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**Acoustic, genetic, and morphological analysis of the
Canarian common chaffinch complex (*Fringilla coelebs* ssp.)
reveals a cryptic diversification process**

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Keywords:	Avian radiation, Incipient speciation, Integrative taxonomy
Abstract:	<p>The common chaffinch (<i>Fringilla coelebs</i>) is the extant avian species with the highest level of differentiation across North Atlantic archipelagos. Such a degree of diversification has been traditionally recognised within the subspecies category, with one endemic subspecies occurring in Azores (<i>F. c. moreletti</i>), one in Madeira (<i>F. c. maderensis</i>), and three in the Canary Islands (<i>F. c. canariensis</i>, <i>F. c. palmae</i> and <i>F. c. ombriosa</i>). Recent genetic, acoustic, and sperm morphology studies informed us about the significant differentiation of the Gran Canaria population, which is traditionally included within <i>F. c. canariensis</i> subspecies. The goal of this study is to examine the similarity of the Canarian chaffinches, with the objective of determining if the Gran Canaria chaffinches represent an isolated and distinct population. In order to achieve this aim, we used a double approach: (1) we analysed new morphological and genetic data from the Canary Islands, and (2) we reviewed and synthesised the vast acoustic, morphological and genetic information available for these taxa in Macaronesia, with special emphasis on the Canary Islands. Genetic, acoustic, and sperm morphological data, and to a lesser extent phenotypic data, strongly support the existence of a cryptic taxon in Gran Canaria. Moreover, our findings also reveal an incipient speciation process on going in the Canary Islands, mostly driven by genetic differentiation. Overall, our synthesis suggests that individuals occurring in Gran Canaria should be considered as a novel taxon that we formally described as <i>Fringilla canariensis bakeri</i> ssp. nov.</p>

5 **Abstract**

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7 level of differentiation across North Atlantic archipelagos. Such a degree of
8 diversification has been traditionally recognised within the subspecies category, with
9 one endemic subspecies occurring in Azores (*F. c. moreletti*), one in Madeira (*F. c.*
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26 **Key words:** Avian radiation, Gran Canaria, *Fringilla coelebs bakeri*, incipient
27 speciation, integrative taxonomy, island biogeography, Macaronesia.

28

29 **Introduction**

30 Oceanic islands support high levels of speciation events due to the role of founder
31 events, drift, mutation, limited gene flow, and selection acting on a small contingent of
32 colonisers over time (Emerson 2002, Grant and Grant 2008). Such divergence events
33 have produced a plethora of forms and colours that taxonomists have frequently
34 described and classified as distinct taxa. Different types of information have been used
35 to understand the origin and variation of biodiversity, for instance, biometry (e.g. Grant
36 1979a, 1979b, Dennison and Baker 1991), acoustic (e.g. Lynch and Baker 1990, Päckert
37 et al. 2006, Tietze et al. 2015), genetic (e.g. Avise 2000, Alström et al. 2015, Stervander
38 et al. 2015), or a combination of methods (Illera et al. 2014). However, cryptic
39 differentiation, that is, species evolving similar morphologies, makes the correct
40 identification of unique taxa difficult, which increases the risk of underestimating
41 biodiversity (Padiál et al. 2010; Fišer et al. 2018).

42 The Canary Islands are an oceanic archipelago situated about 100 and 460 km
43 from the African mainland. The archipelago consists of seven principal volcanic islands
44 with a well studied variation of geological ages increasing towards the African
45 continent. El Hierro appears as the youngest island (1 Mya) and Fuerteventura as the
46 oldest (~ 20 Mya). The Canary Islands harbour a high number of terrestrial endemic
47 species, making this archipelago one of the most important centres for biodiversity in
48 the temperate region (Juan et al. 2000, Illera et al. 2012). As an example, the more than
49 150 native land vertebrate taxa inhabiting the archipelago, 21 (13%) are endemic
50 (Arechavaleta et al. 2010). This value is even higher considering the plants where the
51 endemic taxa (> 550 species) represent around 40% of the native flora (Francisco-
52 Ortega et al. 2000). In relation to extant breeding birds, six species and more than 30
53 subspecies are endemics (Illera et al. 2012, 2016), while considering the extant and

54 extinct species the number is much higher (Illera et al. 2012, 2016). Interestingly, the
55 Canarian birds have recently provided several examples of cryptic differentiation. For
56 instance, four subspecies of the Canarian blue tit (*Cyanistes teneriffae*) had traditionally
57 been recognised in the Canary Islands based on morphology, plumage and song (Martín
58 and Lorenzo 2001). However, Kvist et al. (2005) provided significant genetic
59 divergences not only among the classical subspecies but also between Gran Canaria and
60 the remaining populations. Such differences were used three years later to support the
61 description of a new subspecies in Gran Canaria (Dietzen et al. 2008). Indeed, with such
62 a level of differentiation in all Canarian blue tit subspecies have been suggested that
63 each is treated as a full species (Sangster 2006, Illera et al. 2016). The goldcrest
64 (*Regulus regulus*) provides another interesting case of cryptic differentiation. Päckert
65 and colleagues (2006) studied the acoustic, morphology and genetics of the goldcrests
66 in Macaronesia. They found an unforeseen colonisation pattern with two distinct
67 lineages within the Canary Islands, suggesting two independent waves of colonisation
68 from the Iberian Peninsula. Such findings supported the description of a new subspecies
69 (*R. r. ellenthalerae*), occurring in the western islands of La Palma and El Hierro,
70 meanwhile the former subspecies (*R. regulus teneriffae*) inhabits the islands of Tenerife
71 and La Gomera. In addition, similar scenarios have been documented to occur with the
72 robin (*Erithacus rubecula*), and the blue chaffinch (*Fringilla teydea*) in the Canary
73 Islands (Dietzen et al. 2003, 2015, Lifjeld et al. 2016, Sangster et al. 2016). Overall, all
74 these results show an interesting pattern at species level of independent but repeated
75 bouts of colonisation from the continental areas to the Canaries, with subsequent
76 processes of genetic isolation (and sometimes of extinction) producing new taxa over
77 time. According to these results, it seems clear that the avian Canarian taxonomy needs

78 to be reshuffled using unambiguous, diagnostic and independent traits (Illera et al.
79 2016).

80 The common chaffinch (*Fringilla coelebs*) has been one of the species most
81 intensively studied using molecular tools in Macaronesia. The pioneer study carried out
82 by Baker et al. (1990) using protein electrophoresis of 42 loci found support for two
83 genetic groups within the Canary Islands. One of them would occur on the western
84 islands of El Hierro and La Palma, and the other on Tenerife, La Gomera and Gran
85 Canaria. Nonetheless, the first comprehensive phylogeographic study to understand the
86 evolutionary history of this taxon in Macaronesia was performed by Marshall and Baker
87 (1999). These authors using nucleotide sequences of four mitochondrial genes revealed
88 an unforeseen colonisation pathway from north to south in a stepping stone mode
89 starting in Azores and ending in Gran Canaria Island (Figure 1). In addition, Marshall
90 and Baker (1999) found a strong genetic structure among the three Macaronesian
91 archipelagos where the common chaffinch occurs, suggesting long periods of isolation
92 mostly without gene flow. This finding has been also confirmed in a subsequent
93 multilocus approach using both mitochondrial and nuclear genes (Samarasin-
94 Dissanayake 2010, Rodrigues et al. 2014). Recently, Suárez and co-workers (2009)
95 studying the genetic structure of the common chaffinch in the Canary Islands found an
96 unexpected result in Gran Canaria. These authors showed a strong genetic structure in
97 Gran Canaria, which was compatible with a subspecific rank.

98 In addition to the molecular markers, the evolutionary biology of this passerine
99 has been repeatedly analysed according to morphological, sperm length, and acoustic
100 datasets (Grant 1979b, Dennison and Baker 1991, Lynch and Baker 1994, Marshall and
101 Baker 1999, Rando et al. 2010, Stensrud 2012). Interesting, in a recent study analysing
102 the loss of acoustic variability along the pathway of colonisation in Macaronesia,

103 Lachlan et al. (2013) provided evidence of a significant loss of syllable sequencing
104 within songs in the Gran Canaria chaffinches, which makes this song distinctive from
105 any other Canarian chaffinch population. However, much of this information, and the
106 interpretation of these findings, is tackled on individual traits, which limits the general
107 understanding of the evolutionary consequences of experiencing long periods of
108 isolation. In addition, there is mixed evidence of how morphology can be used to
109 discriminate common chaffinches, and when the genetic divergence occurred within the
110 Canary Islands. Such information is also necessary to reshuffle the taxonomy of this
111 passerine within the Canary Islands. With these precedents, our main goal is to
112 scrutinize whether the Gran Canarian birds can be characterised and identified by
113 multiple traits. To achieve this aim we will use published information, but also new
114 morphological and genetic data to re-analyse and re-evaluate the similarity of the
115 Canarian common chaffinches. Our analysis will show that the common chaffinch in
116 Gran Canaria is a distinguishable population from other Canarian populations from
117 genetic and acoustic perspectives, and to a lesser extent from phenotypic characteristics,
118 representing a new case of cryptic differentiation in the Canary Islands. Our final aim is
119 to perform a formal taxonomic description of this novel taxon, and discuss the
120 evolutionary implications of such a radiation in the Canary Islands.

