

1   **Why don't long-finned pilot whales have a widespread post-reproductive**  
2   **lifespan? Insights from genetic data.**

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13   **Running Header: kinship dynamics in pilot whales**

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19      **Abstract**

20            In a handful of mammals, females show an extended post-reproductive lifespan  
21 (PRLS), leading to questions over why they spend a substantial portion of their lifespan non-  
22 reproductive. Theoretical and empirical studies suggest that PRLS may evolve when (1)  
23 demographic patterns lead to increasing local relatedness as females age, and (2) females  
24 come into reproductive competition with their daughters, as these conditions lead to high  
25 relative benefits of helping kin versus reproducing in later life. However, evolutionary  
26 pathways to PRLS are poorly understood and empirical studies are scarce. Here, we use a  
27 dataset of 1522 individuals comprising 22 pods to investigate patterns of reproduction and  
28 relatedness in long-finned pilot whales *Globicephala melas*; a toothed whale without  
29 species-wide PRLS. We find a similar relatedness structure to whales with PRLS: pods appear  
30 composed of related matrilines, and relatedness of females to their pod increases with age,  
31 suggesting that this species could benefit from late-life help. Furthermore, females with a  
32 large number of philopatric adult daughters are less likely to reproduce, implying  
33 intergenerational reproductive competition between females. This suggests that individuals  
34 may display a plastic cessation of reproduction, switching to investing in existing offspring  
35 when they come into competition with their daughters. To the best of our knowledge, this is  
36 the first time such a relationship has been described in relation to PRLS, and it raises  
37 questions about whether this represents a step towards evolving PRLS or is a stable  
38 alternative strategy to widespread post-reproductive periods.

39      **Key words:** post-reproductive lifespan, menopause, cetacean, fecundity, relatedness,  
40 demography, plasticity

41

42      **Introduction**

43            Mammalian reproductive systems mostly age at approximately the same rate as  
44    somatic tissue and females continue to reproduce until death (Ellis et al., 2018a). However,  
45    in a small number of species, reproductive and somatic ageing are decoupled and females  
46    stop reproducing long before they die, creating a widespread and extended period of post-  
47    reproductive lifespan (PRLS) representing a distinct life stage (Cohen, 2004; Croft et al.,  
48    2015; Ellis et al., 2018a). Why older animals do not increase their direct fitness by continuing  
49    to reproduce has been hotly debated and a number of hypotheses have been proposed  
50    (Cant and Johnstone, 2008; Cohen, 2004; Ellis et al., 2018a; Huber and Fieder, 2018;  
51    Lahdenperä et al., 2004; Levitis et al., 2013; Packer et al., 1998). Humans provide the best-  
52    studied example. Women tend to have their last birth at around 38 (Towner et al., 2016),  
53    followed by a menopause some 10 years later, precluding further reproduction. Post-  
54    reproductive women often have long and healthy lives, even in modern day hunter-gatherer  
55    populations (Emery Thompson et al., 2007) and historic populations without access to  
56    modern medical care (Levitis et al., 2013). Other examples are rare, but include some  
57    toothed whales such as killer whales *Orcinus orca* (Foster et al., 2012), short-finned pilot  
58    whales *Globicephala macrorhynchus* (Kasuya and Marsh, 1984), narwhals *Monodon*  
59    *monoceros* (Ellis et al., 2018b), beluga whales *Delphinapterus leucas* (Ellis et al., 2018b)  
60    Asian elephants *Elephas maximus* (Chapman et al., 2019) and possibly also false killer  
61    whales *Pseudorca crassidens* (Photopoulou et al., 2017) (but see Ellis et al. (2018b)).

62            Explanations for PRLS fall into two main classes; non-adaptive and adaptive. Non-  
63    adaptive decoupling of reproductive and somatic ageing may occur if traits that are strongly  
64    selected early in life have negative consequences on reproduction in late life, and/or if traits  
65    associated with aging are less visible to natural selection because few individuals live to  
66    express them (Hamilton, 1966; Packer et al., 1998; Williams et al., 2006). Similarly, PRLS may  
67    evolve due to links with other aspects of life-history even without impacts on fitness. For  
68    example, in guppies, *Poecilia reticulata*, selection on reproductive lifespan appears to co-  
69    select for post-reproductive lifespan (Reznick et al., 2005). Furthermore, disease and other  
70    stochastic processes are likely to explain why, in many mammalian species, a small  
71    proportion of females have been observed to have post-reproductive periods (Cohen,

72 As this is unlikely to represent a distinct life-stage, this phenomenon is termed post  
73 reproductive viability (Levitis et al., 2013) to distinguish it from PRLS affecting all females.

74 While short periods of postreproductive viability may arise non-adaptively, the  
75 extended periods of PRLS are likely to be the result of adaptive processes (Nichols et al.,  
76 2016). Adaptive explanations for PRLS focus on the fitness benefits that older females may  
77 continue to accrue through behaviors that increase the fitness of their descendants (Croft et  
78 al., 2015). Such explanations have received empirical support in humans, where the  
79 presence of grandmothers increases the production of grand-offspring (Lahdenperä et al.,  
80 2004; Levitis et al., 2013; Sear and Mace, 2008) and in killer whales, where post-  
81 reproductive females substantially enhance the survival of their own offspring (Foster et al.,  
82 2012), for example by providing valuable ecological knowledge (Brent et al., 2015). The  
83 relative benefits of helping rather than reproducing may be enhanced by rising costs of  
84 gestation and birth with age (Grimes, 1994) and by extended periods of offspring  
85 dependency during which offspring lose fitness if the mother dies (Shanley and Kirkwood,  
86 2001).

87 Where adaptive PRLS evolves through kin selection, the social system likely plays a  
88 critical role. Specifically, older females need access to close relatives to help, which will only  
89 occur in species that live in family groups (Nichols et al., 2016); a situation that usually arises  
90 through offspring remaining with their mothers beyond weaning. Indeed, philopatry has  
91 been proposed to be particularly important for the evolution of PRLS because it can lead to  
92 an increase in average relatedness to other group members throughout the lifetime of a  
93 female (Johnstone and Cant, 2010). For example, ancestral human females probably  
94 dispersed to new family groups before reproducing, leading to an initial low relatedness to  
95 their new families which increases over time as a result of her subsequent descendants  
96 (Johnstone and Cant, 2010). In cetaceans such as killer whales, both sexes are philopatric,  
97 but mating occurs outside of the group (Croft et al., 2017; Pilot et al., 2010). Here, average  
98 relatedness between a young female and her social group is relatively low because she was  
99 the product of an extra-group mating. However, her offspring remain within the social  
100 group, and hence average relatedness between the female and other group members  
101 increases over the female's lifespan (Croft et al., 2017). This change in relatedness over time  
102 may lead to a predisposition towards the evolution of an adaptive period of post-

103 reproductive helping (Johnstone and Cant, 2010). Such a link between philopatry and  
104 prolonged PRLS is supported by a comparative study of mammals (Nichols et al., 2016).

105        Although philopatry generates a relatedness structure within which kin selection can  
106 favor late-life helping, the evolution of PRLS also depends on a balance between its relative  
107 costs and benefits (Cant and Johnstone, 2008; Cant et al., 2009; Johnstone and Cant, 2010).  
108 First, there is unlikely to be a fitness benefit to older females from ceasing reproduction if  
109 there is no fitness cost to their relatives when they do breed. PRLS should therefore only  
110 evolve where inter-generational reproductive competition occurs (Cant and Johnstone,  
111 2008). Evidence for this from humans is mixed (Croft et al., 2015), but support has been  
112 found in killer whales, where local group relatedness increases with age and the costs of co-  
113 breeding with kin are higher for older than for younger females (Croft et al., 2017). Second,  
114 post-reproductive females must be able to contribute towards increasing the fitness of their  
115 relatives. For example, post-reproductive resident killer whales have been shown to act as a  
116 repository for ecological information, leading their groups to find salmon in times of food  
117 shortage (Brent et al., 2015). Maternal death consequently has a strong impact on offspring  
118 survival, especially on sons, even when the offspring are adult (Foster et al., 2012). Similarly,  
119 PRLS has been proposed to be associated with foraging niches that require the build-up of  
120 neural capital, and hence result in older individuals being able to acquire an excess of  
121 resources, which they may redistribute to their relatives (Aimé et al., 2017). Thus, where  
122 there is no reproductive competition, the benefits of ecological knowledge are limited  
123 and/or there are few opportunities for alloparental care, adaptive PRLS should not evolve.

