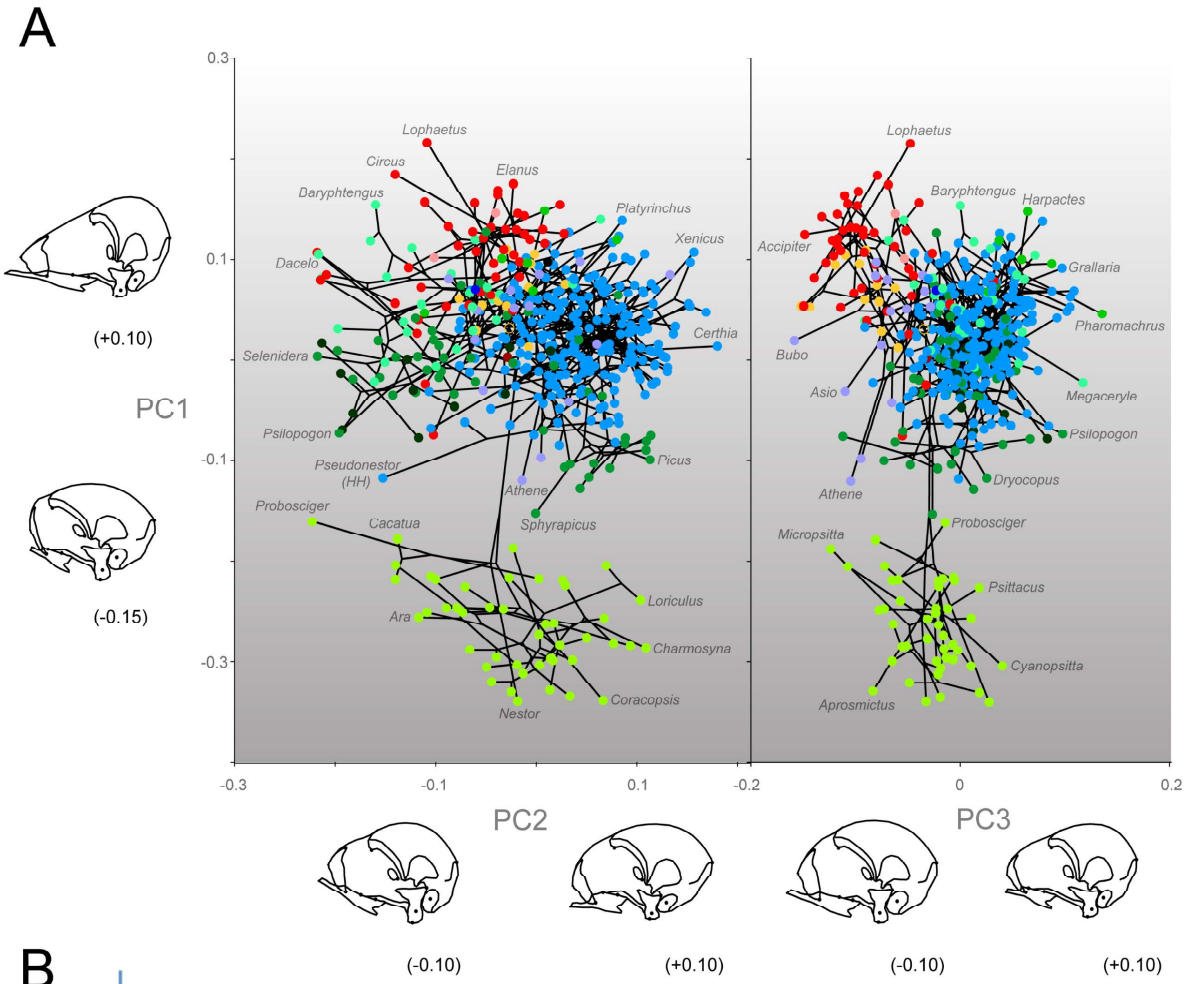

B
Frequency log relative rate
0
0.5
1
1.5
PP of rate shift
>0.7
>0.8
>0.9
Passeriformes
Passeri
Sylvioidea
Tyranni
Acanthisitti
Opisthocomiformes
Accipitrimorphae
Strigiformes
Leptosomatiformes
Trogoniformes
Bucerotiformes
Coraciformes
Eucavllaves
Piciformes
Coliiformes
Cariamiformes
Falconiformes
Psittaciformes