121 **Material and Methods**

122 *The species*

123 The common chaffinch with five subspecies described provides the best example of
124 diversification within extant land birds in Macaronesia (Illera et al. 2016; Figure 1). The
125 species is distributed from Europe to the North of Africa, including three Macaronesian
126 archipelagos (Azores, Madeira and the Canary Islands). At present between 15 to 18
127 subspecies are recognised (Cramp and Perrins 1994, Clement 2018), with one endemic

128 subspecies per Macaronesian archipelago, except in the Canary Islands where three
129 endemic subspecies are traditionally recognised (Martín and Lorenzo 2001). Azorean
130 populations show no significant morphological (Grant 1979b, Dennison and Baker
131 1991) or genetic (Baker et al. 1990; Samarasin-Dissanayake 2010, Rodrigues et al.
132 2014) differentiation among islands, and they are routinely grouped in a single
133 subspecies *F. c. moreletti* Pucheran, 1859. Such a result is compatible with high levels
134 of gene flow among populations (Rodrigues et al. 2014), which contrasts with the
135 significant levels of mutation rates in the song memes found among populations (Lynch
136 and Baker 1994). In Madeira the species only breeds on the Madeira Island with the
137 exclusive subspecies *F. c. maderensis* Sharpe, 1888. Finally, in the Canary Islands the
138 species occurs in the central and western islands being absent from the eastern islands
139 (Lanzarote and Fuerteventura). Three Canarian subspecies were described according to
140 their phenotypic differences: *F. c. palmae* Tristram, 1889 on La Palma, *F. c. ombriosa*
141 Hartert, 1913 on El Hierro, and *F. c. canariensis* Vieillot, 1817 on Gran Canaria,
142 Tenerife and La Gomera islands (Cramp and Perrins 1994, Martín and Lorenzo 2001).

143 Macaronesian chaffinches have in general shorter and rounded wings, and longer
144 tarsus and bills than continental populations (Grant 1979b). Colour pattern also differs
145 between mainland and oceanic island populations. Thus, like in European populations,
146 cheek front part is ochre, but it is still dark bluish on the side of the head and neck.
147 Canarian male chaffinches have an intense blue colour on the back. However, they
148 show a variable extension of reddish-orange-pinkish colour on the breast, which differs
149 from the greenish-brownish back of African chaffinches (*F. c. africana/spodiogenys*)
150 (Corso et al. 2015; Figure 1) and from the ochre-greyish back of European subspecies
151 (*F. c. coelebs*) (see Cramp and Perrins 1994, and references therein). White on tail and

152 wings is less extensive, especially the lower wing bar, compared to *F. c. coelebs*, and
153 the white wing-bars are less extensive, especially the lower bar (Figure 1).

154 *Morphological analyses*

155 *a) Skeletal measurements*

156 Dennison and Baker (1991) studied morphological variances in the Macaronesian
157 finches using skeletal measurements (after skeleton preparation) of fresh individuals.
158 They found that Canarian populations are morphologically less variable than Azorean
159 finches, with no significant morphological differentiation within the Canary Islands.
160 However, our own measurements obtained from live individuals caught in different
161 ringing sessions across the five islands suggested conspicuous morphological
162 differences among populations (J.C. Illera unpublished data). Thus, we decided to take
163 morphological measurements from the same individuals (i.e. skeletons) used by
164 Dennison and Baker (1991).

165 In total, we measured 110 adult male Canarian chaffinches from 5 islands (El
166 Hierro, La Palma, La Gomera, Tenerife and Gran Canaria) stored at Royal Ontario
167 Museum (Supplementary Table 1). We took measurements from 10 skeletal traits
168 (Table 1, Figure 4). Bones were photographed with a Nikon 3200 digital camera on a
169 graphic paper measured in millimetres, and measurements were scored using the
170 program ImageJ version 1.45s (Rasband 1997). Bones were systematically placed in the
171 same position on the graphic paper and photographed by the same person (JCI) in order
172 to standardise the measurements taken.

173 Length differences among the Canarian common chaffinches were analysed through
174 two (cranial and postcranial variables) Multivariate Analysis of Variance (MANOVA).
175 In addition, we explored variation in the morphological traits performing two Principal

176 Component Analysis (PCA), one with cranial (i.e. head and bill) measurements (traits 1-
177 5), and the other with postcranial lengths (traits 6-10). We performed the statistical
178 analyses using the software SPSS, version 15.0.

179 *b) Plumage characters*

180 We roughly compared the external appearance of the Canarian common chaffinch males
181 belonging to the same subspecies (*Fringilla coelebs canariensis*), that is, populations
182 from Gran Canaria, Tenerife and La Gomera. We focused our analysis on the R4 tail
183 feather because was the only tail feather with some kind of conspicuous variation for the
184 white colour between some islands (S-Figure 1). We grouped individuals into two
185 categories: 1) R4 with 0-3 mm tipped white, 2) R4 with ≥ 4 mm tipped white. We
186 performed a contingency table analysis to investigate the association of each population
187 to these categories.

188 *Genetic differentiation*

189 Rando et al. (2010) and Valente et al. (2017) estimated time of colonisation and
190 diversification of common chaffinches in Macaronesia using mitochondrial DNA
191 dating. However, these authors did not consider time of diversification within the
192 Canarian subspecies. Thus, we estimated time of diversification of each subspecies
193 and/or group of islands using the program BEAST version 1.8.1 (Drummond et al.
194 2012). We used the same alignment provided by Rando et al. (2010), adding six new
195 sequences obtained from Gran Canaria (Genbank accession numbers: MH170890-5,
196 Supplementary Table 2).

197 We extracted DNA from tissues stored at -80 °C, following Malagó's et al.
198 (2002) protocol. We carried out PCR reactions in a 12.5 μ l volume, with a buffer
199 consisting of 10 mM Tris-HCl pH 8.3, 2.5 mM MgCl₂, 50 mM KCl, 0.2 mM dNTPs,
200 0.5 μ M of the primers b1 (Kocher et al. 1989) and b6 (Morris-Pocock et al. 2010), and

201 0.25 U Taq polymerase (Invitrogen). We performed PCRs with an initial denaturation
202 for 1 minute at 94°C, followed by 36 cycles of 45 seconds at 94°C, 45 seconds at 52°C,
203 60 seconds at 72°C, and a final extension for 2 minutes at 72°C. PCR products were
204 separated on 2% agarose gels. Amplicons were recovered from the agarose gel using
205 pipet tip centrifugation (Dean and Greenwald 1995) and sequenced with the primers b1
206 and b6, as well as with a nested primer b3 (Morris-Pocock et al. 2010) using ABI
207 BigDye v.3.1 chemistry. The sequenced products were run on an ABI 3730 Genetic
208 Analyzer (Life Technologies).

209 We ran the Bayesian time-tree analyses only using common chaffinch
210 sequences, that is, excluding all outgroups. We proceeded in this way because
211 outgroups usually provide long branches and are less sampled than ingroups, which
212 could bias the divergence time estimates (Drummond and Bouckaert 2015). We inferred
213 the most appropriated nucleotide substitution model (HKY + G) from the program
214 JModelTest version 2.1.4 (Darriba et al. 2012). We used a strict molecular clock, and
215 defined the rate prior to have a mean of 0.01 and standard deviation of 0.0075
216 substitutions per site per million years (Illera et al. 2008). We used a Yule tree prior
217 following the recommendation of Drummond and Bouckaert (2015), since our analyses
218 included sequences from populations with deep divergences. We conducted two
219 independent MCMC analyses of 50,000,000 steps, with a burn-in of 5,000,000 steps.
220 We assessed the convergence of MCMCs with TRACER v.1.6 (Rambaut et al. 2014).