124        One interesting puzzle regarding PRLS is why it pays to evolve irreversible  
125 reproductive cessation, as appears to occur in all species currently identified as having  
126 significant PRLS (Ellis et al., 2018b). If females maintained plasticity in PRLS, they may be  
127 able to adaptively switch resources between producing further offspring and helping  
128 existing offspring, dependent on their current circumstances. For example, females with few  
129 or no offspring within their group (those whose previous offspring have died or emigrated)  
130 would likely benefit from further reproduction, regardless of their age. Here, the sex of a  
131 female's philopatric offspring may be important. For example, where both sexes remain  
132 philopatric but mating occurs between groups (as occurs in some toothed whales), older  
133 females come into conflict with their adult daughters as they both produce offspring in the

134 natal group (Croft et al., 2017). However, they are unlikely to come into conflict with  
135 reproductive sons, who's offspring are in other groups. Under these circumstances, older  
136 females may benefit from ceasing reproduction when they have daughters of reproductive  
137 age in their group but would not benefit if they have only philopatric sons.

138 It is currently unclear why PRLS is not a reversible trait, but it is possible that the  
139 physiological mechanisms that govern reductions in fertility may constrain against  
140 reversibility (Huber and Fieder, 2018). However, young females of many cooperatively  
141 breeding species (species with non-reproductive alloparents) experience reversible declines  
142 in fertility when in competition with older relatives (Russell, 2004), suggesting that  
143 reversibility may be possible. A further prospect is that some species may display substantial  
144 plasticity in the timing of reproductive cessation or may have reversible pauses in  
145 reproduction, but these possibilities could be difficult to detect on a population level due to  
146 the presence of older reproductive females and because plasticity in fertility in older age  
147 may be difficult to distinguish from reproductive senescence (a decline over age in fertility).

148 Toothed whales (Odontoceti) provide an interesting opportunity to investigate  
149 patterns of reproduction and their relationship to social organization for several reasons.  
150 Firstly, maternal investment tends to be high, either due to high energetic costs of lactation  
151 or long periods of offspring dependency (Oftedal, 1997). Secondly, in several species,  
152 offspring of one or both sexes remain with their mothers well beyond weaning and may  
153 continue to receive maternal care (Brent et al., 2015; Pilot et al., 2010). Third, reproductive  
154 senescence is common, with 10 of the 16 species investigated by Ellis et al. (2018b)  
155 experiencing reproductive senescence, and at least four (possibly five) of these species  
156 exhibiting extended PRLS comparable in duration to humans (Cohen, 2004; Croft et al.,  
157 2015; Ellis et al., 2018a; Ellis et al., 2018b). Curiously, although many toothed whales appear  
158 to have similar social systems, PRLS varies greatly in presence, length, and timing. For  
159 example, short-finned and long-finned pilot whales *Globicephala melas* are very closely  
160 related (~1-2mya divergence (Hedges et al., 2006)) sister species that both appear to live in  
161 stable, multigenerational, matrilineal groups where both sexes remain philopatric and  
162 mating is non-local (Foote, 2008). Both have been studied in drive fisheries and show  
163 similar maximum longevities of around 55-60 years, although life-expectancy is generally  
164 shorter in long-finned pilot whales (Ellis et al., 2018b). Despite this, the oldest pregnant

165 females found so far for the two species differ greatly in age: 35 years in short-finned  
166 (Kasuya and Marsh, 1984) and 55 years in long-finned pilot whales (Martin and Rothery,  
167 1993). Accordingly, periods of PRLS differ greatly between the species: PrR (a population-  
168 level measure of the proportion of female years spent post-reproductive (Levitis and Lackey,  
169 2011)) is 0.26 in the short-finned pilot whale and 0.002 in the long-finned pilot whale (Ellis  
170 et al., 2018a). This raises the question of why these two species differ so greatly in PRLS  
171 despite having similar social systems and lifestyles.

172 Here, we use data collected in the late 1980s from a long-finned pilot whale drive  
173 fishery to help understand why this species does not show PRLS. Specifically, we use  
174 microsatellite genotypes of individuals from 22 social groups to test the hypothesis that  
175 long-finned pilot whales lack widespread PRLS because older females lack suitable relatives  
176 to direct late-life help towards. To do this, we test three predictions: if the relatedness  
177 structure of long-finned pilot whales acted as a barrier to the evolution of PRLS, we would  
178 expect (1) a lack of relatives within pods, (2) in particular an absence of philopatric adult  
179 offspring, and/or (3) no increase in relatedness between females and other group members  
180 as females age. Finally, we investigate the hypothesis that individual females could exhibit  
181 plasticity in the timing of PRLS by testing the prediction that females are more likely to be  
182 pregnant if they have few philopatric offspring in their social group, after accounting for  
183 age-related changes in fecundity. Furthermore, as females are likely to experience  
184 competition from reproductive daughters but not sons, we also test the prediction that the  
185 probability of pregnancy depends on the number of philopatric daughters present in the  
186 social group, but is independent of the number of philopatric sons.

187 **Methods**

188 *Physiological and genetic data collection*

189 Data were obtained from 1522 long-finned pilot whales *Globicephala melas*  
190 comprising 95% of individuals from 22 pods harvested between 1986 and 1989 as part of a  
191 legal traditional subsistence hunt in the Faroe Islands (Zachariassen, 1993). Scientific  
192 observers of the harvest were certain that there was no splitting or merging of the pods  
193 during the hunt, hence these pods comprised of entire naturally occurring social groups  
194 (Bloch et al., 1993a). Pods ranged in size from 16 to 175 individuals (median 57) and

195 contained adults and juveniles of both sexes. Pilot whale social behavior is currently poorly  
196 understood, but observational studies suggest that pods may sometimes temporarily split  
197 into smaller subunits of ~7 individuals (Augusto et al., 2017b; De Stephanis et al., 2008;  
198 Ottensmeyer and Whitehead, 2003). As our data are not longitudinal, we cannot comment  
199 on the long-term stability of the pods captured in the hunt, but we have no reason to  
200 believe that the pods we sampled are not representative of those found in the wild  
201 population (and therefore representative of the social structure within which females find  
202 themselves). Nevertheless, as relatedness is likely to be diluted in larger pods, we took pod  
203 size into account in our analyses where appropriate.

204 Upon capture, the total body length and sex of whales were recorded, and age was  
205 determined by counting the growth layer groups visible in a tooth section (Lockyer, 1993).  
206 Skin samples were taken for genetic analysis and females were dissected to confirm  
207 whether they were pregnant at the time of capture. Due to time-constraints when sampling  
208 a large number of whales, it was not possible to take every measurement for each  
209 individual, hence gaps in the data occurred. For individuals without tooth sections (9.7% of  
210 whales), age was estimated from length data where possible, following Nichols et al. (2014).  
211 Females over 400 cm and males over 500 cm long were likely fully grown so age could not  
212 be estimated using length. These individuals were therefore considered as adults but were  
213 excluded from analyses where accurate age data was required.

