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1 BIOLOGICAL SCIENCES

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4 **Title: Genome-wide analyses reveal drivers of penguin diversification**

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50 contributed bioinformatics. L.P. developed the ecological niche models. M.J.F., D.N.,
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65 ABSTRACT

66

67 Extant penguins are the only flightless family of diving birds. They comprise at least 18
68 modern species, distributed from polar to tropical environments in the Southern
69 Hemisphere. The history of their diversification and adaptation to these diverse
70 environments remains controversial. We employed 22 new genomes from 18 penguin
71 species to reconstruct the order, timing, and location of their diversification, track changes
72 in thermal niche through time, and test for associated adaptation across the genome. The
73 penguin crown-group originated during the Miocene in New Zealand and Australia, and
74 not in Antarctica as previously thought. *Aptenodytes* appears as sister taxon of all other
75 penguin species. We show that lineage diversification in penguins was driven by changing
76 climatic conditions and by the development of the Antarctica Circumpolar Current (ACC).
77 Changes in thermal niche were accompanied by adaptations in genes that govern
78 thermoregulation and oxygen metabolism. Our reconstruction of changes in ancestral
79 effective population sizes (N_e) recovered three different demographic trajectories in
80 deeper time, the most common (11/18 penguin species) being an increased N_e between
81 0.04 and 0.07 Mya; N_e drops precipitously after the Last Glacial Maximum (LGM) most
82 likely as a consequence of the overall decline in marine productivity following the last
83 glaciation.

84

85 Significance Statement

86 Penguins have long been of interest to the scientific community. However, their
87 evolutionary history is not well understood. Using genomes we investigate macro- and
88 microevolutionary drivers of penguin diversification. Crown-group penguins diverged in
89 the early Miocene in the Australia/New Zealand region. We found that *Aptenodytes*
90 (emperor and king penguins) form a separated clade, sister of all other penguin lineages,
91 in contrast with previous studies that placed them as sister taxa of *Pygoscelis*. Analyses
92 suggest that penguins first radiated from temperate environments and then occupied cold
93 Antarctic waters. Although the onset of the ACC (35 Mya) was suggested to have a role
94 on penguins diversification, our findings of more recent time estimates of divergence

95 suggest that the intensification of the ACC (11.6 Mya) may have promoted their
96 diversification and geographic expansion.

97

98 **Introduction**

99

100 Few organisms have been as successful at colonizing the globe as seabirds, a large
101 ecological assemblage of oceanic and nearshore species that undergo some of the most
102 remarkable foraging and migratory journeys on Earth (1, 2). Despite their ubiquitous
103 presence, surprisingly little is known about the mechanisms that spurred their
104 diversification and allowed for their adaptation to diverse and often dynamic oceanic
105 habitats.

106 As the only living clade of flightless diving birds, penguins (order Sphenisciformes)
107 occupy both terrestrial and marine habitats. They forage across a wide range of ocean
108 temperatures and depths, from Antarctic to tropical waters (3). Our understanding of
109 penguin diversification and adaptation is hampered by disagreements about their
110 phylogenetic relationships (4–10) and the chronology of their radiation. When these
111 estimations are made using few genetic markers from different sections of the genome,
112 discordant results are to be expected as genomic regions vary in their mutation rates and
113 evolutionary history, including unknown patterns of gene introgression when different
114 species hybridize (11). Accordingly, estimates of ordinal crown-age vary between the
115 Miocene and Eocene (9.9–47.6 million years ago [Mya]) (4, 5, 8, 9). The earliest crown-
116 group fossil dates to the late Miocene (12).

117 In addition, reconstructions of ancestral distributions and climatic niches are critical
118 to extend our knowledge of penguin diversification, but existing hypotheses are
119 conflicting: (i) an Antarctic origin, with later expansion towards warmer areas (5) or (ii) a
120 sub-Antarctic origin, with subsequent colonization of Southern Ocean islands and
121 Antarctica (7, 13). Testing these alternative hypotheses on a broad scale requires
122 accurate knowledge of the evolutionary history of penguins, including branching patterns
123 and timing of diversification.

124 The extent of ice and changes in the currents of the Southern Ocean during
125 repeated glacial cycles likely played a significant role in structuring penguin populations
126 and lineage diversification (14-16). Biogeographic boundaries in the Southern Ocean,
127 particularly the Antarctic Polar Front (APF) and the sub-tropical Front (STF), serve as
128 barriers to dispersal of some penguin species (14, 15, 17, 18). Differences in abiotic (e.g.,
129 temperature and salinity) and biotic (e.g., types of food resources) variables on either side
130 of these two fronts may promote local adaptation and enable niche divergence among
131 penguins (19). Furthermore, associated currents have varied significantly over time in
132 latitude and strength in response to changing global circulation patterns (20). These
133 changes have been implicated in the colonization, isolation, and local extinction of some
134 penguin populations and species (4, 9).

135 We report here the reconstruction of the history of penguin diversification and
136 adaptation using 22 newly sequenced genomes representing 18 extant species and one
137 outgroup. We determined phylogenetic relationships and biogeographic histories, and
138 consequently the divergence of niche space through time. Finally, we also assessed the
139 extent of introgression between species that may have contributed to previous
140 disagreements on phylogenetic reconstructions, and adaptations of penguins across
141 environmental gradients.