221 We used the program MEGA version 7.0 (Kumar et al. 2016) to obtain the
222 uncorrected pairwise genetic distances among populations. Finally, Suárez et al. (2009)
223 inferred the genetic structure within the Canarian common chaffinches, but they did not
224 consider the remaining Macaronesian and continental chaffinches. Thus, we built a
225 haplotype network using Macaronesian and nearby continental cytochrome b sequences

226 (Supplementary Table 2) to track the connections among and within common
227 chaffinches using the software TCS version 1.21 (Clement et al. 2000). We performed
228 the analysis fixing a limit of connection to 94%. Missing data or gaps were considered
229 as a fifth state.

230 **Results**

231 *Morphological differentiation*

232 *a) Cranial morphology*

233 The MANOVA performed with skull and bill measurements (traits 1-5) identified
234 significant morphological differences among the Canarian common chaffinches (Wilk's
235 Lambda = 0.11; d.f. = 20, 209; $p < 0.001$). These differences were identified for all
236 traits except premaxilla width (trait 1) ($F = 1.33$; $p = 0.27$). Significant differences
237 found in premaxilla height were due to La Gomera chaffinches. This population showed
238 the highest premaxilla height with all comparisons being significant ($p < 0.015$).
239 However, there were no significant differences among the remaining populations ($p >$
240 0.12). In addition, the common chaffinches from La Gomera showed the longest head
241 and mandible of all Canarian populations ($p < 0.002$ for all comparisons). We did not
242 find any significant differences in any trait between Gran Canaria and Tenerife ($p > 0.1$
243 for all traits). Finally, La Palma and El Hierro showed significant differences only in the
244 mandible length ($p = 0.01$).

245 The PCA performed with skull and bill measurements (traits 1-5) produced two
246 principal components explaining 76.5% of the total variance. PC1 explained 60.3%, and
247 showed a high positive weighting for traits 2-5 (premaxilla height, skull length,
248 mandible length and width), and a moderate positive weighting for premaxilla width
249 (trait 1). PC2 explained 16.2% of the variance and showed a high positive weighting for

250 premaxilla width, and a negative weighting for traits 2-5 (Figure 2a). PC1 plot depicted
251 all La Gomera individuals with values over zero being most of them segregated from
252 other islands (Figure 2a).

253 *b) Post-cranial morphology*

254 The postcranial MANOVA (traits 6-10) showed significant differences in all traits
255 among populations (Wilk's Lambda = 0.11; d.f.= 20, 203; $p < 0.001$). Such a result was
256 a consequence of significant differences found with any trait comparison between
257 Tenerife and Gran Canaria with the remaining islands ($p < 0.005$). However, we did not
258 find any significant differences between Tenerife and Gran Canaria ($p > 0.25$).

259 Postcranial PCA (traits 6-10) provided two principal components explaining
260 91% of the total variance. PC1 explained 80% of the total variance and showed a high
261 positive weighting for all traits. PC2 explained the 11% of variance showing a negative
262 weighting for scapula, humerus and ulna lengths (traits 6-8), a moderate positive weight
263 for femur (trait 9) and a high positive weight for tarsometatarsus length (trait 10)
264 (Figure 2b). PC1 plot scored all Gran Canaria individuals and most from Tenerife under
265 zero, whereas most birds from the remaining islands scored over zero. Thus, almost all
266 birds of both groups appear segregated on this axis (Figure 2b).

267 *c) Plumage characters*

268 The three populations of *Fringilla coelebs canariensis* (i.e. Gran Canaria, Tenerife and
269 La Gomera) are in appearance and size similar. However, significant differences are
270 found at R4 tail feather. There is a highly significant association between the extension
271 of tipped white at R4 and the island ($\chi^2 = 43.15$, $P < 0.01$). This result is explained
272 because males on Gran Canaria show a tiny white edges (81.5%, $n = 22$) or $\leq 3\text{mm}$
273 white spots (18.5%, $n = 5$), whereas, Tenerife and La Gomera populations develop a

274 clear tendency to show ≥ 4 mm extended white spots on R4 (S-Figure 1a). Such a
275 pattern is especially strong on common chaffinch males occurring in Tenerife (85%, n =
276 27) than in La Gomera (65%, n = 29) (S-Figure 1b, 1c).

277 *Dating and genetic differentiation*

278 The sequence divergence (i.e. percentage of base differences between sequences)
279 between Canarian common chaffinches subspecies, obtained from 46 sequences of 829
280 base pairs (bp) for the mtDNA cytochrome b (cyt-b) gene is as follows. *Fringilla*
281 *coelebs bakeri* (new subspecies from Gran Canaria) and *F. c. canariensis* (Tenerife and
282 La Gomera) differ between 0.72-1.21%. Meanwhile, the divergence between *F. c.*
283 *bakeri* and *F. c. palmae/ombriosa* (La Palma and El Hierro) ranged between 1.21-
284 1.69% (Supplementary Table 3). The diagnostic characteristics (i.e. variable sites) in the
285 mitochondrial sequences are shown in Table 2.

286 The haplotype network showed a clear differentiation among archipelagos and
287 the continental areas (Figure 3), which agrees with the pattern previously reported in
288 Macaronesia (Marshal and Baker 1999, Rando et al. 2010, Rodrigues et al. 2014).
289 Within the Canary Islands, our results also agree with the pattern found by Suárez et al.
290 (2009), and support a genetic structure determined by three distinctive nodes. One node
291 includes all Gran Canaria sequences; another node is grouping sequences from Tenerife
292 and La Gomera and, finally, the third node clumps birds from La Palma and El Hierro
293 (Figure 3). Population connections between the Canarian chaffinches and their
294 Macaronesian counterparts suggests a common ancestor to all of them. In addition, the
295 central islands of Tenerife and La Gomera appear directly connected with the remaining
296 common chaffinch populations.

297 Our dating shows slightly lower dates of colonisation and diversification of
298 common chaffinches in Macaronesia than was previously reported (Rando et al. 2010,

299 Valente et al. 2017). The age estimated for the colonisation of the extant common
300 finches in Macaronesia suggests that this species arrived in the Azores during the
301 middle Pleistocene (824,000 years; 0.21-1.87 Mya, lower and upper 95% highest
302 posterior density values, respectively). Shortly after this event, chaffinches colonised
303 Madeira (708,000 years; 0.18-1.62 Mya) and the Canary Islands (601,000 years; 0.17-
304 1.38 Mya). The Gran Canarian population diverged from the remaining Canary Islands
305 approximately 493,000 years (0.13-1.11 Mya) ago. Meanwhile, Tenerife, La Gomera,
306 El Hierro and La Palma appear to have commenced their differentiation processes
307 383,000 (0.09-0.87 Mya) years ago.

308 **Discussion**

309 The family Fringillidae constitutes an iconic group for evolutionary biologists to study
310 avian speciation because of the high number of species raised by adaptive radiation and
311 hybridisation (Grant and Grant, 2008; Price, 2008; Lamichhaney et al., 2018). In
312 Macaronesia, only the common chaffinch shows a moderate level of differentiation at
313 the subspecies level, and it is not possible to state whether such a differentiation process
314 is a consequence of selection (natural or sexual), or alternative evolutionary forces such
315 as mutation, drift and founder effects (Spurgin et al. 2014, Illera et al. 2016, van Doren
316 et al. 2017). According to our results it is plausible to conclude that common
317 chaffinches in Gran Canaria are isolated from the remaining Canarian populations, that
318 is, there is no evidence of dispersal movements among islands. As result, Gran Canarian
319 common chaffinches are characterised by multiple distinctive traits. For all the
320 aforementioned reasons, we conclude that the common chaffinch lineage in Gran
321 Canaria differs from other Canarian common chaffinches and should be ranked as a new
322 taxon. The formal description is presented in the section taxonomic account.

323 *Genetic and morphological differentiation*

324 Delimiting a cryptic differentiation process is challenging because only few traits can
325 experience visible changes. Thus, the limited skeletal differentiation found within the
326 Canary Islands suggests that changes on other less conspicuous traits such as the genetic
327 ones have been independently fixed and maintained on each population over time. The
328 phenotypic similarities found among the Canarian populations could be a direct
329 consequence of homoplasious evolution among lineages, perhaps because birds are
330 experiencing similar environmental and sexual pressures across islands (Illera et al.
331 2014).