214 Genotyping was carried out as described in Fullard et al. (2000) using a panel of nine  
215 highly polymorphic microsatellite loci: 199/200, 417/418, 468/469, 409/470, 415/416, and  
216 464/465 (Amos et al., 1993); EV37, EV94, EV1 (Valsecchi and Amos, 1996). A subset of pods  
217 for which sampling and morphometric data collection was particularly comprehensive  
218 ( $N=737$  individuals comprising 11 pods) were genotyped at an additional seven loci: D14 and  
219 D22 (Shinohara et al., 1997); FCB6/17, FCB3 and FCB1 (Buchanan et al., 1996); SW10  
220 (Richard et al., 1996); Gm8 (Fullard et al., 2000). Although this meant that pods differed in  
221 the number of microsatellites used in maternity assignments, previous analyses revealed no  
222 effect on patterns of maternity (Nichols et al., 2014). Consequently, we did not include this  
223 as a separate factor in our models. Individuals genotyped at fewer than seven markers or  
224 that lacked sufficient age and sex information were excluded from downstream analyses.

225 Our analyses always used the maximum number of individuals for which data were  
226 available.

227 *Relatedness calculations*

228 Pairwise relatedness was calculated using the program Kingroup (Konovalov et al.,  
229 2004). We selected Lynch and Ritland's (1999) measure of relatedness following  
230 recommendations by Csilléry et al. (Csilléry et al., 2006), who compared the performance of  
231 various measures of relatedness. As relatives are likely to be present within groups, we  
232 applied a bias correction that excludes other group-members when calculating relatedness  
233 for that pair, as recommended by Konovalov et al. (2004).

234 *Parentage analysis*

235 Maternity analysis was conducted following Nichols et al. (2014) using the program  
236 Cervus (Marshall et al., 1998). In brief, females were considered as potential mothers if they  
237 were in the same pod and at least 6 years older than the candidate offspring. A threshold of  
238 6 years was chosen as females as young as 5 and 6 were very occasionally found to be  
239 pregnant. As pods include relatives, simulations to generate the critical value of delta  
240 allowed for 10% of candidate mothers being related to the true mother by 0.25. Although  
241 almost-complete pods were sampled, it is likely that some mothers had died or emigrated  
242 since the offspring was born. Hence, we included the conservative estimate of 50% mothers  
243 having been sampled. Re-genotyping 45 samples revealed an average per-allele error rate of  
244 0.012, which was incorporated into simulations to generate critical delta.

245 Our downstream analyses incorporated 472 offspring assigned to 280 mothers at a  
246 minimum of 90% confidence. A further 250 potential mothers in our dataset had no  
247 offspring genetically assigned, bringing the total number of females analyzed to 530.  
248 Dissections revealed that 104 of the 530 females (19.6%) were pregnant at the time of  
249 capture. The 104 unborn fetuses were assigned to the mother they were dissected from  
250 without the need for genetic analyses.

251 *Statistical analyses*

252 Statistical analyses were conducted in R version 3.5.3 using the lme4 package (Bates  
253 et al., 2013). Data included multiple individuals from each pod, so generalized linear mixed  
254 models (GLMMs) were used to control for pseudoreplication, with pod fitted as a random  
255 factor in all models. We tested for a quadratic effect of age in our models, and retained this  
256 where significant ( $P > 0.05$ ), tested using analysis of deviance. P values presented are those  
257 associated with removing the term from the model.

258 In order to investigate patterns of relatedness between different sex and age groups  
259 of individuals, we first calculated the relatedness between all intra-pod comparisons. We  
260 then extracted 3 sets of data: 1) relatedness between all females and adult males, 2)  
261 relatedness between all females and adult females, and 3) relatedness between all females  
262 and all juveniles. Individuals were considered Juvenile if under 10 years of age (Bloch et al.,  
263 1993b): although females occasionally give birth younger, parentage analysis assigned just  
264 1.6% of offspring to females below 10. We then fit normally-distributed GLMMs to each of  
265 these datasets with relatedness as the response variable and pod size, female age and age<sup>2</sup>  
266 plus the interaction between age and pod size as explanatory variables. Since the data were  
267 pairwise relatedness values, individuals were present in the data several times.  
268 Consequently, we included individual identity as a random effect in these models in addition  
269 to pod identity.

270 To investigate whether the number of offspring assigned to a female changes  
271 throughout her lifespan, we constructed a Poisson-distributed GLMM with the number of  
272 offspring assigned to each female as the response term and female age and age<sup>2</sup> included as  
273 explanatory terms. To investigate the influence of existing offspring on fecundity, we  
274 constructed a binomial-distributed GLMM with whether or not a female was pregnant at  
275 the time of capture as the response term and age, age<sup>2</sup> and the number of existing  
276 philopatric offspring as the explanatory terms. To investigate whether reproductive  
277 competition may influence fecundity, we refitted this model including the number of male  
278 and female philopatric adult offspring as separate explanatory variables, instead of the total  
279 number of offspring.

280 *Ethical note*

281 Data were collected from long-finned pilot whales harvested in the late 1980s as part  
282 of a legal traditional subsistence hunt in the Faroe Islands. Whales have been hunted there  
283 for at least 700 years (probably considerably longer) and hunts are non-commercial, with  
284 the resultant meat being processed and consumed by local communities. No animals were  
285 killed for the purposes of scientific data collection; instead, researchers collected data from  
286 dead whales with permission from the Faroese government. No payment was made for  
287 access to harvested whales or genetic samples. Data collection therefore did not fuel the  
288 trade or consumption of whale meat. The authors do not condone whaling. This research  
289 was approved by Swansea University College of Science Ethics Committee: SU-Ethics-Staff-  
290 290119/111.

291 **Results**

292 *Are pods composed of relatives?*

293 Average levels of relatedness within pods (derived from genetic markers rather than  
294 pedigrees) were low but highly variable (mean relatedness within 22 pods = 0.06, range 0.01  
295 – 0.23). Low average relatedness is perhaps not surprising given the large sizes of many  
296 pods (median 57 individuals, range 16 to 175). While the majority of pod-members had low  
297 relatedness, there is also evidence of close relatives being present within pods,  
298 demonstrated by the left skew in Figure 1.

299 Furthermore, the vast majority of individuals had multiple close relatives present in  
300 their pods, here defined as relatedness over 0.25; the average expected level of relatedness  
301 between half siblings (Figure 2a). Some pods appear to comprise several family units,  
302 possibly representing separate matrilines (for a clear example, see pod 131 in Figure 2a).  
303 These family units are also related to each other, with several ties linking lesser relatives  
304 (here defined as relatedness being above 0.125; the average expected level of relatedness  
305 between first cousins) between units (e.g. see pod 131, Figure 2b). Similar patterns are  
306 shown in other pods (Figures 2a and b). This supports the idea that pods represent extended  
307 family groups composed of multiple related matrilines.

308 A small proportion of individuals (43 individuals representing 3.1% of the  
309 population) had no close relatives ( $r>0.25$ ) present in their pod (median 1.5 individuals per  
310 pod, range 0-7). There was a greater proportion of males than females with no close

311 relatives (4.6% males, 2.1% females, two-proportions z-test;  $X^2 = 6.51$ , df=1, p=0.0107),  
312 possibly indicating that some males are temporarily associating with a non-natal group in  
313 search of mating opportunities. It is also possible that individuals with no close relatives  
314 could be present in their natal pod but their closest relatives have died, migrated or may be  
315 present in the pod but are not included in our analysis due to PCR failures during genotyping  
316 or missing tissue samples (95% of individuals were sampled). Almost all individuals had  
317 lesser relatives ( $r>0.125$ ) present within the pod; just 4 individuals, representing 0.29% of  
318 the population had no within-pod relatives at  $r>0.125$ .

319 *Are philopatric adult offspring present with their mothers?*

320 Of the 530 genotyped potential mothers of known age, at least one offspring was  
321 genetically assigned to 280 females (mean offspring per female = 0.89, range 0-4). The  
322 number of offspring assigned to females increased with age in a quadratic fashion (GLMM:  
323  $X^2 = 34.52$ , df = 1, p =  $4.23 \times 10^{-9}$ , Figure 3, Table 1). Each female can expect to have one  
324 offspring present in their pod by the age of 25, rising to almost two by age 40 (Figure 3). The  
325 number of assigned offspring declined in females over 40, possibly due to the death or  
326 dispersal of mature offspring, but few data are available for older females so this decline  
327 should be interpreted with caution.