142

143 **Results**

144 The penguin and petrel outgroup genomes were sequenced to ~30x coverage (Tables
145 S1–S3). All, but one genome sequences contained >90% of the conserved single-copy
146 genes identified across avian genomes (complete BUSCOs >90%; Table S4, Figs. S1–
147 4). From the assembled genomes we extracted 23,108 loci: Ultra Conserved Elements
148 (UCE: 4,057 loci), coding sequences (CDS: 11,011), and introns (8,040). We applied
149 species tree and concatenation methods to construct a phylogenetic hypothesis for extant
150 penguins using all loci together, and for each set of loci independently (Figs. 1, S5–8,
151 Table S5–S6).

152

153 **Phylogenetic history and patterns of introgression of crown-group penguins**

154 All analyses supported a similar phylogenetic hypothesis, all placing *Aptenodytes* as
155 sister taxon of all other extant penguin species (Fig. 1), distinct from other clades
156 comprising the genera *Pygoscelis*, *Spheniscus+Eudyptula*, and *Megadyptes+Eudyptes*.
157 The phylogeny based on mitogenomes was similar to that retrieved from the genomic
158 datasets, with a few minor differences in *Eudyptes* penguins that are likely explained by
159 genome-wide introgression among closely related species (Figs. 2, S7, S9, Table S7) as
160 we found evidence that some species may have hybridized during the course of their
161 diversification. Genomic introgressions were detected between i) erect-crested and the
162 ancestral rockhopper penguin species (17–23%); ii) erect-crested and macaroni/royal
163 (25%) penguins (Fig. 2), and iii) an ancestor of the Galápagos/humboldt and magellanic
164 penguins (11%; Fig. 2). Our divergence time estimated the divergence of the crown-group
165 penguins in the early Miocene at 21.9 Mya (95% CI 19.06–25.19; Figs. 1, S10, Table S8).

166

167 **Biogeographic history and ancestral niche reconstruction**

168 The reconstruction of ancestral geographical occurrence identified the coastlines of
169 Australia, New Zealand, and nearby islands as the most likely range of the ancestor of
170 extant penguins (Figs. 1, S11; Table S9). The first branching event (20.3–19.7 Mya) led
171 to the establishment of the genus *Aptenodytes* in the Antarctic, and reconstructions of the
172 ancestral *Pygoscelis* species indicate that they colonized the Antarctic Peninsula (area
173 C; Fig. 1, Table S9) soon after *Aptenodytes*, pointing to a long history of occupation in
174 Antarctica. In the mid-Miocene, the lineage leading to the *Spheniscus/Eudyptula* ancestor
175 colonized the South American coast (A), with members of the genera *Eudyptes*,
176 *Eudyptula*, *Megadyptes*, and *Spheniscus* progressively diversifying and colonizing
177 warmer oceanic environments (Fig. 1).

178 Consistent with the above findings, our reconstruction of sea surface temperatures
179 (SST) as a proxy for ecological niche disparity through time (DTT) suggests that penguins
180 originated from areas with a maximum SST of 9°C (Figs. 1, S12-S13) which is in
181 alignment with present-day temperatures of sub-Antarctic waters (21). Southern and
182 eastern rockhopper penguins have retained a thermal preference for a maximum SST of
183 9°C, while other closely related species (northern Rockhopper, fiordland, erect-crested)
184 have shifted towards warmer at-sea conditions (SST of 11–17°C; Figs. 1, S13). This

185 thermal shift was most likely driven by divergence across the STF over the past 4.5 Mya.
186 In contrast, Macaroni penguins have shifted to occupy colder at-sea conditions to feed in
187 the nutrient-rich waters off Antarctica (Fig. S13). Lower latitude geographical locations,
188 such as the South African continental coasts (G) and the Galápagos Islands (J), were
189 colonized in the Pleistocene (0.59 Mya). Galápagos penguins are present in Pacific
190 tropical waters near the equator, where SST reach up to 27°C, and exhibit a significant
191 increase in thermal tolerance compared to their sister-species, humboldt penguins (>6°C
192 higher; DTT results, Fig. 1).

193

194 **Genes under positive selection**

195 We detected 104 genes under positive selection (BEB value >0.95 and FDR $q < 0.1$) using
196 a site model across all branches of the Spheniscidae (Table S10-12, Fig. S14). Using a
197 gene interaction network analysis, we found that many of these positively selected loci
198 are functionally connected and formed two major clusters (Fig. 3): one primarily related
199 to broad cellular functions, and the other containing genes that affect specific phenotypes
200 including immunity, renal function and cardiovascular activities (e.g., blood pressure,
201 oxygen metabolism, coagulation). Our gene ontology analysis revealed a concordant
202 pattern of pathway enrichment, including terms related to angiotensin regulation, blood
203 pressure, and oxygen metabolism (Fig. 3, Table S11–12). All of these adaptations are
204 related to diving and maintenance of high core body temperatures.