332 Our genetic results have provided robust evidence that, individuals from each
333 archipelago consistently group together, which suggests long isolation processes with
334 strong genetic differentiation on each archipelago. Strikingly, despite that Azores is
335 composed by nine islands, which appear arranged along 600 kilometres (i.e. furthest
336 than the Canary Islands), our findings confirm that the genetic differentiation found in
337 the Canary Islands is deeper than in Azores (Suárez et al. 2009, Rando et al. 2010,
338 Rodrigues et al. 2014). Reasons to explain this pattern are unknown. However, it seems
339 plausible to suggest that such circumstance is a direct consequence of contemporary
340 gene flow, which would preclude genetic differentiation between the Azorean
341 populations (Rodrigues et al. 2014). The high chaffinch abundances reported in the
342 Azores in relation to the Canary Islands (Carrascal et al. 2008, Ceia et al. 2009)
343 supports this hypothesis. Thus, in the Azores, there could be a recurrent density-
344 dependent dispersal process, perhaps mediated by competition among individuals
345 (Matthysen 2005). Under this scenario, common chaffinches inhabiting islands with
346 high population densities could have developed a dispersal strategy to avoid competitive
347 interactions. In contrast, the lower abundances of common chaffinches recorded in the
348 Canary Islands could preclude a similar behaviour in this archipelago. The high genetic

349 differentiation found among some of the Canarian populations provides evidence for the
350 existence of limited gene flow.

351 Our findings support the pattern of three clades within the Canary Islands
352 (Suárez et al. 2009), where common chaffinches first came to the central islands of
353 Tenerife and/or La Gomera. This result suggests that both populations have served as
354 the cradle of diversification of the Canarian common chaffinches and acted as source
355 for the western and Gran Canaria islands. Our estimates of colonisation and
356 diversification in the Canary Islands suggest that this process started 600,000 years ago,
357 with the longest period of isolation (>490,000 years) recorded for Gran Canaria.
358 Previous studies reported the existence of strong genetic differentiation of some
359 passerine species occurring in Gran Canaria in relation to their Canarian counterparts
360 (Pestano et al. 2000, Dietzen et al. 2003, 2008, Kvist et al. 2005, Padilla et al. 2015).
361 This recurrent pattern could be explained due to the geological age of Gran Canaria
362 (≈ 14 my old), which makes it the third oldest island in the Canaries (Fuerteventura and
363 Lanzarote are the oldest ones). Therefore, the ancient age of Gran Canaria has favoured
364 the genetic isolation and final differentiation in allopatry of many avian taxa there
365 inhabiting (Illera et al. 2012).

366 Our genetic findings agrees with the results obtained by Lachlan et al. (2013)
367 studying the acoustic differentiation within the common chaffinch, and Stensrud (2012)
368 analysing the sperm morphology. Lachlan et al. (2013) tested the degree of
369 differentiation between the populations of Gran Canaria and Tenerife with an
370 experiment. They raised individuals from both islands in isolation conditions from birth,
371 and exposed them to songs from both islands and the mainland. Results showed the
372 highest responses when the call came from individuals belonging to the same island.
373 Such a result highlights two main ideas: 1) the acoustic characteristics in the common

374 finches were more inherited than learned, which is the reverse of patterns found in
375 oscines where song has a strong cultural component (Grant and Grant 2008), and 2)
376 Tenerife and Gran Canaria have a long history of isolation, which agrees with our
377 estimate of divergence. On the other hand, Stensrud (2012) found that Gran Canarian
378 finches showed the lowest sperm length on average, being significantly differentiated
379 from the remaining Canarian populations analysed, although with a high variance.
380 Again, Gran Canarian finches appeared clearly distinguishable from the remaining
381 populations.

382 Interestingly, morphological differences between individuals from large
383 (Tenerife and Gran Canaria) and small (La Gomera, El Hierro and La Palma) islands
384 match with the co-existence or absence of other *Fringilla* extant species, whose
385 individuals show the largest cranial and postcranial trait values (Rando et al. 2010).
386 Thus, when common chaffinches co-exist in sympatry with the blue chaffinches in
387 Tenerife (*F. teydea*) and Gran Canaria (*F. polatzeki*), they do not show significant
388 morphological differences between them. However, when common chaffinches do not
389 co-occur with other finch species (i.e. El Hierro, La Palma and La Gomera) they show
390 larger scapula, humerus and ulna values (traits 6-9), than the common chaffinches from
391 Tenerife and Gran Canaria ($p < 0.05$ in all the cases). In addition, individuals from these
392 three islands (El Hierro, La Palma and La Gomera) show the highest morphological
393 variation in skull traits and, overall, show longer hindlimb bones (Table 1). This
394 morphological pattern suggests the existence of an ecological character displacement
395 process driving morphological differentiation between big and small chaffinch species
396 in Tenerife and Gran Canaria. Such a mechanism could explain how sympatric finch
397 species minimise the competition for food resources in Tenerife (Grant and Grant 2006,
398 2010, Rando et al. 2010). In contrast, the biggest sizes and the highest morphological

399 variation recorded in La Gomera, La Palma and El Hierro provide evidence for an
400 expansion of their ecological niche, which is compatible with a competitive release
401 phenomenon (Grant and Grant 2008). Although these phenomena are considered central
402 to understand how species appear and multiply (Schluter 2000), alternative explanations
403 such as phenotypic plasticity or sexual selection cannot be rule out (Stuart and Losos
404 2013). Experimental approaches where the potential role of interspecific competition
405 can be inferred through estimating the population growth in sympatry and allopatry
406 (Germain et al. 2018) are now needed to comprehend the ultimate reasons behind the
407 morphological pattern here found.

408 **Taxonomic account**

409 **Genus:** *Fringilla* Linnaeus 1758

410 **Species:** *Fringilla coelebs* Linnaeus 1758

411 *Fringilla coelebs bakeri* ssp. nove.

412 **Diagnosis:**

413 **a) Appearance**

414 *Fringilla coelebs bakeri* is in appearance and size similar to *F. c. canariensis* from
415 Tenerife and La Gomera islands. However, *F. c. bakeri* males are different from *F. c.*
416 *canariensis* in the pattern of tail feather R4. *F. c. bakeri* males show a tiny white edge
417 or small white spot ($\leq 3\text{mm}$), whereas, *F. c. canariensis* males develop a significant
418 tendency to show conspicuous and extended white spot on R4 ($\geq 4\text{mm}$) (S-Figure 1a).

419 **b) Holotype**

420 ROM 151158, adult male (skin and skeleton) from Fontanales (Gran Canaria Island,
421 Canary Islands) collected by Michael D. Dennison on 5th May 1985 (Figure 5). Fresh
422 measurements were taken by Michael D. Dennison on 1985, and bone measurements
423 were taken by us for this study such as is described in Methods (Figure 5).

424 *b.1) Genetics*

425 The cytochrome b sequence of this specimen has been deposited in the National Center
426 for Biotechnology Information (NCBI) gene bank database with the MH170895
427 accession number.

428 *b.2) Holotype colour pattern:*

429 Holotype skin shows dark bluish colour from crown to back. Rump is bright green.
430 Upper tail-coverts and centre of tail are bluish-greyish tinged. Tail feathers are blackish-
431 greyish except outer rectrices (R6-R5), which show a variable amount of white, and the
432 internal rectrices (R1) which have pale green edges. Wing mostly black except for white
433 median coverts and narrow white tips of greater coverts. Remiges are black with pale
434 green edges. Face and underparts are pinkish, whitish on belly and under tail-coverts.

435 *b.3) Holotype morphological measurements*436 *b.3.1) Fresh*

437 Data (all in millimetres except weight in grams) from the fresh specimen. Bill exposed
438 (12.6); Bill nasal (10.8); Bill depth (7.8); Bill width (6.6), Tarsometatarsus (20.4),
439 Middle toe (11.2); Wing length (not available); Tail (not available), Weight (22.5 g).

440 *b.3.2) Bones*

441 Bone measurements (in mm): Premaxilla width (7.7); Premaxilla height (5.2); Head
442 length (33.1); Mandible length (23.8); Mandible width (not available); Scapula (20.9),
443 Humerus (19.4); Ulna (23.9); Femur (17.8); and Tarsometatarsus (21.8).

444 *c) Paratypes*

445 Adult males (skins and skeletons): Paratype1 (ROM 151143), Paratype2 (ROM
446 151148), Paratype3 (ROM 151151), Paratype4 (ROM 151153), and Paratype5 (ROM
447 151157). All from the same locality as the holotype, collected between 3rd and 5th May
448 1985, by Michael D. Dennison. Fresh measurements were taken by Michael D.