328 Both males and females were present in the same pod as their mothers, even up to  
329 the ages of 31 (males) and 38 (females) (Figure 4). A total of 69 adult (aged 10+) males  
330 (34.6% male offspring) and 116 adult females (43.9% female offspring) were found to be  
331 present in the same pod as their mother. This confirms previous analyses of a smaller  
332 dataset and demonstrates that both sexes show philopatry well beyond sexual maturity  
333 (Amos et al., 1991; Amos et al., 1993).

334 *Does relatedness between females and other group members increase as females age?*

335 Relatedness of females to adult male and female pod-members increased  
336 significantly throughout the lifespan, with relatedness of females to males increasing at a  
337 faster rate than relatedness between females (Figure 5a; Table 1). The relatedness of  
338 females to juveniles also changed significantly throughout the lifespan, although in a  
339 quadratic fashion, first increasing and then decreasing (Figure 5a, Table 1). These

340 relationships were influenced by pod size, indicated by the significant interaction between  
341 pod size and female age (Table 1, Figure 5b-d), with relatedness being generally lower in  
342 larger pods.

343 Females in an average sized pod (median pod size = 57) can expect their relatedness  
344 to male pod members to increase from 0.06 when they are born to 0.15 by the time they  
345 are 50 years old (Figure 5b). In contrast, their relatedness to adult female pod members  
346 remains relatively stable, increasing from 0.11 to 0.14 over the same time period (Figure 5c),  
347 while their relatedness to juveniles remains relatively low, not exceeding 0.10 (Figure 5d).  
348 These results are similar to the patterns predicted to predispose species to evolving  
349 adaptive PRLS by Johnstone and Cant (2010), and the levels of relatedness are only  
350 marginally lower than empirical data from toothed whales with prolonged PRLS (Croft et al.  
351 (2017) and Table S1).

352 *Are females more likely to be pregnant if they have fewer philopatric offspring?*

353 Dissections found that 104 females of known age were pregnant at the time of  
354 capture. We found a quadratic relationship between female pregnancy state and female  
355 age, with females of intermediate age being most likely to be pregnant (GLMM:  $X^2 = 7.47$ , df  
356 = 1,  $p = 0.00626$ , Figure 6a, Table 1). This is consistent with reproductive senescence  
357 occurring in older females, as has been found previously in long-finned pilot whales and  
358 across several other species of toothed whale (Ellis et al., 2018b). After accounting for age-  
359 related changes in fecundity, we found that the probability of females being pregnant  
360 decreased as the number of existing philopatric offspring belonging to that female increased  
361 (GLMM:  $X^2 = 10.1$ , df = 1,  $p = 0.00148$ , Figure 6b, Table 1). None of the 23 females with 4  
362 philopatric offspring were pregnant, 3 of 29 females (10.3%) with 3 philopatric offspring  
363 were pregnant, while 21.1% of the 478 females with fewer than 3 philopatric offspring were  
364 found to be pregnant at the time of capture.

365 We considered two potential drivers for the relationship between the number of  
366 philopatric offspring and current pregnancy. First, older females may be ceasing  
367 reproduction when they come into conflict with their reproductive daughters. Second  
368 females with a large number of offspring may be more likely to have a current dependent  
369 calf, and females with dependent calves are less likely to become pregnant again:

370 dependent calves were found to affect pregnancy status in a previous study (Nichols et al.,  
371 2014). To investigate whether the relationship could be explained by reproductive  
372 competition, we re-fitted the model of pregnancy status, this time including only adult (aged  
373 10+) philopatric offspring. We found that the probability of females being pregnant  
374 significantly decreased as the number of existing philopatric daughters increased (GLMM:  $X^2$   
375 = 4.68, df = 1, p = 0.0305, Table 1), but this relationship was not found with the number of  
376 philopatric sons (GLMM:  $X^2$  = 1.39, df = 1, p = 0.238, Table 1).

## 377 Discussion

378 *Is the relatedness structure of long-finned pilot whales likely to act as a barrier to the  
379 evolution of widespread PRLS?*

380 We used genetic data to show that social groups (pods) of long-finned pilot whales  
381 are composed of networks of relatives, often containing several clusters of close relatives  
382 ( $r > 0.25$ ) linked together by a mixture of close and lesser relatives ( $r > 0.125$ ). Consistent with  
383 this, we confirmed earlier reports of lifelong philopatry of both sexes (Amos et al., 1991;  
384 Amos et al., 1993), with sons and daughters being present in the same pod as their mothers  
385 well into adulthood and mothers being accompanied by up to four philopatric offspring. The  
386 social system of the long-finned pilot whale appears to sit within the bounds of other whale  
387 species that have PRLS (Table S1). Resident killer whales, the best studied example, show  
388 lifelong philopatry of both sexes (Barrett-Lennard, 2000; Pilot et al., 2010) and bisexual  
389 philopatry is possible in the remaining species, although data are extremely limited and  
390 some dispersal of one or both sexes is likely (Table S1). These dispersal patterns are  
391 supported by evidence from mitochondrial DNA, which shows a single mtDNA haplotype in  
392 killer whale pods, indicating a single extended matriline (Barrett-Lennard and Ellis (2001),  
393 Table S1), while long-finned pilot whales (Oremus, 2008), false killer whales (Chivers et al.,  
394 2010) and a larger aggregation of narwhal (Palsbøll et al., 1997) all comprise multiple  
395 haplotypes that represent multiple, potentially related, matrilines.

396 Although long-finned pilot whales live in groups of relatives, average within-pod  
397 relatedness is generally lower than in short-finned pilot whales and resident killer whales  
398 (Table S1); we found that mean relatedness within pods was 0.06 (range 0.01 – 0.23) in  
399 comparison to 0.097 (range -0.1 to 0.38) from incomplete sampling of short finned pilot

400 whale pods (Alves et al., 2013), and average pedigree relatedness values of 0.22-0.33  
401 between female resident killer whales and the rest of their pod (Croft et al., 2017). These  
402 differences in relatedness are likely due to differences in pod size; long-finned pilot whale  
403 pods are marginally larger than those of short-finned pilot whales and are considerably  
404 larger than those of resident killer whales (Table S1). However, note that studies have used  
405 different measures of relatedness, have collected data from different populations and have  
406 used different methods to define group-membership (see Table S1 and references therein)  
407 so comparisons should be interpreted with appropriate caution.

408 Relatively low relatedness within long-finned pilot whale pods may reduce the  
409 benefits of helping (Hamilton, 1964), and hence reduce the probability of late-life help  
410 evolving. This might be particularly important if help is directed towards pod-members at  
411 random, and if help carries high costs. However, if help is preferentially directed towards  
412 related group-members (such as philopatric offspring), relatively low average relatedness  
413 may not preclude the evolution of altruistic behavior. Indeed, observational studies of  
414 other populations suggest that larger long-finned pilot whale pods may be composed of  
415 small, stable sub-units in which average relatedness could be much higher (Augusto et al.,  
416 2017b; De Stephanis et al., 2008; Ottensmeyer and Whitehead, 2003). Similar social  
417 systems have been observed or hypothesized for all six species of whales with PRLS, with  
418 long-term associations between small groups of close relatives that in turn form larger  
419 aggregations (although data is severely limited for some species; see Table S1 and  
420 references therein). Despite lower average relatedness within groups than some other  
421 species with PRLS, it therefore seems unlikely that the social structure of long-finned pilot  
422 whale pods constrains against the evolution of a post-reproductive period by preventing  
423 females from directing late life help towards relatives, specifically philopatric young.