205

206 **Ancestral effective populations sizes (N_e)**

207 Our reconstruction of changes in ancestral effective population sizes (N_e) recovered three
208 different demographic trajectories in deeper time. Eleven species of penguin (emperor,
209 king, Adélie, chinstrap, gentoo [Kerguelen Population], humboldt, magellanic, African,
210 eastern rockhopper, little) increased N_e between 0.04 and 0.07 Mya, with N_e dropping
211 precipitously during the Last Glacial Maximum. In contrast, three species (northern
212 rockhopper, southern rockhopper, erect-crested) increased N_e during the Penultimate
213 Glaciation Period (PGP) between 0.130–0.194, but were in decline by 0.07 Mya. Finally,

214 two species (gentoo [Antarctica, Falkland Is. populations], Galápagos) have been in
215 steady decline since at least the Naynayxungla Glaciation (0.50–0.72 Mya; Fig. 4, S16).
216 Why Galápagos penguins and southern populations of gentoo penguins have been in
217 decline over such a considerable period of time remains uncertain, as there are no large
218 life-history or ecological differences that distinguishes these two species from other
219 penguins (Table S2). One possibility is that both Galápagos penguins and southern
220 populations of gentoo penguins represent recent divergence events (Fig 1. S7, S10), and
221 hence, the demographic reconstructions may be reflective of a founder event with larger
222 deep time N_e reflecting ancestral population sizes.

223 For erect-crested, southern and northern rockhoppers, and magellanic penguins
224 distributed around the tip of South America and on islands north of the APF, N_e was
225 highest during the PGP with a decline starting in or shortly after the subsequent
226 interglacial. This pattern could reflect changes in ecosystem productivity over deep time,
227 but it could be an artifact of the inability of the PSMC method to account for introgression.
228 Our analyses suggest that for these four species ancestral introgression (Fig. S9) would
229 have elevated estimates of N_e and could have offset the time interval when a peak in N_e
230 occurred (Fig. S16). The largest ancestral N_e we observed was for Adélie penguins
231 ($>10^5$), a primarily cold-water species (Fig. 1) widely distributed south of the APF;
232 decreases in temperatures and increases in ice cover may have promoted the expansion
233 of that population. Smaller historical peaks for N_e ($\sim 2\text{--}3 \times 10^4$) were recovered for island
234 endemic species, such as fiordland (southern New Zealand) and northern rockhopper
235 penguins (Tristan da Cunha and Gough Island).

236

237 **Discussion**

238 Phylogenetic reconstructions recovered by this study show that the large emperor and
239 king penguins (i.e., *Aptenodytes*) are sister to all other extant penguins, refuting the
240 hypothesis that *Aptenodytes* and *Pygoscelis* are sister-taxa (4, 8, 9). While genome-wide
241 data used in our trees allowed for the detection of the deep lineage split between
242 *Aptenodytes* and all other penguins, the short internal branch recovered by our analysis
243 at this split likely indicates a rapid diversification event (<1 Mya) (22). Such rapid
244 speciation events may explain the discrepancies among the previous proposed

245 phylogenetic hypothesis generated using that few molecular markers, which are known
246 to be insufficient in resolving such deep and short branches (23). As the clades become
247 more divergent, the phylogenetic position of the remaining genera and species are
248 consistent with phylogenetic hypotheses generated in other studies (4–10). Reticulated
249 evolution may also have contributed to some inconsistencies in penguin phylogenetic
250 reconstructions. Genome analyses detected deep and shallow introgression events
251 across the phylogeny of extant penguins. Species of crested penguins (*Eudyptes*) appear
252 to have exchanged genes throughout much of their evolutionary history. The directionality
253 of introgression among these lineages is consistent with the clockwise direction of the
254 Antarctic Circumpolar Current (ACC) connecting sub-Antarctic islands and promoting
255 dispersal. We also detected extensive genomic introgression between an ancestor of the
256 galápagos/humboldt penguin and the magellanic penguin; such introgression is still
257 observed at present between magellanic and humboldt penguins for which hybridization
258 has been reported in the wild (24).

259 Our divergence time estimates are consistent with the fossil record (12), placing
260 the ancestor of crown-group penguins in the early Miocene. Our biogeographic
261 reconstruction for crown-group penguins pointed to the coastlines of Australia and New
262 Zealand and nearby islands as the most likely range of the ancestor of extant penguins,
263 supporting earlier suggestion (7), rather than Antarctica as place of origin (5). Because of
264 the recency of most diversification events (2–9 Mya), we propose an alternative
265 hypothesis regarding their geographic expansion, namely that the opening of the Drake
266 Passage around the tip of South America led eventually to the full development of a deep,
267 strong ACC by ~11.6 Mya (26) which in turn may have contributed to colonization of new
268 areas and diversification of penguins, rather than the initial formation of the ACC ~35 Mya
269 (26)(Fig. 1). Global climate cooling intensified with the strengthening of the ACC and
270 possibly led to the extinction of several species inhabiting Antarctica (20, 27). The ACC
271 also reinforced the isolation of taxa inhabiting Antarctica from those on continental
272 shelves and islands to the north (20, 27), while promoting eastward colonization of
273 available sub-Antarctic islands.

274 Acceleration of the decline in surface temperatures since the Pliocene (20) may
275 have facilitated the colonization of new areas such as islands in the Indian Ocean. This

276 hypothesis is supported by our analysis of the divergence of the four gentoo penguin
277 lineages across thermal and salinity gradients to the north and south of the APF (Figs.
278 S5–S8). The Pliocene-Pleistocene cooling, along with the expansion of ice shelves
279 across the Southern Ocean (20), would have reduced connectivity among penguin
280 populations and facilitated speciation across *Pygoscelis*, *Spheniscus*, *Eudyptes* and
281 *Aptenodytes* between 2 and 5.5 Mya (Fig. 1).