449 Dennison on 1985, and bone measurements were taken by us for this study such as is
 450 described in Methods (Figure 5).

451 *c.1) Genetics*

452 The cytochrome b region sequenced of these specimens have been deposited in the
 453 NCBI gene bank database with the following accession numbers: Paratype1
 454 (MH170890); Paratype2 (MH170891); Paratype3 (MH170892); Paratype4
 455 (MH170893); and Paratype5 (MH170894).

456 *c.2) Paratype colour pattern*

457 As Holotype.

458 *c.3) Paratype morphological measurements*

459 In the same order of those of the Holotype. n.a.: not available measurement.

460 *c.3.1) Fresh specimen measurements*

461 All data in mm except Weight in grams:

462 1) ROM 151143: 12.3; 10.9; 7.6; 6.9; n.a.; 10.7; 82.0; n.a.; 23.5 g

463 2) ROM 151148: 12.8; 11.1; 7.5; 6.5; 21.5; 10.8; n.a.; n.a.; 22.5 g

464 3) ROM 151151: 12.0; 10.4; 7.4; 6.5; 20.7; n.a.; 83.0; n.a.; 23.5 g

465 4) ROM 151153: 12.9; 11.1; 7.8; 7.0; n.a.; 10.6; 82.0; n.a.; 23.0 g

466 5) ROM 151157: 12.8; 10.8; 7.7; 6.5; 20.6; 11.0; n.a.; n.a.; 24.0 g

467 *c.3.2) Bone measurements*

468 All data in mm

469 1) ROM 151143: 7.2; 5.0; 34.6; 24.4; n.a.; n.a.; 19.5; n.a.; n.a.; n.a.

470 2) ROM 151148: 7.3; 4.8; n.a.; 24.3; 13.7; 20.9; 19.4; 23.7; 18.0; n.a.

471 3) ROM 151151: 7.3; n.a.; n.a.; 23.9; 14.5; 20.8; 19.7; 23.7; 18.1; n.a.

472 4) ROM 151153: 7.6; 4.5; 33.9; 24.1; n.a.; 19.8; 19.2; 23.5; 17.9; n.a.

473 5) ROM 151157: n.a.; 4.3; n.a.; 23.9; 14.2; n.a.; 19.1; 23.2; 17.8; 22.0 g

474 d) *Institution Housing Material (holotype and paratypes):*

475 Royal Ontario Museum (ROM), Toronto, Canada.

476 e) *Status*

477 Extant

478 f) *Etymology:*

479 The subspecies name is in honour of Professor Allan John Baker who contributed
480 immensely to our understanding of genetic structure, acoustic, and phylogeography of
481 common chaffinches in the Macaronesian islands and nearby continental areas.

482 g) *Distribution*

483 Gran Canaria Island (Canary Islands)

484 h) *Habitat*

485 This taxon is associated with “monteverde” habitats, which represents both laurel forest
486 and ‘fayal-brezal’ (*Myrica faya-Erica arborea*) woodlands. In addition, this taxon also
487 occurs on chestnuts (*Castanea sativa*) and Canary pine (*Pinus canariensis*) forests.
488 Furthermore, it extends its distribution on lower elevations exploiting the dense
489 vegetation of willows (*Salix canariensis*) and reeds (*Phragmites communis*), being able
490 to be found in areas as low as 100 meters above sea level (e.g. Barranco de Moya)
491 (Martín and Lorenzo 2001).

492

493

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- 686
- 687

688 **Figure 1.** Distribution of the common chaffinch (*Fringilla coelebs*) in Macaronesia and
689 nearby continental areas. Green lines depict pathway of colonisation of chaffinches in
690 Macaronesia suggested by Marshall and Baker (1999).

691 **Figure 2.** Principal Component Analysis (PCA) plots for the cranial (A) and post-
692 cranial (B) traits. Cranial PCA (A) includes the following traits: bill width and height,
693 head length, mandible length and width (traits 1-5). Post-Cranial PCA (B): includes:
694 scapula, humerus, ulna, femur and tarsometatarsus lengths (traits 6-10). Common
695 chaffinches (*Fringilla coelebs*) from Gran Canaria (yellow circles), Tenerife (blue
696 triangles), La Gomera (red rhombus), La Palma (green squares) and El Hierro (black
697 stars).

698 **Figure 3.** Parsimony network of the common chaffinch (*Fringilla coelebs*) in
699 Macaronesia and the nearby continental areas (Iberian Peninsula and North Africa)
700 based on the cytochrome b. Open small circles depict one-step mutation edge. The size
701 of haplotypes (circles) represents its abundance, that is, the number of individuals
702 sharing such a haplotype. The three groups (clusters) identified with the mitochondrial
703 cytochrome b are shaded in blue.

704 **Figure 4.** Morphological (cranial and post-cranial) traits measured on the Canarian
705 common chaffinches (*Fringilla coelebs*). 1: Premaxilla width, 2: Premaxilla height, 3:
706 Skull length, 4: Mandible length, 5: Mandible width, 6: Scapula length, 7: Humerus
707 length, 8: Ulna length, 9: Femur length, and 10: Tarsometatarsus length.

708 **Figure 5.** *Fringilla coelebs bakeri*'s holotype. Frontal, back and right lateral views.

709 **Supplementary Figure 1.** Tail colour pattern of common chaffinches of adult
710 (EURING 6) and sub-adult (EURING 5) in Gran Canaria (*Fringilla coelebs bakeri*), La
711 Gomera and Tenerife (*F. c. canariensis*). A: Gran Canaria, B: La Gomera, C: Tenerife.

712

For Review Only

713 **Table 1.** Morphological measurements (mean \pm standard error) of extant *Fringilla coelebs* occurring in the Canary Islands. Sample
 714 size (in brackets) and range (in square brackets) are also provided. Numbers before morphological trait names correspond with the
 715 trait numbers used in the text.

716

	El Hierro	La Palma	La Gomera	Tenerife	Gran Canaria
¹Bill width	7.3 \pm 0.2 (15) [6.8-7.6]	7.4 \pm 0.2 (14) [7.1-7.7]	7.3 \pm 0.3 (23) [6.6-7.8]	7.2 \pm 0.2 (20) [6.7-7.6]	7.3 \pm 0.3 (19) [6.8-7.7]
²Bill height	5.0 \pm 0.3 (13) [4.5-5.5]	5.0 \pm 0.2 (17) [4.6-5.4]	5.3 \pm 0.2 (22) [4.9-5.8]	4.9 \pm 0.3 (20) [4.2-5.6]	4.7 \pm 0.3 (22) [4.1-5.2]
³Head length	32.5 \pm 0.5 (14) [31.7-33.6]	33.3 \pm 0.9 (17) [31.8-34.8]	34.4 \pm 1 (22) [32.1-36.1]	32 \pm 0.8 (18) [31-33.8]	32.8 \pm 1.1 (18) [30.6-34.6]
⁴Mandible length	24.4 \pm 0.3 (10) [23.8-24.8]	24.9 \pm 0.4 (20) [24.1-25.9]	25.9 \pm 0.4 (19) [25.1-27]	24.3 \pm 0.5 (16) [23.6-25.1]	23.8 \pm 0.4 (22) [22.7-24.6]
⁵Mandible width	14.5 \pm 0.3 (9) [14.1-14.9]	14.6 \pm 0.3 (19) [14-15.2]	15.4 \pm 0.4 (15) [14.9-16.1]	14.6 \pm 0.3 (17) [14-15]	14.1 \pm 0.2 (15) [13.7-14.5]
⁶Scapula	21.5 \pm 0.5 (16) [20.6-22.3]	21.7 \pm 0.5 (18) [20.5-22.7]	21.8 \pm 0.4 (23) [21.2-22.5]	20.9 \pm 0.4 (17) [20.1-21.7]	20.7 \pm 0.5 (24) [19.8-21.5]
⁷Humerus	20.4 \pm 0.3 (15) [19.7-21]	20.4 \pm 0.5 (24) [19.6-21.2]	20.5 \pm 0.4 (21) [19.8-21.1]	19.6 \pm 0.4 (19) [18.5-20.3]	19.1 \pm 0.4 (26) [18.3-19.8]
⁸Ulna length	25.2 \pm 0.3 (12) [24.4-25.9]	25.1 \pm 0.5 (21) [24-26]	25.1 \pm 0.5 (21) [24.2-26]	24 \pm 0.6 (18) [22.6-25]	23.5 \pm 0.5 (25) [22.7-24.2]
⁹Femur	18.1 \pm 0.4 (16) [17.3-19]	18.3 \pm 0.4 (24) [17.6-19.1]	18.7 \pm 0.4 (22) [18-19.4]	17.9 \pm 0.5 (21) [16.8-18.7]	17.8 \pm 0.4 (24) [17-18.5]
¹⁰Tarsometatarsus	22.0 \pm 0.4 (15) [21.2-22.7]	22.1 \pm 0.6 (20) [20.9-22.9]	22.5 \pm 0.6 (21) [21.5-23.7]	21.5 \pm 0.7 (19) [20.1-22.8]	21.8 \pm 0.5 (21) [20.7-22.7]