424 A particularly strong piece of evidence suggesting that long-finned pilot whales have  
425 demographic patterns that could predispose them to evolving PRLS comes from age-related  
426 changes in relatedness. Johnstone and Cant (2010) predict PRLS will be favored by  
427 philopatry when this causes females to become more related to their social group, and  
428 particularly to males, as they age. This is what we find for long-finned pilot whales: a  
429 female's relatedness to adult males in a median sized pod can be expected to increase from  
430 0.06 to 0.15 over her lifespan, while her relatedness to other females increases from 0.11 to

431 0.14. A similar pattern is found in resident killer whales, with pedigree relatedness to other  
432 females remaining stable at around 0.33, while relatedness to males increases from 0.16 to  
433 0.33, but then decreases again when females enter their post-reproductive period,  
434 presumably as they do not continue to produce philopatric offspring beyond this point to  
435 compensate for the mortality of existing offspring (Croft et al., 2017). Such patterns are also  
436 found in some human populations. For example, matrilineal Mosuo of southwest China  
437 display an unusual dispersal system whereby both sexes are philopatric to their natal  
438 homestead (Wu Jia-Jia et al., 2013). Men do not live with their wives or children, instead  
439 visiting them at night, resulting in a relatedness structure that closely matches Johnstone  
440 and Cant's (2010) model predictions (Johnstone and Cant, 2019).

441 *Why don't long-finned pilot whales have PRLS?*

442 Despite displaying a relatedness structure that may predispose them to evolving  
443 PRLS, long-finned pilot whales do not show widespread PRLS; only ~4% of adult female long-  
444 finned pilot whales had ceased ovulating compared with 25% in short-finned pilot whales  
445 (Foote, 2008; Martin and Rothery, 1993), a species that does show PRLS. We also found a  
446 pregnant female aged 45, close to the maximum life expectancy. However, we did find  
447 evidence of reproductive senescence; there was a peak of pregnancy in females aged in  
448 their 20s but relatively few pregnant females over 40 years old. Such patterns are consistent  
449 with previous work on a larger dataset of long-finned pilot whales (Martin and Rothery,  
450 1993) and are common across many species of mammal in the wild (Nussey et al., 2013).

451 There are several reasons why long-finned pilot whales may not show PRLS. First,  
452 there may be few opportunities for helping. In resident killer whales, food can be  
453 unpredictable and the ecological knowledge of older females appears to aid its location and  
454 results in increased survival of philopatric adult offspring (Brent et al., 2015). Long-finned  
455 pilot whales feed mainly on squid, particularly *Loligo pealei* (Desportes and Mouritsen,  
456 1988), supplemented with Atlantic mackerel *Scomber scombrus* (Abend and Smith, 1997).  
457 Their prey move seasonally with changes in water temperature and with time of day  
458 (Serchuk FM and WF, 1974). While it is possible that ecological knowledge could be  
459 important in locating mobile prey, local knowledge may be considerably less important if  
460 prey are continually followed over long distances, which may happen to a greater degree in

461 long-finned pilot whales than resident killer whales and short-finned pilot whales. However,  
462 helping is not necessarily limited to finding food, and older females might offer other forms  
463 of help. Augusto et al (Augusto et al., 2017a) found that long-finned pilot whale calves were  
464 often ‘escorted’ by individuals unlikely to be parents. This might provide protection,  
465 allowing mothers to spend more time foraging, particularly during deeper dives. Similar  
466 behavior is observed in sperm whales (which do not appear to have PRLS) (Konrad et al.,  
467 2018). However, little is known about the costs and benefits of escorting and in long-finned  
468 pilot whales it does not seem to be primarily conducted by older females (Augusto et al.,  
469 2017a), although data are extremely limited, so its relevance to PRLS evolution is unclear.  
470 Allonursing, whereby non-mothers suckle young, has also been observed in toothed whales,  
471 including wild sperm whales where closer relatives are more likely to allonurse calves  
472 (Konrad et al., 2018) and also in captive beluga whales (Leung et al., 2010). Long-finned pilot  
473 whales are not known to allonurse, but data on this behavior is extremely difficult to collect  
474 due to the difficulties of sexing and ageing individuals and identifying mothers from  
475 observational data (Augusto et al., 2017a). Future work on the costs and benefits and  
476 distribution of helping behavior in toothed whales with and without PRLS will help to reveal  
477 the degree to which patterns of PRLS are explained by helping behavior, however collecting  
478 behavioral data on these species is a challenging and time-consuming process.

479 A second potential reason for the absence of PRLS in long-finned pilot whales relates  
480 to the possibility that older females in species with PRLS cease reproduction to reduce  
481 competition with their own descendants (Cant and Johnstone, 2008; Cant et al., 2009). If  
482 competition between generations is low, for example because food is generally not limiting,  
483 female long-finned pilot whales may be able to continue to reproduce without reducing the  
484 reproductive output of their philopatric offspring. A similar situation appears to exist in the  
485 African elephant *Loxodonta africana*, where matriarchs act as a repository for knowledge,  
486 and groups led by older, still reproductive, matriarchs have higher reproductive success than  
487 groups led by younger females (McComb et al., 2001). Unfortunately, the longitudinal data  
488 required to fully understand intergenerational competition in long-finned pilot whales is  
489 currently lacking. However, our finding that the probability of being pregnant declines with  
490 the number of philopatric daughters suggests that females may refrain from breeding to  
491 avoid reproductive competition with existing daughters, and can do so plastically (rather

492 than via an fixed and irreversible PRLS). Reproductive competition between females and  
493 their philopatric daughters may therefore be substantial in long-finned pilot whales.

494 Third, it is possible that long-finned pilot whales lack sufficient variation in post-  
495 reproductive viability to evolve PRLS. Post-reproductive viability (short post-reproductive  
496 periods that don't represent a distinct life stage (Levitis et al., 2013; Levitis and Lackey,  
497 2011)) appears to arise by chance in some mammals and may evolve into longer periods of  
498 PRLS under appropriate demographic conditions (Nichols et al., 2016). Long-finned pilot  
499 whales have higher late-life mortality rates than species with PRLS (Foote, 2008), which  
500 could result in too few females reaching a sufficient age to for selection pressure to extend  
501 the post-reproductive period (Foote, 2008). However, since post-reproductive viability is  
502 found in closely related species (Ellis et al., 2018b), it is unclear why this trait appears to be  
503 particularly reduced in long-finned pilot whales. Additionally, our study finds that  
504 pregnancy likelihood is influenced by existing offspring, suggesting that there is individual  
505 variation in the amount of time spent post-reproductive in long-finned pilot whales. Even if  
506 small, this existing variation could present sufficient material for selection on extended  
507 PRLS.

508 A final possibility is that PRLS in toothed whales and humans is a result of non-  
509 adaptive processes. For example, it may result due to oocytes having a limited 'shelf life'  
510 and hence resulting in longer-lived species undergoing early reproductive senescence in  
511 comparison to shorter-lived species, unless there is strong selection to the contrary (Huber  
512 and Fieder, 2018). However, this seems unlikely to explain why toothed whales with PRLS  
513 stop reproducing considerably earlier than species without PRLS (Ellis et al., 2018b). It is also  
514 possible that PRLS can result from selection on other traits, such as an extended lifespan in  
515 males (Tuljapurkar et al., 2007). However, males of post-reproductive species tend to have  
516 shorter lifespans than females, making this possibility unlikely.

517 *Is there any evidence of plasticity in the timing of reproductive cessation?*

518 We found that females were less likely to be pregnant if they had a larger number of  
519 genetically assigned offspring present in the pod (while controlling for age dependent  
520 changes in fecundity), indicating that female fertility depends on previous reproduction. We  
521 note that this relationship persisted after dependent calves were removed from the dataset,

522 suggests that females may refrain from breeding when they have adult offspring present in  
523 their pod, rather than simply when they have dependent offspring. This suggests that  
524 females with several existing offspring may invest in enhancing the quality of these  
525 offspring, rather than in producing further offspring. Such trade-offs appear to occur in  
526 other long-lived species with extended periods of maternal care. In humans, for example, a  
527 study of 163,827 births to 101,195 mothers across sub-Saharan Africa found that the  
528 probability of a child surviving to age 5 decreases by 14% for each subsequent child born to  
529 the mother, likely due to increased competition for maternal resources between siblings  
530 (Lawson et al., 2012). However, we note that in humans there is currently no evidence that  
531 women refrain from reproducing once they have a certain number of children (Towner et  
532 al., 2016).