282 During the Quaternary glaciations (1.8–0.01 Mya), sea-ice is thought to have
283 reached c. 40°S at the coast of South America (28). This extent of sea-ice would have
284 promoted the northern expansion of *Spheniscus* to the subtropics, and subsequently
285 enabled colonization of the Galápagos Islands, home to rich feeding resources for
286 penguins due to the upwelling of cooler, nutrient rich waters. Strong north-flowing currents
287 – the Humboldt Current and the Benguela Current – would have further facilitated penguin
288 colonization of subtropical habitats in the Pacific (Galápagos) and Atlantic (southern
289 Africa), respectively. Neither of these current systems penetrate beyond the equator; this,
290 together with their sub-Antarctic origins and preference for cooler waters, may explain
291 why crown-group penguins never successfully colonized the Northern Hemisphere.

292 The genes for which signals of positive selection were detected are associated with
293 thermoregulation (e.g., vasoconstriction/vasodilation: ENPEP, MME, BDKRB2),
294 osmoregulation (e.g., balance of fluids and salt: SCL6A19, ACE2, AGT), and diving
295 capacity (e.g., oxygen storage: MB), thereby reflecting adaptations that enabled penguins
296 to colonize both colder and warmer habitats, away from their ancestral thermal maximum
297 of c. 9°C (Fig. 1, S12-13). In Antarctica, emperor penguins are exposed to temperatures
298 as low as -40°C and forage in waters of -1.8°C (29), whereas Galápagos penguins are
299 exposed to SST >27°C and air temperatures exceeding 40°C. These high temperatures
300 are mostly associated with El Niño events, which may cause heat stress, high mortality,
301 and low recovery of the penguin colonies (30, 31). Regulating blood pressure selectively
302 through the constriction of blood vessels can further conserve oxygen consumption and
303 facilitate the maintenance of high core body temperatures (32).

304 Penguins spend most of their lives at sea, often performing prolonged dives while
305 foraging. They store oxygen in their lungs, blood, and muscles (33), and their rates of

306 oxygen consumption can be very low (34). The two largest penguin species, the emperor
307 and king penguins, can achieve depths of >300 meters and maximum dive durations of
308 22 and 8 minutes, respectively (33, 35, 36). Smaller penguin species tend to dive in
309 shallow waters (<50 m) with dives of 1–2 minutes in duration (33), although the chinstrap
310 penguins often dive off-shelf (>200 m, (37)). In this sense, nucleotide differences in
311 Myoglobin (MB, overall positive selection, $Z=2.645$, $p=0.005$) across species groups
312 could be associated with differences in diving capacity. For example, we found several
313 non-synonymous substitutions that were common within *Pygoscelis*, *Eudyptes*, and
314 *Aptenodytes* penguins, but differed in their amino acid composition (Fig. S15). It is
315 possible that these non-synonymous mutations encode greater oxygen-binding capacity,
316 which would facilitate the deep and prolonged dives performed by *Aptenodytes* and some
317 species of *Pygoscelis* penguins compared with *Eudyptes* (higher dN/dS ratios, Table
318 S13).

319 Our results suggest that adaptive evolution, implicating genes involved in multiple
320 interconnected genetic pathways, has increased the foraging success and survival of
321 penguin species across diverse temperature and salinity gradients. Foraging success is
322 associated with reproductive success (38, 39) and also with survival during long periods
323 of fasting while caring for eggs and chicks (40). Collectively, such adaptations would have
324 enabled the radiation of penguin species across the Southern Hemisphere.

325 Penguins have a remarkable evolutionary history. Their radiation from the
326 temperate coasts of New Zealand and Australia into other parts of the Southern
327 Hemisphere was facilitated by changes in global circulation patterns over the past 20
328 million years. Our analysis detected positive selection across several gene networks,
329 suggesting that molecular adaptation enabled the establishment of penguin populations
330 in Antarctic and tropical regions, and enhanced the ability of some species to dive deeply.
331 Demographic reconstructions over the past million years show that most penguin species
332 have declined during the severe ice conditions during the LGM in the Southern Ocean, a
333 result concordant with that recovered for several other bird species (41, 42).

334 Our results suggest that penguins originated from areas with a maximum SST of
335 9°C and diversified over millions of years, occupying colder Antarctic and warmer tropical

336 waters. As such, it seems unlikely that locally adapted species will be able to keep pace
337 with rapid climate change, especially as marine species may be more vulnerable to global
338 warming than terrestrial species (43, 44). This vulnerability is especially pertinent for
339 penguins, as illustrated by the massive mortality of Adélie penguin chicks and by the
340 relocation of emperor penguins in response to suboptimal sea ice conditions (45, 46). As
341 large-scale genomic studies become increasingly feasible and data for more
342 sophisticated global climate models become available for niche modelling, the application
343 of approaches like those in the present study hold significant promise for revealing new
344 insights into the evolutionary history and climatic vulnerability of many of the world's
345 poorly understood taxonomic groups.

