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Ecological separation of two sibling species

1 **Surreptitious sympatry: exploring the ecological and genetic separation**
2 **of two sibling species**

3

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5

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*Ecological separation of two sibling species***1 Abstract**

2 Climate change is having profound impacts on animal populations, and shifts in geographic range
3 are predicted in response. Shifts that result in range overlap between previously allopatric
4 congeneric species may have consequences for biodiversity through inter-specific competition,
5 hybridization, and genetic introgression. Harbour seals (*Phoca vitulina*) and spotted seals (*Phoca*
6 *largha*) are parapatric sibling species and areas of co-occurrence at the edges of their range, such as
7 Bristol Bay, Alaska, offer a unique opportunity to explore ecological separation, and discuss
8 potential consequences of increased range overlap resulting from retreating sea ice. Using telemetry
9 and genetic data from 14 harbour seals and 6 spotted seals, we explored the ecological and genetic
10 separation of the two species by comparing their utilization distributions, distance from haul-out,
11 dive behaviour (e.g. depth, duration, focus), and evidence of hybridization. Firstly, we show that
12 harbour and spotted seals, which cannot be visually distinguished definitively in all cases, haul-out
13 together side-by-side in Bristol Bay from late summer to early winter. Secondly, we observed subtle
14 rather than pronounced differences in ranging patterns and dive behaviour during this period.
15 Thirdly, most spotted seals in this study remained close to shore in contrast to what is known of the
16 species in more northern areas, and lastly, we did not find any evidence of hybridization. The lack
17 of distinct ecological separation in this area of sympatry suggests that inter-specific competition
18 could play an important role in the persistence of these species, particularly if range overlap will
19 increase as a result of climate-induced range shifts and loss of spotted seal pagophilic breeding
20 habitat. Our results also highlight the added complexities in monitoring these species in areas of
21 suspected overlap, as they cannot easily be distinguished without genetic analysis. Predicted
22 climate-induced environmental change will likely influence the spatial and temporal extent of
23 overlap in these two sibling species. Ultimately, this may alter the balance between current isolating
24 mechanisms with consequences for species integrity and fitness.

25

26

27 Keywords

28 Climate change, range shift, hybridization, inter-specific competition, dive behaviour, habitat
29 utilisation.

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*Ecological separation of two sibling species***1 Introduction**

2 Reproductive isolation and divergent natural selection are often central elements in speciation
3 (Mayr 1970; Schluter 2009). When the geographic ranges of closely related or similar species
4 overlap inter-specific competition may increase adaptive divergence and maintain reproductive
5 isolation (Brown & Wilson 1956; Grant & Grant 2006; Pfennig & Pfennig 2009). Alternatively, in
6 species where reproductive barriers are not absolute, range overlap may result in successful
7 hybridization that facilitates genetic introgression and phenotypic convergence, which can lead to a
8 loss of unique adaptations and the emergence of new genotypes and phenotypes with different
9 fitness (Grant et al. 2004; Lancaster et al. 2007). Latitudinal and elevational climate-induced range
10 shifts have recently been observed in a variety of species worldwide, and future climate scenarios
11 predict further distribution shifts (Parmesan 2006). Such shifts may create geographic overlap
12 between previously allopatric species, resulting in increased inter-specific competition and potential
13 ‘hybrid zones’ in closely related species with implications for biodiversity (Garroway et al. 2010;
14 Grant et al. 2004; Shurtliff 2013). Recent literature indicates that hybridization amongst mammals
15 is more common than previously thought (Shurtliff 2013; Koen et al. 2014; Ellington & Murray
16 2015; Lehman et al. 1991; Schwartz et al. 2004). In time this may become more apparent in polar
17 species as a result of climate-induced northward boundary shifts causing a ‘polar squeeze’ whereby
18 species ranges are condensed and more likely to overlap as a result of a reduction in available
19 habitat (Gilg et al. 2012). Hybridization is already evident in some arctic mammals, such as polar
20 and grizzly bears, and several arctic species considered at risk of hybridization are also listed either
21 as threatened or endangered with extinction (Kelly et al. 2010). Furthermore, polar species may
22 suffer additional detrimental effects from retreating sea ice, resulting in habitat loss, and opening of
23 new corridors allowing disease transfer to naïve populations (Comiso et al. 2008; Kovacs &
24 Lydersen 2008; Kovacs et al. 2011). The mitigation and management of these impacts therefore
25 requires an understanding of the likely ecological or evolutionary impacts of impending climate-
26 induced sympatry, and the broader consequences for biodiversity in polar regions (Kovacs et al.
27 2011).