533 A particularly interesting finding is that the fecundity of female long-finned pilot  
534 whales was significantly reduced by the presence of philopatric daughters but not sons. This  
535 relationship suggests that females may refrain from reproducing (or possibly are actively  
536 suppressed) when this brings them into conflict with their reproductive daughters. This  
537 could be viewed as a plastic adaptive post-reproductive period, only occurring in females  
538 with high potential for reproductive conflict. We suggest that long-term studies of wild long-  
539 finned pilot whales investigate this possibility further. Inter-generational reproductive  
540 conflict has been shown to occur in killer whales, whereby the mother's offspring are less  
541 likely to survive than the daughter's offspring if they are born at the same time (Croft et al.,  
542 2017). This conflict has been proposed to be an important factor in the evolution of PRLS in  
543 killer whales (Croft et al., 2017), however it is not known whether plasticity in the timing of  
544 the onset of PRLS occurs in the species, and if so whether plasticity serves to reduce conflict.

545 It is currently unclear whether patterns of pregnancy in long-finned pilot whales  
546 represent flexibility in the timing of reproductive cessation, or represent a reversible pause  
547 in reproduction such that a female may begin to reproduce again should her existing  
548 offspring disperse or die. If reversibility is important for this species, there may be  
549 disadvantages to losing the ability to reproduce and undergoing a physiological menopause.  
550 Future studies investigating the mechanisms determining fecundity in this species would  
551 shed light on these possibilities. Although the underlying mechanisms are not yet  
552 understood, our study suggests that in long-finned pilot whales a post-reproductive period

553 may occur in individuals that benefit from it, but be rare on a population-wide level, and  
554 thus be difficult to distinguish from reproductive senescence. This plastic cessation of  
555 reproduction may represent a first step towards the evolution of irreversible species-wide  
556 PRLS, or alternatively could represent a stable alternative strategy to widespread post-  
557 reproductive periods. The possibility of adaptive plasticity in reproductive cessation  
558 warrants further attention in this species, and in other species that may benefit from late-  
559 life helping, both in cases where population-wide post-reproductive life stages occur, and  
560 where they do not. Given that we find that long-finned pilot whales meet the demographic  
561 conditions which should promote the evolution of PRLS (which occurs in the very closely  
562 related short-finned pilot whales), but they seem to have evolved a plastic cessation of  
563 reproduction, our results raise the question of why some species evolve irreversible PRLS if  
564 adaptive plasticity is possible?

565

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567 manuscript; KF carried out the molecular lab work; WA collected field data, coordinated molecular  
568 data collection and helped draft the manuscript; KA conducted statistical analyses and helped draft  
569 the manuscript. All authors commented on the manuscript and gave final approval for publication.

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577 **Data Accessibility** Analyses reported in this article can be reproduced using the data provided by  
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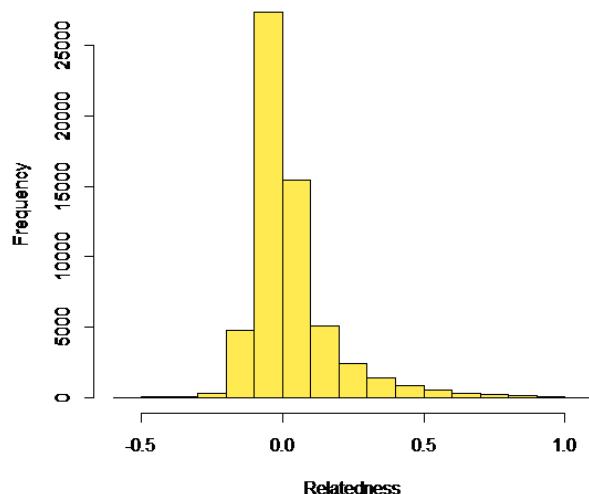
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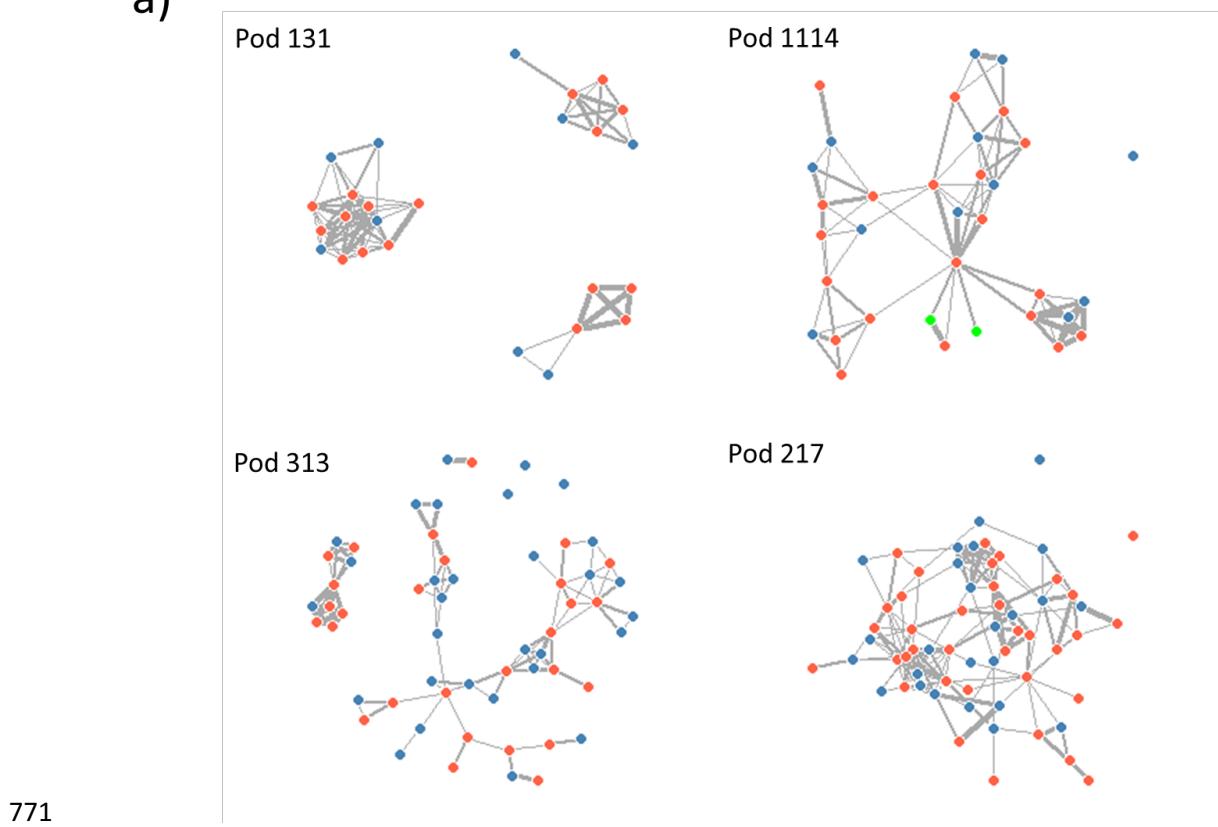
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764 **Figures and Legends**