346

347 **Materials and Methods**

348 Detailed methods for each of the sections below are provided in the supplementary
349 documents.

350

351 **Genome sequencing and assembly**

352 The genomes of 18 extant penguin species (22 individuals) as well as the southern giant
353 petrel (*Macronectes giganteus*) were sequenced to ~30x coverage with 150 bp paired-
354 end reads using an Illumina HiSeq X platform at MedGenome (USA; Table S1). We used
355 the giant petrel as outgroup for the analyses reported below. Briefly, duplicate sequences
356 were removed using Super Deduper (<https://github.com/dstreeet/Super-Deduper>) and the
357 reads were then filtered. We aligned the resulting cleaned reads of each individual to the
358 emperor penguin reference genome (<http://gigadb.org/dataset/100005>; scaffold-level
359 assembly) using LAST (<http://last.cbrc.jp/>). The extent to which genome assemblies were
360 complete was assessed using the Benchmarking Universal Single-Copy Orthologs,
361 BUSCO v2 dataset (47)(Fig. S2) and KAT spectra-cn plots (48)(Fig. S3, S4). The CDS,
362 intron and mitogenome sequences were extracted for each genome using the reference
363 genome GFF. We extracted 120 bp Ultra Conserved Element (UCE) loci with 750 bp of
364 length of the flanking sequence padded to each side with scripts from the PHYLUCE
365 pipeline (49). Sequences were aligned using MAFFT (50).

366

367 **Estimation of phylogeny, divergence times, and interspecific introgression**

368 To account for potential genome-wide incompatibilities between taxa and loci, we used
369 Astral III (48) to estimate species tree phylogenies for each of the UCE, intron, and CDS
370 data sets, and for all three data sets combined (Fig S8). We used RAxML-NG (v. 0.5.1b
371 BETA) (51) to generate independent gene trees for each locus of the UCE, intron, and
372 CDS alignments. As input to Astral III, we merged all of the “best” trees generated by
373 RAxML-NG into a single file (Supplement). For the phylogenomic concatenated analysis
374 using all the data from UCEs, CDS, intron, and the mitogenome we carried out maximum
375 likelihood (ML) analyses in IQ-TREE, (52), with 1000 bootstrap replicates (Fig. S5-S7).
376 We estimated divergence times in BEAST v2.5.2 (53) using the computer resources
377 available through the CIPRES Science Gateway (Fig S7, S10) (54) calibrating the
378 topology with five fossils (Table S8). This phylogeny was used for all subsequent analysis
379 that required this information. Analyses to investigate the extent of interspecific
380 introgression across the phylogeny were performed using a partitioned *D*-statistics
381 approach implemented in DFOIL (55) for possible taxa combinations (eight) respecting
382 the priors of a symmetrical tree composed of four taxa and an outgroup, one ingroup
383 clade being younger than the other (Fig. 2, S9, Table S7). To perform the tests, we split
384 the genome-wide alignments into 100 kb, non-overlapping windows with Bedtools and
385 custom scripts.

386

387 **Ancestral Distribution and Niche Reconstruction**

388 For the historical biogeographic analysis, we estimated the ancestral range of the extant
389 penguin species in the R package BioGeoBEARS (56) implementing three models of
390 ancestral area reconstruction with and without long distance dispersal (the parameter *j*:
391 “jump dispersal”). We subdivided the extant penguin geographic distribution into 10
392 different areas. Occurrence records for all penguin species and six marine variables were
393 used to create raw models with MaxEnt–Javascript (57). Niche overlap was estimated
394 between all penguin species for the set of variables considered. We used the package
395 ‘Phyloclim’ to create Predicted Niche Occupancy (PNO) profile values and plots.
396 Subsequently we combined this information with the phylogenetic tree to generate the

397 Divergence Through Time (DTT) plots and climatic tolerance chronograms depicted in
398 Figure 1.

399

400 **Detection of signatures of positive selection**

401 We performed a dN/dS ratio test using the CodeML algorithm implemented in ETE3 (58,
402 59) for all species and sub-groups in the phylogeny. Due to the large number of analyzed
403 genes, we performed a multiple comparisons (false-discovery rate [FDR]) test
404 implemented in R. Genes that persisted on the list (i.e. remained significantly different
405 from neutral expectations, supporting a positive selection regime) were then used to
406 perform a gene ontology analysis using WebGestalt (WEB-based GENE SeT AnaLysis
407 Toolkit) (60) and network analysis performed with StringDB (61) (Figure S14-S15).

408

409 **Demographic history**

410 To address questions about how climate may have influenced effective population size
411 for each penguin species, we performed a demographic analysis using a pairwise
412 sequential Markovian coalescent (PSMC) method (62). PSMC was run with parameters
413 “-N25 -t15 -r5 -p 4 + 25*2 + 4 + 6”, and an estimated generation time (g) for the different
414 penguin species (Figure 4, S16, Table S2) using a substitution rate derived from chicken
415 pedigrees (63).

416

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418

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576

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582 **Data and materials availability:** Penguins and giant petrel raw fastq reads,
583 reconstructed genomes (BioProject PRJNA530615, BioSample accession
584 SAMN11566608-SAMN11566630) and mitogenomes (MK760983-MK761004,
585 MK761006) were deposited in Genbank. All UCE, CDS, intron and mitogenome
586 alignments, dated phylogenies and codes for all data analyses are available at Dryad
587 (<https://doi.org/10.5061/dryad.pk0p2ngj2>). All other data needed to evaluate the
588 conclusions in this paper are present either in the main text or the supplementary
589 materials.