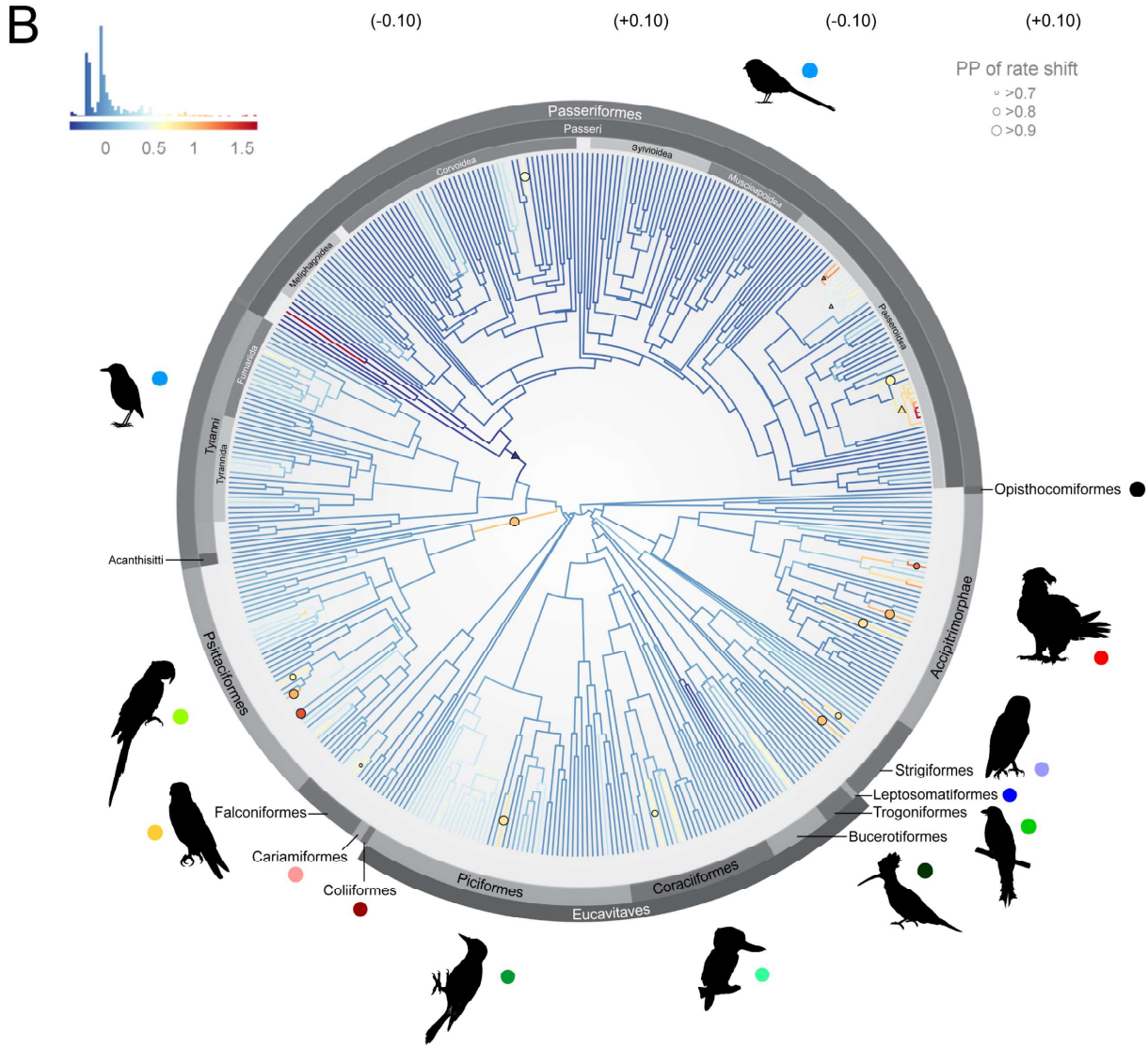
A

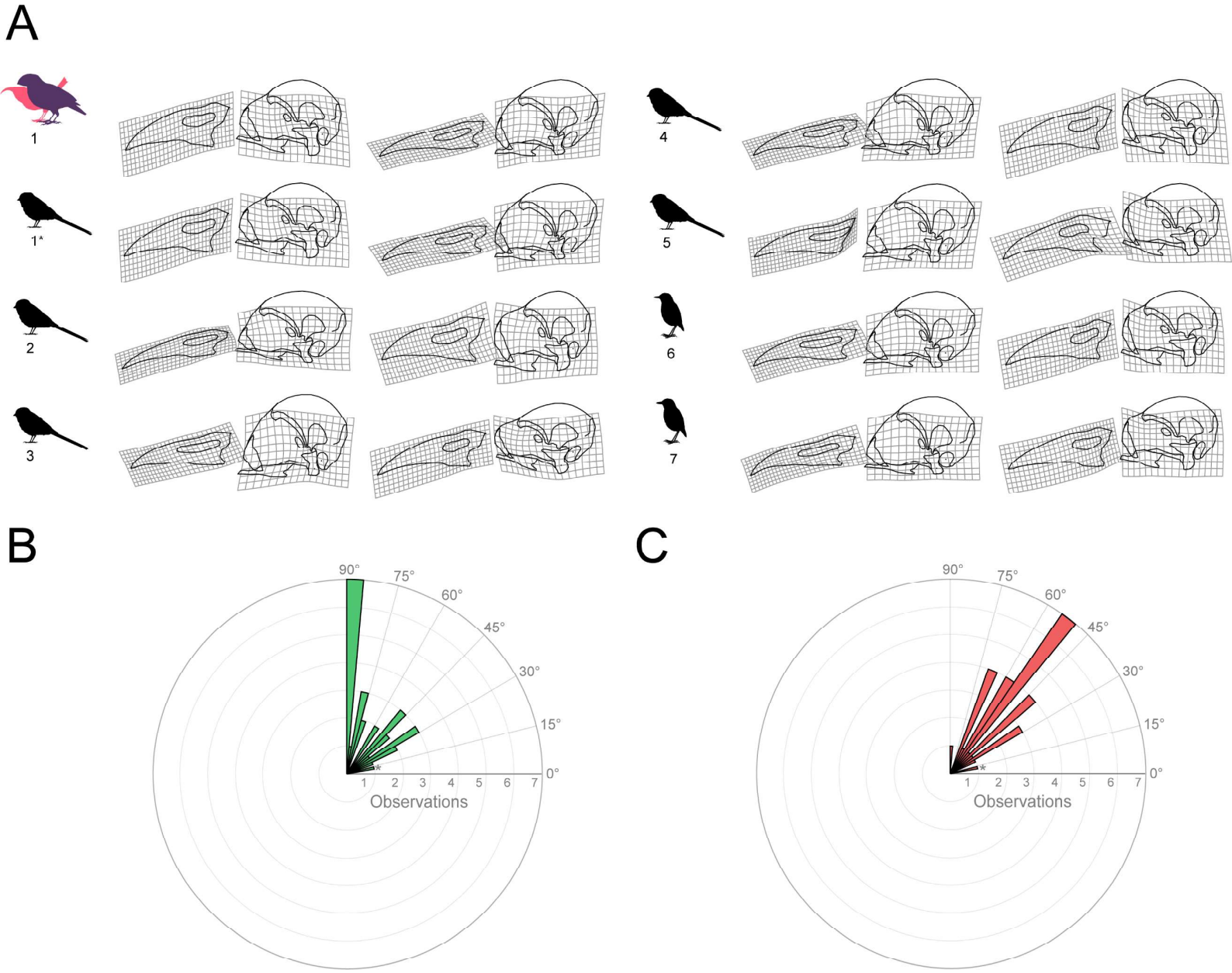

PC1
PC2
PC3
(+0.15)
(-0.25)
(-0.15)
(+0.15)
(-0.10)
(+0.10)
Phylidonyris
Myiagra
Leptosomus
Upupa
Epimachus
Cathartes
Bucorvus
Strix
Nestor
Ramphastos
Paradoxornis
Harpagus
Eclectus
Pithecophagus
Cacatua alba
Acanthisitta
Philemon
Rupicola
Pityriasis
Plectophenax
Opisthocomus
Hieraetus
Polihierax
Agapornis
Cacatua sulphurea