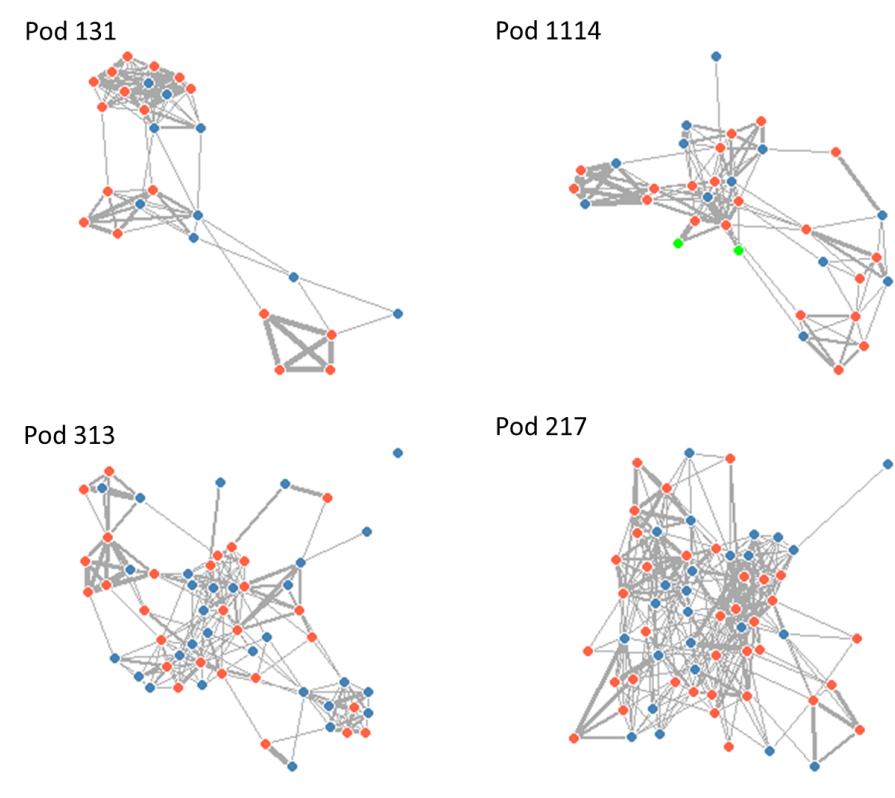


765  
766 Figure 1. The distribution of within-pod relatedness values is left-skewed; most individuals  
767 have multiple close relatives within their pod but have low relatedness to the remainder of  
768 their pod. Data comprises 58792 pairwise relatedness values between individuals from the  
769 same pod. Note that relatedness values below zero represent individuals that are less  
770 genetically related to each other than the population average.

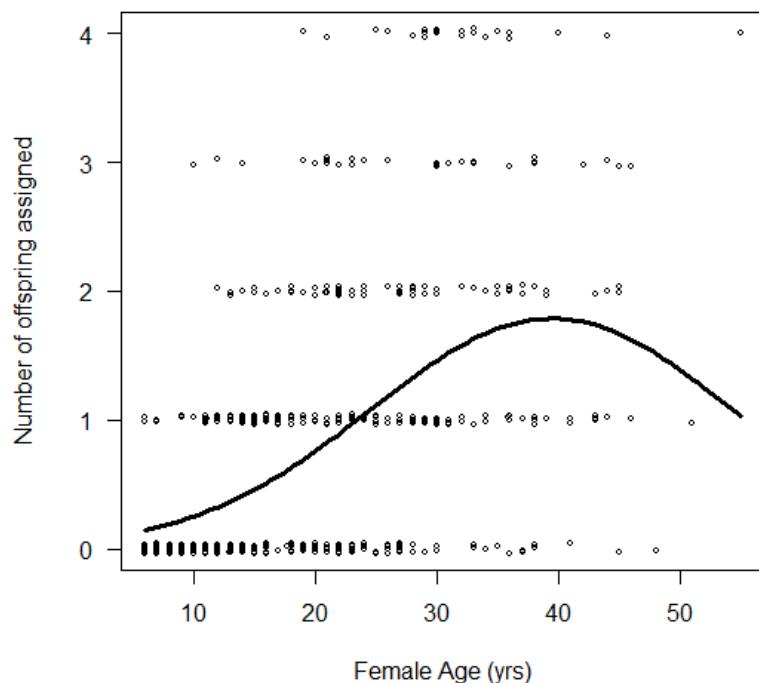
a)



b)

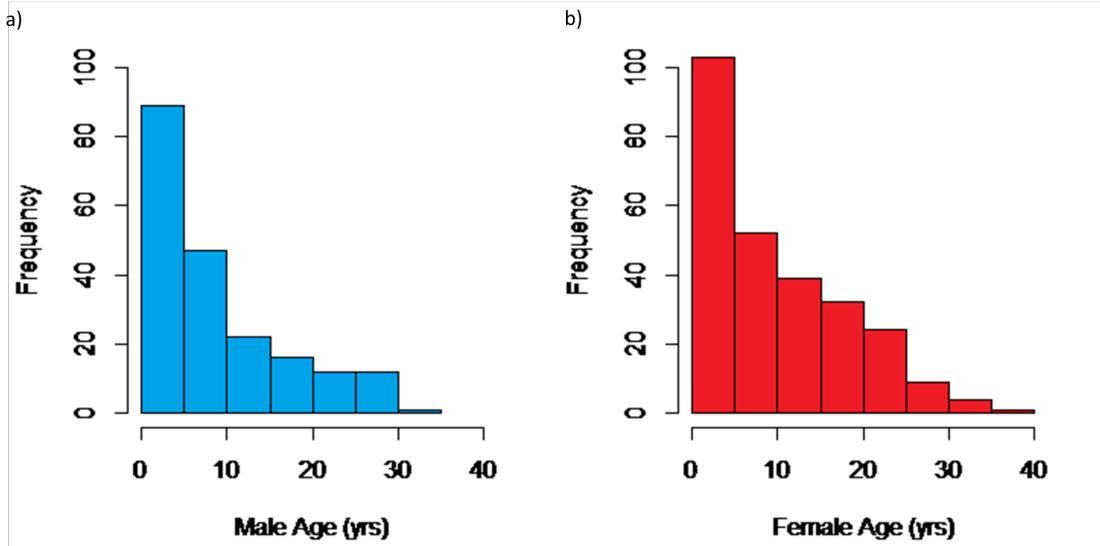


773 Figure 2. Relatedness networks within four pods: 131 (total pod size is 26 individuals, all  
774 genotyped), 1114 (total pod size is 32 individuals plus 3 fetuses, 34 genotyped whales are  
775 included), 313 (total pod size is 57 individuals plus 6 fetuses, 58 genotyped whales are  
776 included), 217 (total pod size is 59 individuals plus 5 fetuses, 61 genotyped whales are  
777 included). Blue dots represent males, red dots represent females, and green dots represent  
778 unsexed fetuses. Grey lines show cases where relatedness between two individuals is above  
779 (a) 0.25, the expected average value between half siblings, and (b) 0.125, the expected  
780 average value between cousins. Thicker grey lines indicate higher relatedness values.