590

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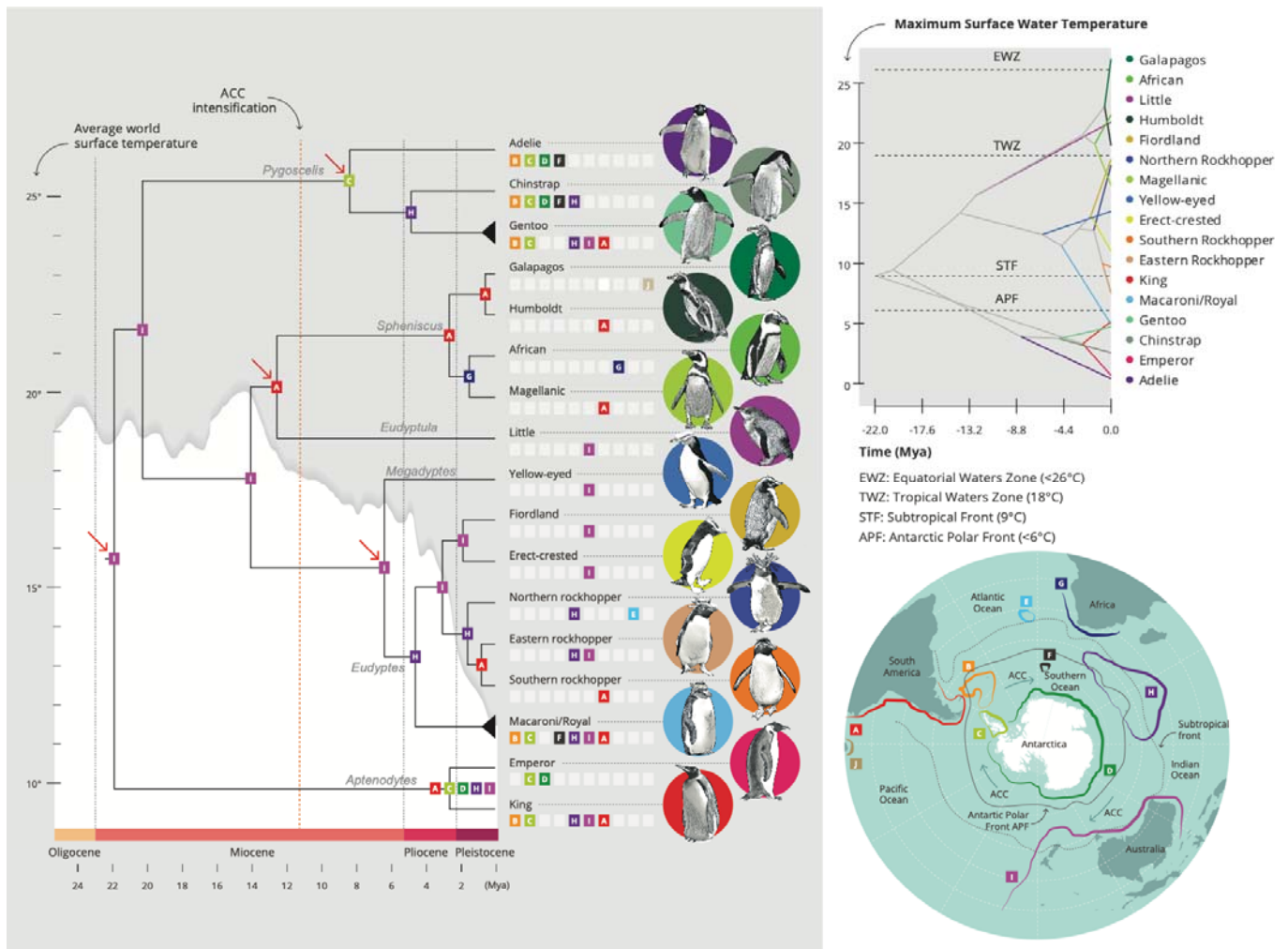
592 **Supplementary Materials:**