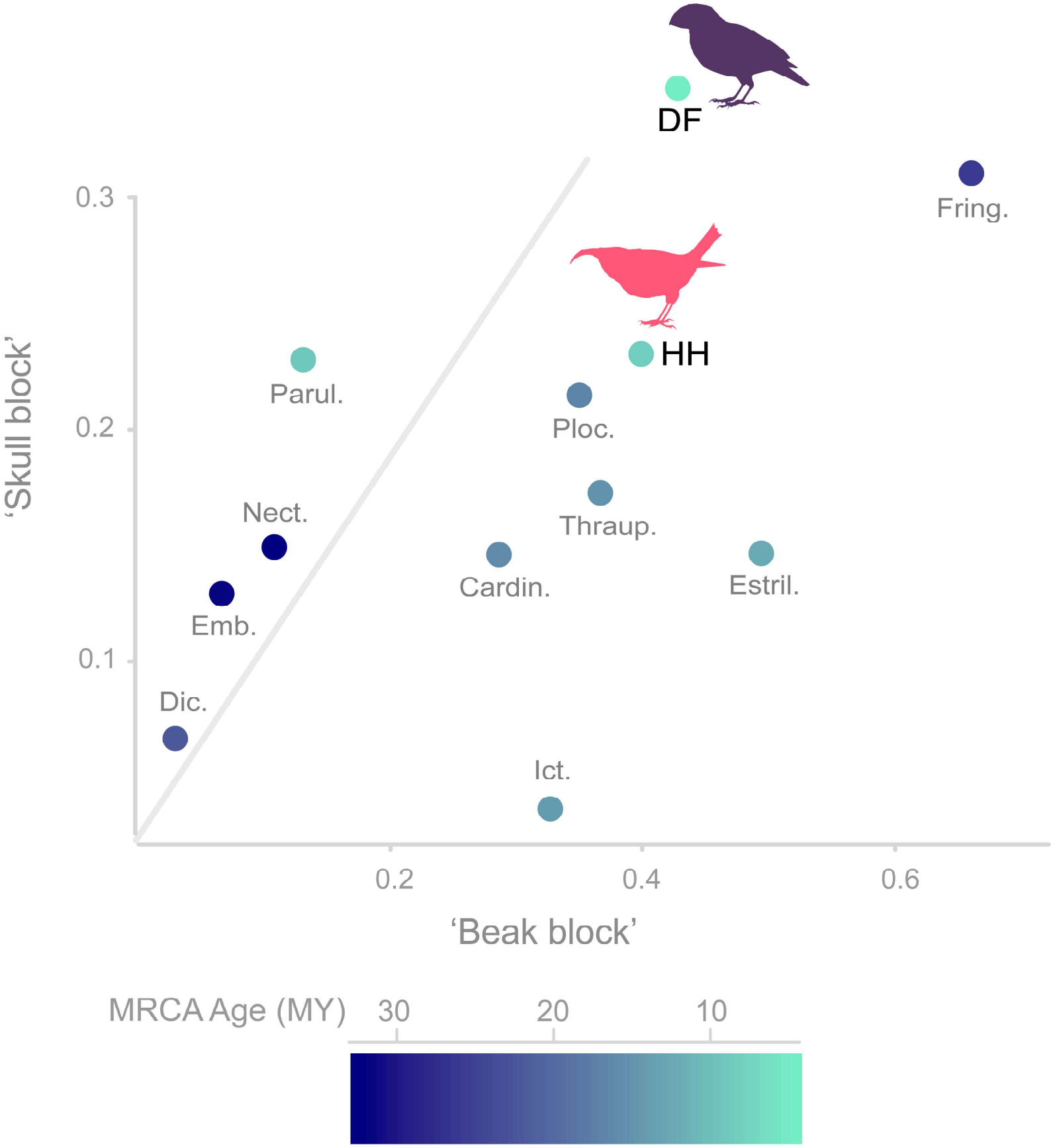
B

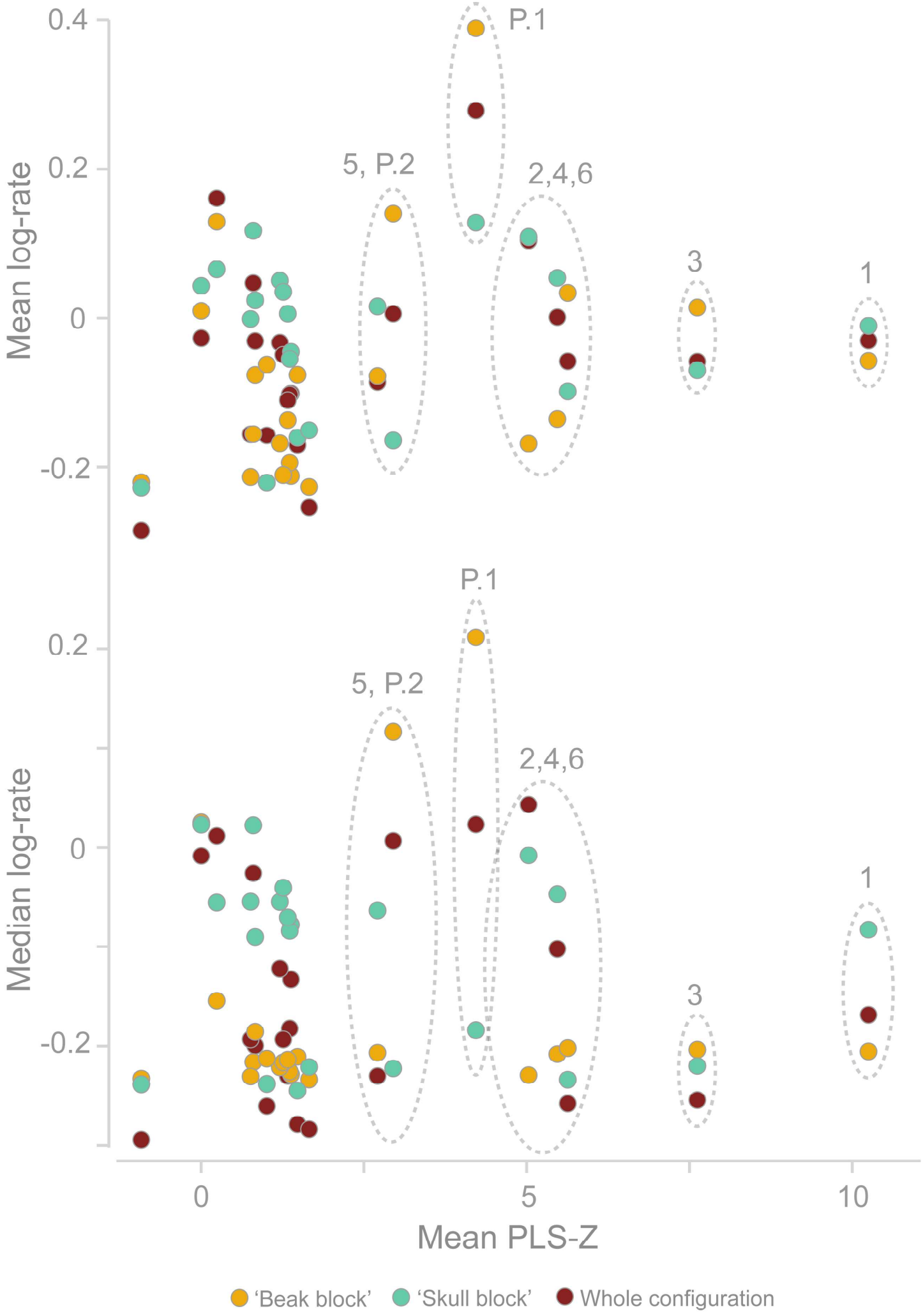

PP of rate shift
>0.7
>0.8
>0.9
0
0.5
1
1.5
Passeriformes
Passeri
Corvoidea
Sylvioidea
Muscicapoidea
Meliphagoidea
Passeroidea
Furnaridae
Tyranni
Tyrannida
Opisthocomiformes
Acanthisitti
Psittaciformes
Accipitrimorphae
Strigiformes
Leptosomatiformes
Trogoniformes
Bucerotiformes
Falconiformes
Cariamiformes
Coliiformes
Piciformes
Coraciiformes
Eucavitaves