717

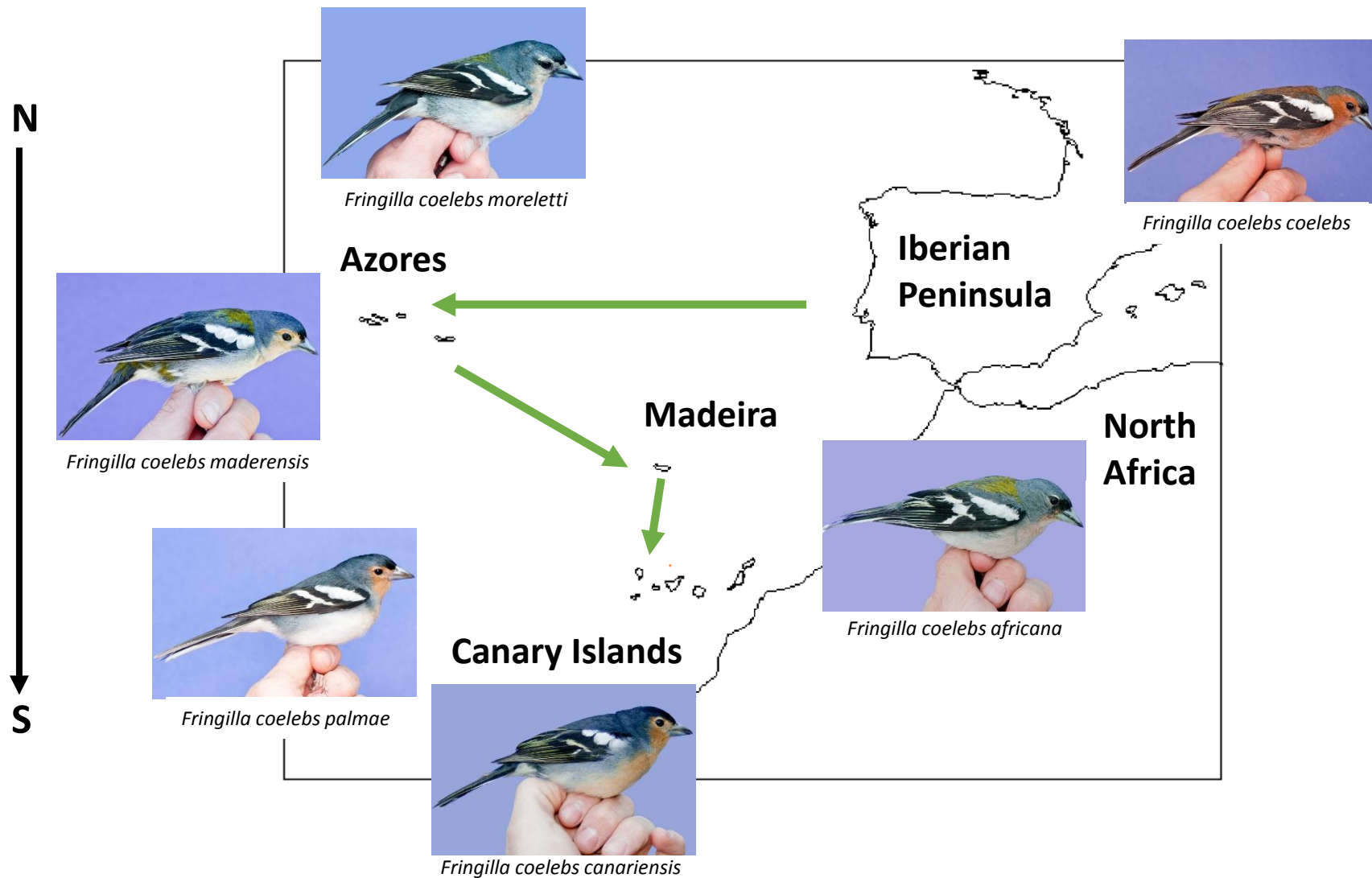
718 **Table 2.** Cytochrome b diagnostic bases (i.e. variable sites) for *Fringilla coelebs bakeri* in relation to the remaining Canarian common chaffinch
 719 subspecies. Pure cyt-b diagnostic bases for discriminating all *F. c. bakeri* individuals from other Canarian populations for cyt-b are shown in red.
 720 Numbers are according to the base position along a cyt-b fragment of 829 bp.

721

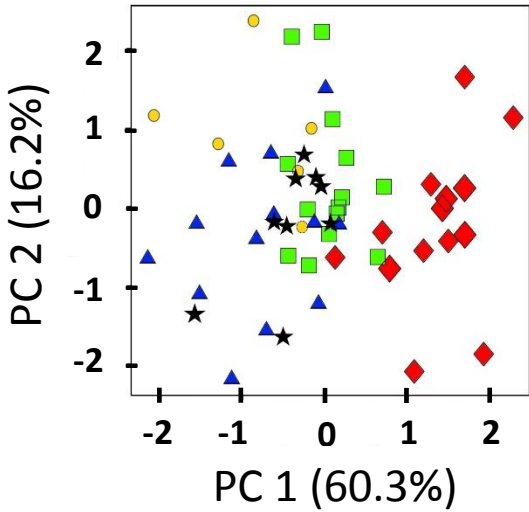
Position	293	299	305	374	390	443	503	659	707	785
<i>F. c. bakeri</i>	G	C	C	T	T	T	A	A	T	A
<i>F. c. canariensis</i>	G	T	T	C	T/C	C	C	A	C	A
<i>F. c. ombriosa</i>	A	T	T	C	C	C	C	T	C	G
<i>F. c. palmae</i>	A	T	T	C	C	C	C	T	C	G