593 Materials and Methods

594 Figures S1-S16

595 Tables S1-S13

596 References (1-42)

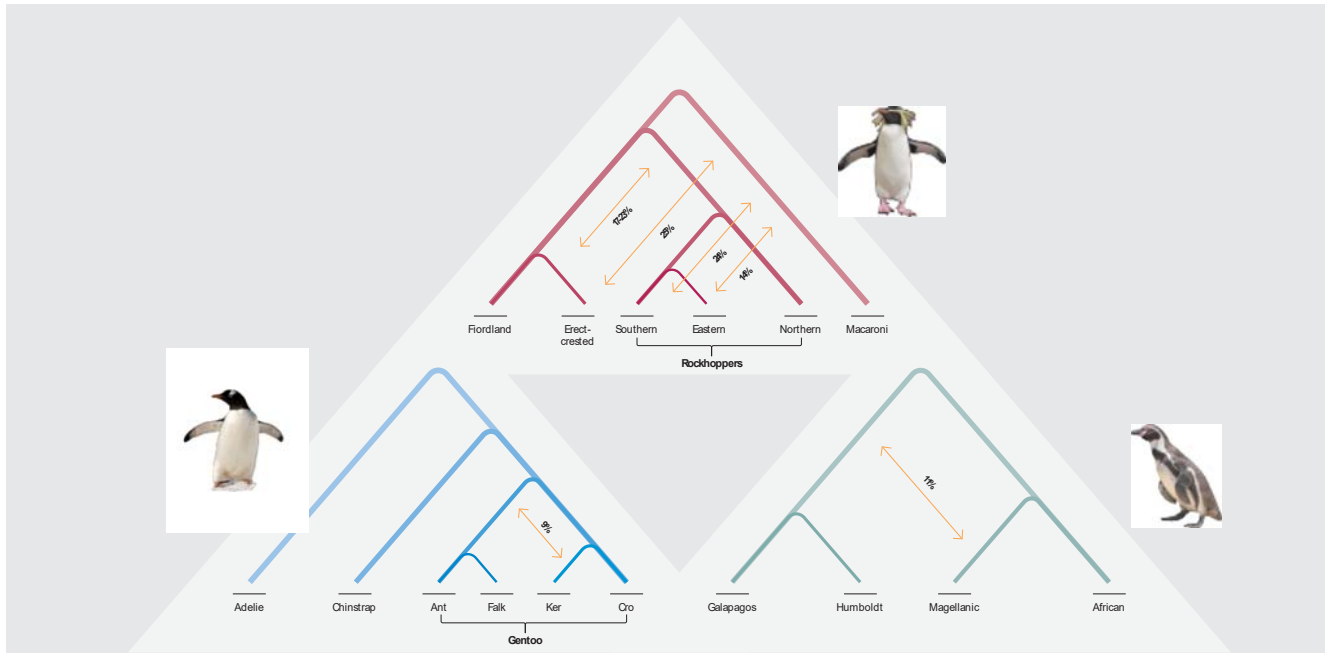


598

599 **Fig. 1. Evolutionary history of penguins.** Phylogenetic hypothesis of penguin species
 600 and divergence time estimates using UCE dataset. Red arrows represent the four fossil
 601 calibration points (fifth point corresponds to the node with the outgroup which not
 602 represented). Each node is represented by the ancestral distribution before the
 603 cladogenesis event using Ancestral range reconstruction based on the best-fit model
 604 (DIVALIKE+J) and is associated with one or more of the ten geographic locations
 605 depicted on the map in the lower right (different letters A–J and colors); areas at branch
 606 tips represent the current range of species. Average world surface temperature in the
 607 past is represented by the white graph behind the phylogeny (41) and onset of the
 608 strengthening of the Antarctic Circumpolar Current (ACC) by a dashed red line. At the
 609 top right: Ecological niche disparity through time (DTT) for penguins (top right), with the
 610 phylogeny projected onto niche parameter space on the y-axis (maximum surface water

611 temperature) with predicted niche occupancy (PNO) over time (x-axis) reconstructed for
612 internal nodes.