A
PC1
PC2
PC3
(+0.10)
(-0.15)
(-0.10)
(+0.10)
(-0.10)
(+0.10)
Lophaetus
Circus
Elanus
Daryphtengus
Platyrinchus
Xenicus
Dacelo
Certhia
Selenidera
Psilopogon
Pseudonestor (HH)
Picus
Athene
Probosciger
Cacatua
Sphyrapicus
Loriculus
Ara
Charmosyna
Coracopsis
Nestor
Baryphtengus
Harpactes
Accipiter
Grallaria
Pharomachrus
Bubo
Asio
Megaceryle
Dryocopus
Micropsitta
Psittacus
Cyanopsitta
Aprosmictus


B
0
0.5
1
1.5
PP of rate shift
>0.7
>0.8
>0.9
Passeriformes
Passeri
Corvoidea
Sylvioidea
Muscicapoidea
Meliphagoidea
Passeroidea
Eurylaimida
Tyranni
Tyrannida
Acanthisitti
Psittaciformes
Falconiformes
Cariamiformes
Coliiformes
Piciformes
Coraciiformes
Eucavitaves
Strigiformes
Leptosomatiformes
Trogoniformes
Bucerotiformes
Accipitrimorphae
Opisthocomiformes


A
1
1*
2
3
4
5
6
7
B
90°
75°
60°
45°
30°
15°
0°
1 2 3 4 5 6 7
Observations
C
90°
75°
60°
45°
30°
15°
0°
1 2 3 4 5 6 7
Observations


DF
Fring.
HH
Parul.
Ploc.
Thraup.
Nect.
Cardin.
Estril.
Emb.
Dic.
Ict.
0.3
0.2
0.1
'Skull block'
0.2
0.4
0.6
'Beak block'
MRCA Age (MY)
30
20
10


0.4
0.2
0
-0.2
Mean log-rate
P.1
5, P.2
2,4,6
3
1
0.2
0
-0.2
Median log-rate
P.1
5, P.2
2,4,6
3
1
0
5
10
Mean PLS-Z
'Beak block'
'Skull block'
Whole configuration

Label	Family
Acanth.	Acanthisittidae
Acc.	Accipitridae
Alaud.	Alaudidae
Alced.	Alcedinidae
Brachyp.	Brachypteraciidae
Buc.	Bucerotidae
Bucc.	Bucconidae
Cacat.	Cacatuidae
Cardin.	Cardinalidae
Cath.	Cathartidae
Cistic.	Cisticolidae
Corac.	Coraciidae
Corv.	Corvidae
Coting.	Cotingidae
Crac.	Cracticidae
DF	Darwin's finches (Geospizinae, Thraupidae)
Dic.	Dicaedidae
Ember.	Emberizidae
Estril.	Estrildidae
Euryl.	Eurylaimidae
Falc.	Falconidae
Fring.	Fringillidae (excluding Hawaiian honeycreepers)
Furn.	Furnariidae
Galb.	Galbulidae
HH	Hawaiian honeycreepers (Drepanidinae, Fringillidae)
Hirun.	Hirundinidae
Ict.	Icteridae
Lyb.	Lybiidae
Megal.	Megalaimidae
Melip.	Meliphagidae
Merop.	Meropidae
Momot.	Momotidae
Nect.	Nectariniidae
Paradi.	Paradisaeidae
Parul.	Parulidae
Phoen.	Phoeniculidae
Pic.	Picidae
Pipr.	Pipridae
Pitt.	Pittidae
Ploc.	Ploceidae
Psitt.	Psittacidae
Ptilon.	Ptilonorhynchidae
Ramph.	Ramphastidae
Strig.	Strigidae
Sturn.	Sturnidae
Sylv.	Sylviidae
Tham.	Thamnophilidae
Thraup.	Thraupidae (excluding Darwin's finches)
Timal.	Timaliidae
Tity.	Tityridae
Trog.	Trogonidae
Tyran.	Tyrannidae
Vang.	Vangidae

ϴ			
BEAK	**Passeriformes**	**Passeri**	**Tyranni**
Passeroidea	27.57	23.17	44.37
Passeroidea*	31.35	28.70	43.59
Muscicapoidea	71.24	70.33	82.03
SKULL			
Passeroidea	30.98	27.51	41.32
Passeroidea*	33.69	29.63	43.42
Muscicapoidea	56.16	58.51	60.18