722

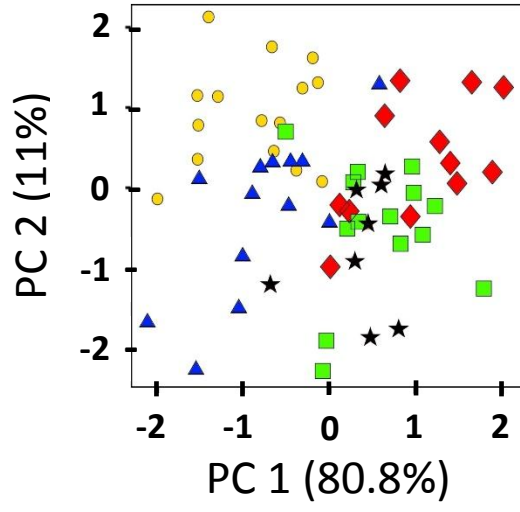
Figure 1



A) Cranial PCA

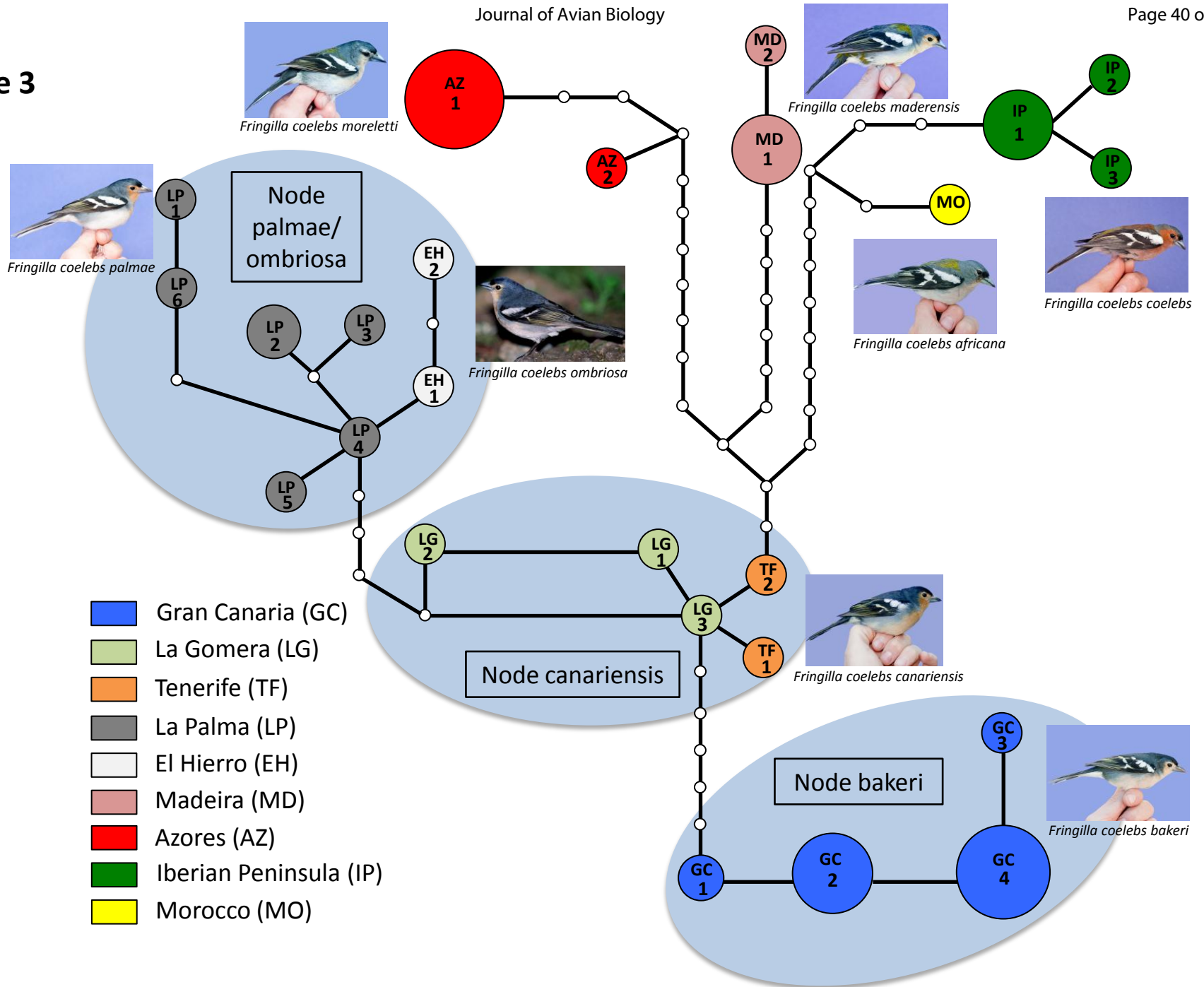


B) Post-Cranial PCA



▲ Tenerife ★ El Hierro ■ La Palma
◆ La Gomera ● Gran Canaria

Figure 3



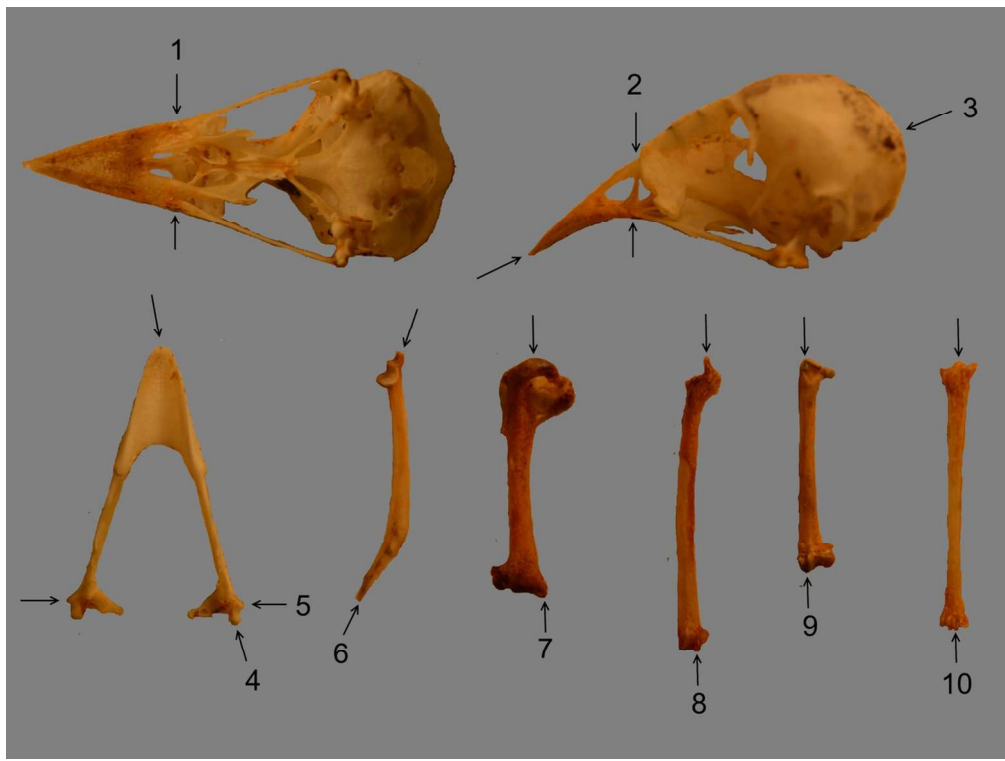


Figure 4

124x93mm (300 x 300 DPI)

Only



Holotype of *Fringilla coelebs bakeri*
ROM 151158 / AJB4561

Supplementary File 1. Specimens of common chaffinches (*Fringilla coelebs*) from the Canary Islands measured for the present study. All individuals were males and adults, and are stored at Royal Ontario Museum (ROM). Dates of capture of each specimen are also shown.

Specimen	Island	Date
ROM_148875	El Hierro	21/04/1984
ROM_148876	El Hierro	21/04/1984
ROM_148877	El Hierro	21/04/1984
ROM_148878	El Hierro	22/04/1984
ROM_148880	El Hierro	22/04/1984
ROM_148883	El Hierro	22/04/1984
ROM_148884	El Hierro	22/04/1984
ROM_148886	El Hierro	22/04/1984
ROM_148888	El Hierro	22/04/1984
ROM_148890	El Hierro	22/04/1984
ROM_148892	El Hierro	22/04/1984
ROM_148896	El Hierro	22/04/1984
ROM_148898	El Hierro	22/04/1984
ROM_148901	El Hierro	22/04/1984
ROM_154227	El Hierro	20/05/1988
ROM_154228	El Hierro	20/05/1988
ROM_154229	El Hierro	20/05/1988
ROM_154230	El Hierro	20/05/1988
ROM_148894	El Hierro	22/04/1984
ROM_151139	Gran Canaria	03/05/1985
ROM_151140	Gran Canaria	03/05/1985
ROM_151142	Gran Canaria	03/05/1985
ROM_151143	Gran Canaria	03/05/1985
ROM_151145	Gran Canaria	03/05/1985
ROM_151147	Gran Canaria	03/05/1985
ROM_151148	Gran Canaria	04/05/1985
ROM_151149	Gran Canaria	04/05/1985
ROM_151150	Gran Canaria	04/05/1985
ROM_151151	Gran Canaria	04/05/1985
ROM_151152	Gran Canaria	04/05/1985
ROM_151153	Gran Canaria	04/05/1985
ROM_151154	Gran Canaria	05/05/1985
ROM_151155	Gran Canaria	05/05/1985
ROM_151156	Gran Canaria	05/05/1985
ROM_151157	Gran Canaria	05/05/1985
ROM_151158	Gran Canaria	05/05/1985
ROM_151160	Gran Canaria	04/05/1985
ROM_151161	Gran Canaria	04/05/1985
ROM_151162	Gran Canaria	04/05/1985
ROM_151163	Gran Canaria	04/05/1985
ROM_151165	Gran Canaria	04/05/1985
ROM_151166	Gran Canaria	04/05/1985
ROM_154204	Gran Canaria	16/05/1988