613

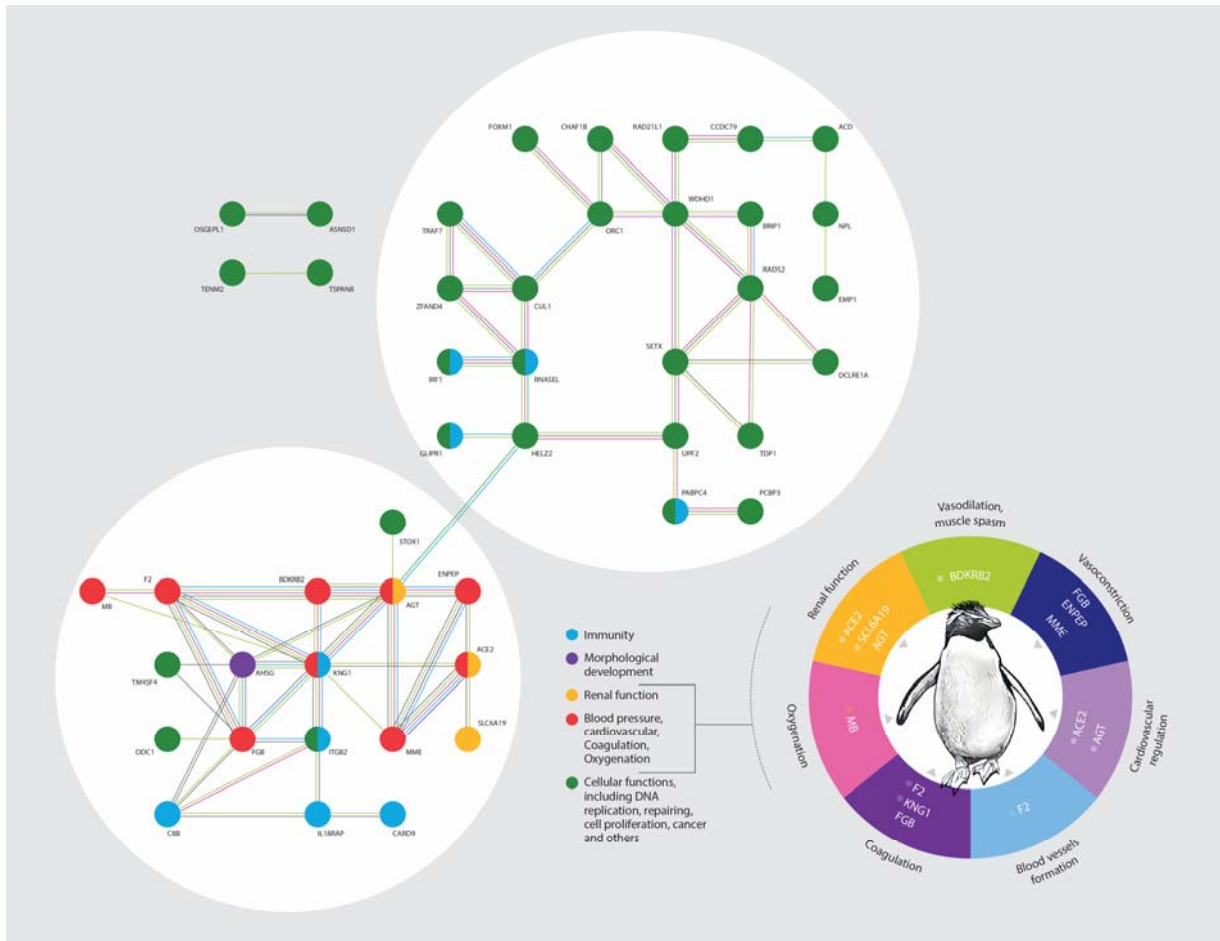


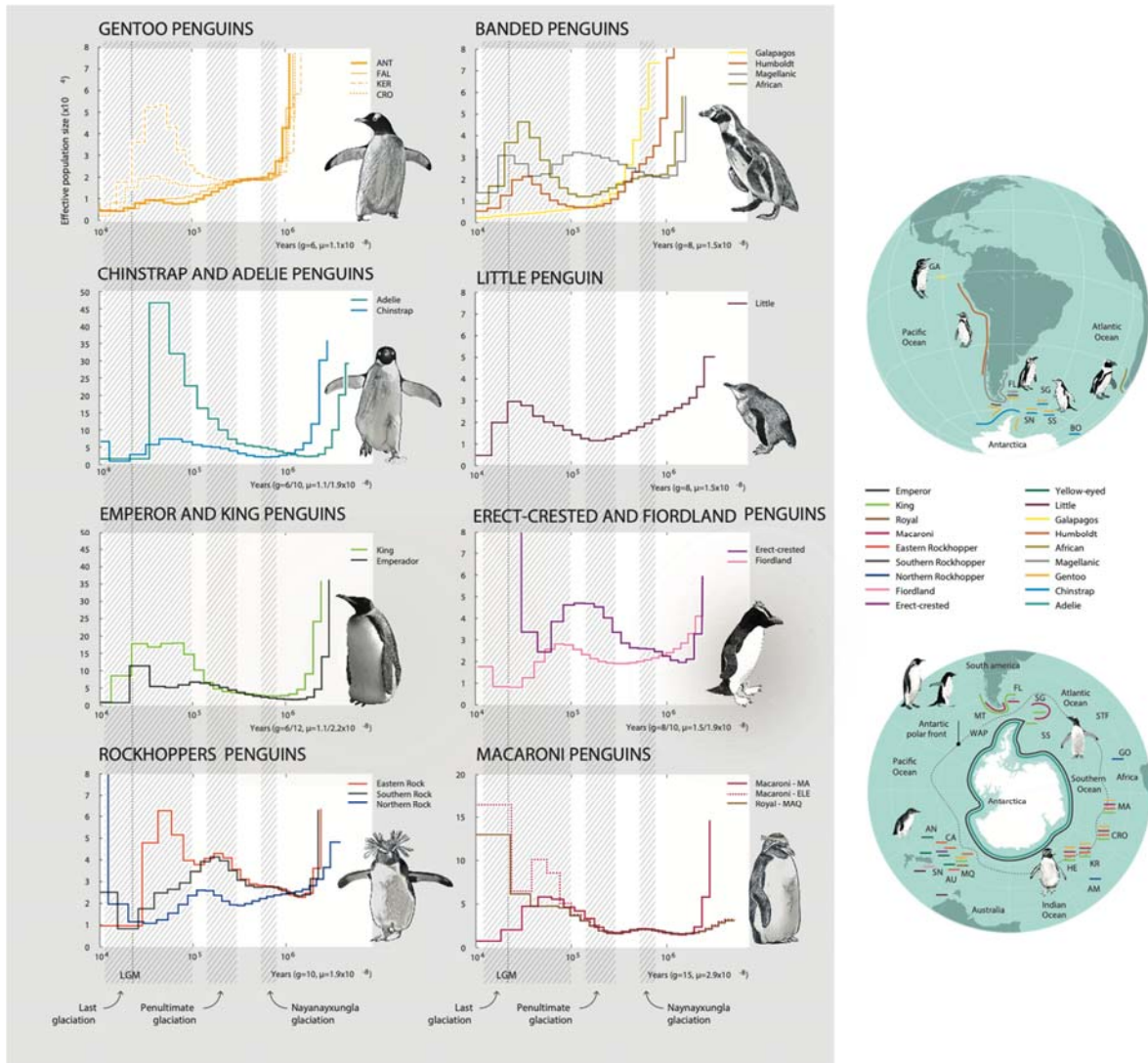
614

615 **Fig. 2. Summary of introgression among penguin taxa.** Arrows represent the
616 percentage of introgression (>2%) between taxa for all 8 combinations of the five-taxa
617 statements evaluated (see Fig. S9, Table S7).

618

619





629

630 **Fig. 4. Demographic history of penguins.** Pairwise Sequentially Markovian
 631 Coalescent (PSMC) plot depicting the demographic history of each lineage inferred from
 632 genomic data represented by different colored lines (see Fig. S16 for bootstrapped
 633 curves). The period of the Naynayxungla glacial, Penultimate glacial and the Last
 634 glacial are represented in the plots, as well as the Last Glacial Maximum (LGM).