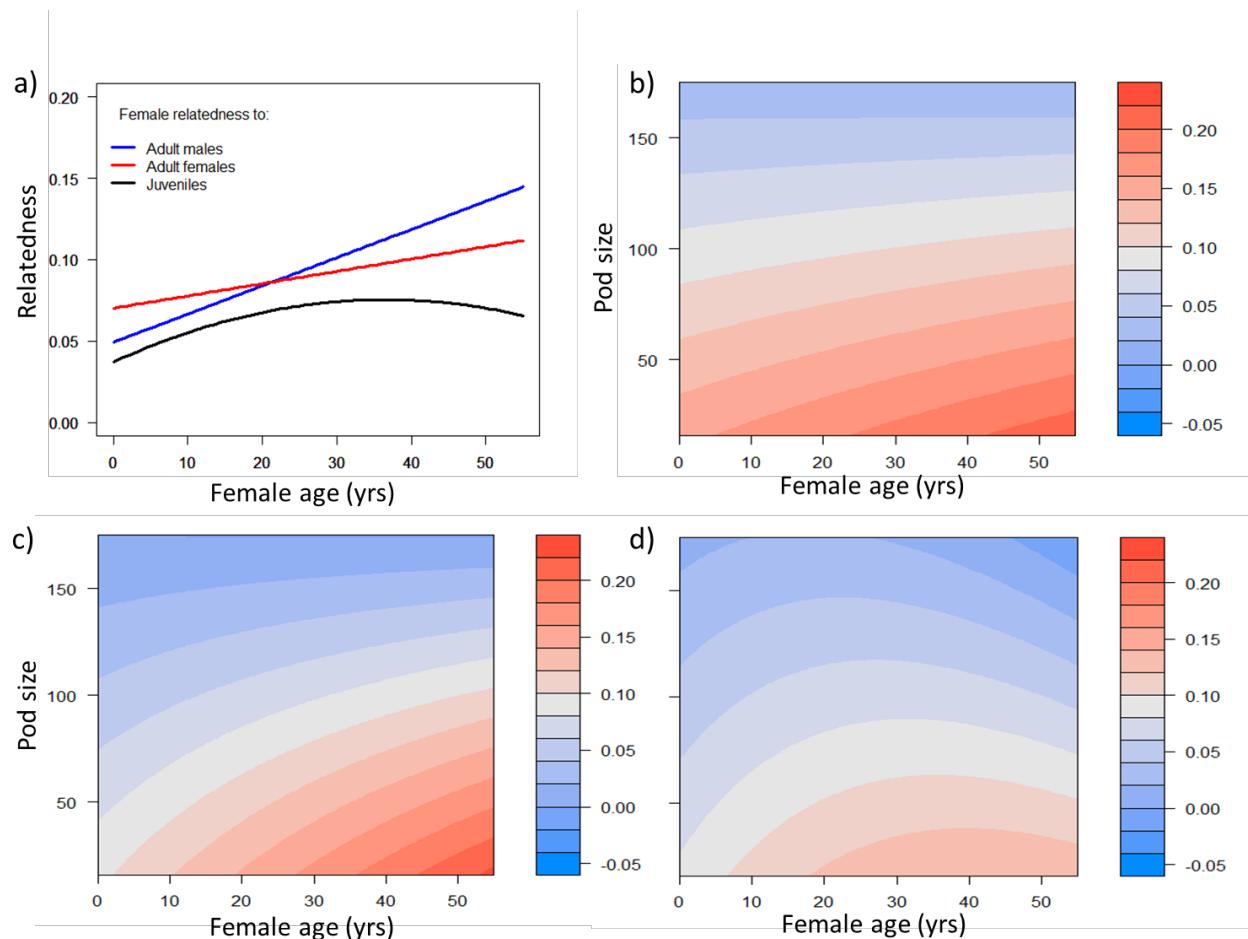
781

782 Figure 3. The number of genetically assigned offspring present in the pod for females of  
783 different ages. Open circles represent the data but note that we have jittered their positions  
784 slightly for clarity since data can only take integer values.



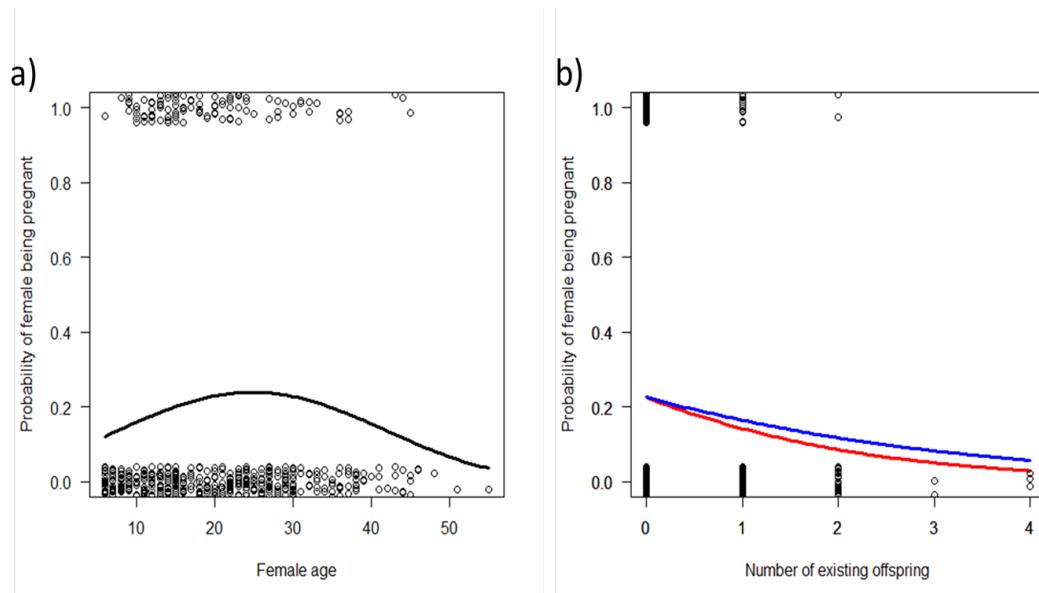
785

786 Figure 4. The number of (a) males and (b) females of different ages, present in the same pod  
 787 as their genetically assigned mother. Data comprises 463 assigned offspring with known sex  
 788 and age.



789

790 Figure 5. Relatedness between females and other members of her pod, predicted from  
791 GLMMs containing pod and individual ID as random effects. (a) Shows average relatedness  
792 between females and adult males (blue), adult females (red) and juveniles (black) over the  
793 female lifespan in a median sized pod (57 individuals). Note that this plot does not include  
794 the interaction between age and group size so does not fully represent the GLMM, but it is  
795 included for comparison with other studies and theoretical models that do not take group  
796 size into account. Contour plots show changes in female relatedness to (b) adult males (c)  
797 adult females and (d) juveniles, dependent on female age and pod size.



798

799 Figure 6. The probability of being pregnant (a) for females of different ages and (b) for  
800 females with different numbers of adult sons (blue – upper line) and daughters (red – lower  
801 line) present in the pod. Lines are predictions from GLMMs containing pod ID as a random  
802 effect. Open circles represent the data but note that we have jittered their positions slightly  
803 for clarity since data can only take values of 0 and 1.

804

## 805 **Tables and Table Legends**

806 Table 1. Summary of all GLMMs conducted. Models of relatedness over the lifespan used  
807 relatedness values from 809 genotyped females (for which the age and sex was also known)

808 in 25 pods. Models of pregnancy status used 530 females from 22 pods. P values presented  
 809 are associated with removing the term from the model.

Model	Term	Effect size	SE	t or z value	p-value
Relatedness between females and adult male pod-members	Intercept	0.0842	0.0255	3.30	NA
	Female age	0.00260	0.000406	6.42	NA
	Pod size	-0.000602	0.000305	-1.97	NA
	Age: pod size	$-1.50 \times 10^{-5}$	$3.46 \times 10^{-6}$	-4.34	$1.52 \times 10^{-5}$
Relatedness between females and adult female pod-members	Intercept	0.0117	0.0239	4.89	NA
	Female age	0.00118	0.000361	3.28	NA
	Pod size	-0.000808	0.000288	-2.81	NA
	Age: pod size	$-7.34 \times 10^{-6}$	$3.19 \times 10^{-6}$	-2.31	0.0213
Relatedness between females and juvenile pod-members	Intercept	0.0634	0.0139	4.56	NA
	Female age	0.00263	0.000351	7.50	NA
	Female age <sup>2</sup>	$-2.88 \times 10^{-5}$	$6.88 \times 10^{-6}$	-4.18	$2.92 \times 10^{-5}$
	Pod size	-0.000455	0.000165	-2.76	NA
	Age: pod size	$-9.07 \times 10^{-6}$	$1.95 \times 10^{-6}$	-4.65	$3.47 \times 10^{-6}$
Number of genetically assigned offspring present in pod	Intercept	-2.94	0.282	-10.4	NA
	Female age	0.178	0.0203	8.77	NA
	Female age <sup>2</sup>	-0.00226	0.000373	-6.07	$4.23 \times 10^{-9}$
Probability of a female currently being pregnant	Intercept	-2.82	0.577	4.90	NA
	Female age	0.154	0.0532	2.90	NA
	Female age <sup>2</sup>	-0.00308	0.00116	-2.65	0.00626
	N existing offspring	-0.448	0.148	-3.04	0.00148
Probability of a female currently being pregnant	Intercept	-2.59	0.561	-4.62	NA
	Female age	0.116	0.0508	2.28	NA
	Female age <sup>2</sup>	-0.00234	0.00113	-2.07	0.0366
	N daughters	-0.566	0.280	-2.02	0.0305
	N sons	-0.392	0.349	-1.13	0.238

810

811