ROM_154205	Gran Canaria	16/05/1988
ROM_154206	Gran Canaria	16/05/1988
ROM_154207	Gran Canaria	16/05/1988
ROM_154208	Gran Canaria	16/05/1988
ROM_154209	Gran Canaria	16/05/1988
ROM_148903	La Gomera	26/04/1984
ROM_148905	La Gomera	26/04/1984
ROM_148907	La Gomera	26/04/1984
ROM_148909	La Gomera	26/04/1984
ROM_148913	La Gomera	26/04/1984
ROM_148915	La Gomera	26/04/1984
ROM_148917	La Gomera	27/04/1984
ROM_148919	La Gomera	27/04/1984
ROM_148921	La Gomera	27/04/1984
ROM_148922	La Gomera	27/04/1984
ROM_148925	La Gomera	27/04/1984
ROM_148926	La Gomera	27/04/1984
ROM_148928	La Gomera	27/04/1984
ROM_148930	La Gomera	27/04/1984
ROM_148931	La Gomera	27/04/1984
ROM_151212	La Gomera	27/02/1985
ROM_151213	La Gomera	28/02/1985
ROM_151216	La Gomera	28/02/1985
ROM_151218	La Gomera	28/02/1985
ROM_151221	La Gomera	28/02/1985
ROM_151223	La Gomera	01/03/1985
ROM_151224	La Gomera	01/03/1985
ROM_151225	La Gomera	01/03/1985
ROM_151226	La Gomera	01/03/1985
ROM_154232	La Gomera	21/05/1988
ROM_154233	La Gomera	21/05/1988
ROM_154234	La Gomera	21/05/1988
ROM_147800	La Palma	06/07/1983
ROM_147801	La Palma	06/07/1983
ROM_147807	La Palma	06/07/1983
ROM_147808	La Palma	06/07/1983
ROM_147809	La Palma	06/07/1983
ROM_147814	La Palma	06/07/1983
ROM_147816	La Palma	06/07/1983
ROM_147817	La Palma	06/07/1983
ROM_147819	La Palma	06/07/1983
ROM_147820	La Palma	06/07/1983
ROM_147824	La Palma	07/07/1983
ROM_147828	La Palma	07/07/1983
ROM_147829	La Palma	07/07/1983
ROM_151191	La Palma	22/02/1985
ROM_151193	La Palma	22/02/1985
ROM_151203	La Palma	24/02/1985
ROM_151205	La Palma	24/02/1985
ROM_151206	La Palma	24/02/1985

ROM_151208	La Palma	24/02/1985
ROM_154218	La Palma	19/05/1988
ROM_154219	La Palma	19/05/1988
ROM_154222	La Palma	19/05/1988
ROM_154223	La Palma	19/05/1988
ROM_147797	Tenerife	24/05/1983
ROM_147798	Tenerife	24/05/1983
ROM_147799	Tenerife	24/05/1983
ROM_147838	Tenerife	11/07/1983
ROM_147841	Tenerife	12/07/1983
ROM_148858	Tenerife	23/05/1983
ROM_148859	Tenerife	23/05/1983
ROM_148867	Tenerife	12/07/1983
ROM_148870	Tenerife	12/07/1983
ROM_148872	Tenerife	12/07/1983
ROM_149093	Tenerife	??/07/1983
ROM_151176	Tenerife	15/02/1985
ROM_151177	Tenerife	15/02/1985
ROM_151178	Tenerife	15/02/1985
ROM_151179	Tenerife	15/02/1985
ROM_151183	Tenerife	16/02/1985
ROM_151186	Tenerife	16/02/1985
ROM_151188	Tenerife	17/02/1985
ROM_154215	Tenerife	18/05/1988
ROM_154216	Tenerife	18/05/1988
ROM_154226	Tenerife	19/05/1988

Supplementary Table S2. List of sequences used in the present study per taxa and Genbank accession numbers. The haplotype codes (in brackets) represent the sequences used in the haplotype network analysis depicted at Figure 3.

Species	Subspecies	Origin	Genbank accession number and haplotype codes
<i>Fringilla coelebs</i>	<i>ombriosa</i>	El Hierro/CI	GQ330543 (EH1) GQ330544 (EH2)
<i>Fringilla coelebs</i>	<i>palmae</i>	La Palma/CI	GQ330545 (LP1) GQ330554 (LP2) GQ330549 (LP2) GQ330550 (LP3) GQ330551 (LP4) GQ330552 (LP5) GQ330553 (LP6)
<i>Fringilla coelebs</i>	<i>canariensis</i>	La Gomera/CI	GQ330546 (LG1) GQ330547 (LG2) GQ330548 (LG3)
<i>Fringilla coelebs</i>	<i>canariensis</i>	Tenerife/CI	GQ330555 (TF1) GQ330556 (TF2)
<i>Fringilla coelebs</i>	<i>canariensis</i>	Gran Canaria/CI	MH170890 (GC1)* MH170895 (GC1)* MH170891 (GC2)* MH170892 (GC2)* GU592658 (GC2) GQ330559 (GC3) MH170893 (GC4)* MH170894 (GC4)* GQ330557 (GC4) GQ330558 (GC4)
<i>Fringilla coelebs</i>	<i>maderensis</i>	Madeira/MD	GU592659 (MD1) GU592660 (MD2)
<i>Fringilla coelebs</i>	<i>moreletti</i>	Terceira/AZ	GU592662 (AZ1) GU592661 (AZ2)
<i>Fringilla coelebs</i>	<i>coelebs</i>	IP	GU592664 (IP1) GU592666 (IP1) GU592663 (IP2) GU592665 (IP3)
<i>Fringilla coelebs</i>	<i>africana</i>	Rabat/MO	GU592667 (MO)

CI: Canary Islands. EH: El Hierro. LP: La Palma. LG: La Gomera. TF: Tenerife. GC: Gran Canaria. MD: Madeira. AZ: Azores. IP: Iberian Peninsula. MO: Morocco. *: new sequences used in this study.

Supplementary Table 3. Percentage of mean divergences (uncorrected pairwise sequence) among populations of common chaffinches (*Fringilla coelebs*). We used 46 sequences of 829 base pairs (bp) for the mtDNA cytochrome b gene. Number of sequences used per population is also shown in brackets.

	El Hierro (2)	La Palma (7)	La Gomera (3)	Tenerife (2)	Gran Canaria (13)	Madeira (4)	Azores (9)	Iberia (5)
La Palma (7)	0.45							
La Gomera (3)	0.88	0.85						
Tenerife (2)	0.97	0.93	0.24					
Gran Canaria (13)	1.41	1.51	1.02	1.02				
Madeira (4)	1.72	1.68	1.40	1.36	1.81			
Azores (9)	2.14	2.11	1.82	1.78	2.24	2.17		
Iberia (5)	2.22	2.18	1.90	1.86	2.31	2.25	2.41	
North Africa (1)	2.29	2.26	1.81	1.69	2.14	2.32	2.48	0.65

(A)



Male_EURING 5_Gran Canaria
Fringilla coelebs bakeri

(B)



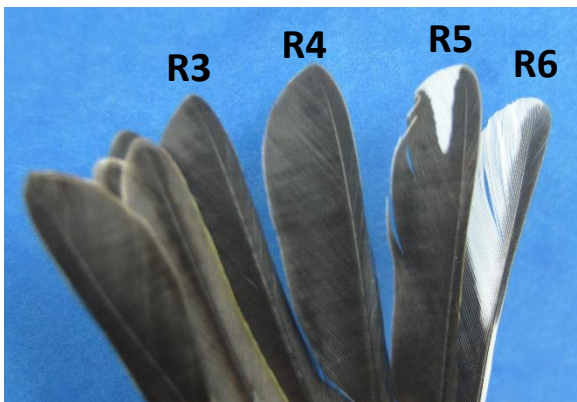
Male_EURING 5_La Gomera
Fringilla coelebs canariensis

(C)



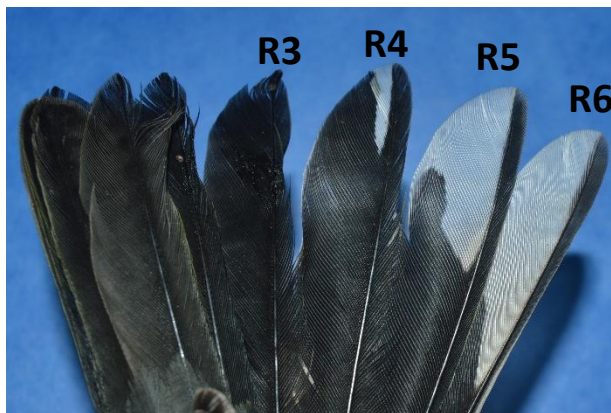
Male_EURING 5_Tenerife
Fringilla coelebs canariensis

R3 R4 R5 R6



Male_EURING 6_Gran Canaria
Fringilla coelebs bakeri

R3 R4 R5 R6



Male_EURING 6_La Gomera
Fringilla coelebs canariensis

R6 R5 R4 R3



Male_EURING 6_Tenerife
Fringilla coelebs canariensis

(A)

(B)

(C)