28

29 In parapatric species, distributions overlap slightly with small contact zones of co-occurrence. The
30 seasonal and spatial extent of contact zones, however, may influence the balance between
31 maintaining reproductive and phenotypic separation on the one hand, and genetic introgression and
32 convergence on the other. These contact zones, therefore, offer a valuable opportunity for exploring
33 the potential impacts of climate-induced range shifts in closely related species and ultimate
34 consequences for biodiversity. Where two species have long occurred in sympatry, character

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1 displacement via inter-specific competition may have taken place; however, if the sympatry is
2 relatively new, evidence of hybridization through morphological intermediates may exist. Harbour
3 seals (*Phoca vitulina*) and spotted seals (*Phoca largha*) are parapatric in the North Pacific and
4 overlap in distribution at the edges of their range on the Kamchatka Peninsula (Russia), Hokkaido
5 Island (Japan), and Bristol Bay (Alaska) (Burns 2002; Nakagawa et al. 2009; Nakagawa et al.
6 2010). Spotted seals are closely associated with the sea ice of the Bering, Chukchi, and Beaufort
7 seas for much of the year, whereas harbour seals of the North Pacific and North Atlantic Oceans
8 haul out on sandbanks, mud flats and skerries, but also on glacial ice floes in some parts of their
9 range (Burns 2002; Silva & Terhune 1988). These two species have distinct ecologies and
10 reproductive biology, with spotted seals pupping on sea ice up to two months earlier (Feb-May)
11 than harbour seals (April-July), which give birth primarily on land (Burns 2002). However, the two
12 species are very similar in gross morphology and in areas of seasonal range overlap both species
13 haul out on terrestrial sites. They were only recognised as two separate species in the 1970s (Burns
14 et al. 1970; Shaughnessy & Fay 1977), and subsequent genetic and morphological investigations
15 have established their sibling species status (Burns et al. 1984; Nakagawa et al. 2009; O’Corry-
16 Crowe & Westlake 1997). Nevertheless, they remain extremely difficult to distinguish from one
17 another using only external morphological features.

18
19 Distinguishing between the two species is possible, if information is available on a suite of
20 characteristics; e.g., pelage (Shaughnessy & Fay 1977) or dentition (Burns et al. 1984). However,
21 distinguishing between the two species using these criteria is a qualitative, not a quantitative
22 process and is not definitive in all cases. The limited information available during our capture
23 operations was insufficient to definitively distinguish the two species. As such, seals we thought to
24 be harbour seals were captured and satellite tagged in Bristol Bay, Alaska, and a few individuals
25 subsequently exhibited long-distance movements, one more than 1500km (Bristol Bay to Chukotka,
26 the north east coast of Russia). Such extensive movements have not been documented for harbour
27 seals, but are typical from what is known about spotted seal behaviour from more northern regions
28 (Boveng et al. 2009; Lowry et al. 1998; Lowry et al. 2000). Although harbour seals have been
29 widely studied across much of their range, less is known about the spotted seal, and no ecological
30 studies have been conducted in any area of co-occurrence. Furthermore, because of their
31 morphological similarity and the paucity of information on the seasonal extent of sympatry, the
32 degree to which both species haul out together is unknown.

33

Ecological separation of two sibling species

1 We focussed our research during the ice-free non-breeding season (September to December in years
2 2000 and 2001) after the summer moult to facilitate tag attachment and when oceanographic
3 conditions might predict the greatest seasonal sympatry and ecological overlap. Using a
4 combination of molecular and telemetric techniques, we employed a multifaceted approach to
5 compare the ecological and genetic separation of harbour and spotted seals in Bristol Bay, Alaska.
6 Our specific objectives were to 1) determine if the two species haul out together; 2) explore if there
7 was evidence of hybridization; and (3) investigate ecological separation in ranging patterns,
8 utilisation distributions, and dive behaviour of the two species.

9

10 Methods**11 Study area and capture**

12 Seal captures took place in Egegik and Ugashik bays, located on the north side of the Alaska
13 Peninsula, in Bristol Bay, Alaska, which is part of the Bering Sea with a maximum depth of ~70m.
14 In September of 2000 and 2001, after both species were known to have moulted, 20 seals (10 in
15 each year) were captured in nets near haulouts within the two bays, which are ~75 km apart in
16 south-eastern Bristol Bay, and then placed in hoop nets and transferred to a research vessel for
17 processing; i.e., sex, mass (kg), tissue biopsy (small ~1 cm wedge-shaped piece of skin at the edge
18 of the flipper), and tag deployment (Table 1a). In each year, captured seals were equipped with
19 satellite linked dive recorders (SDR, T16 model developed by Wildlife Computers) that were glued
20 onto their mid-dorsal surface using quick-setting epoxy. The SDR tags measured 109 x 44 x 22 cm
21 and weighed 143 g. The seals were released near their capture sites within 2-4 hours of capture.
22 Animals were captured and handled under National Marine Fisheries research permits 1000 & 358-
23 1585 issued to the ADF&G.

24

25 Genetic data

26 Tissue biopsy samples collected from tagged seals were preserved in EtOH and total DNA was
27 extracted using standard protocols (O’Corry-Crowe et al. 2003). A 588 base-pair (bp) fragment of
28 the mitochondrial genome was amplified and 435bp sequenced for both light and heavy strands (see
29 Westlake & O’Corry-Crowe 2002). We used mtDNA sequence data (435bp) from over 1,400
30 harbor seal samples from across the North Pacific, including 1,271 from Alaska, and 247 spotted
31 seal samples from across their range (Okhotsk Sea, Bering Sea, and Chukchi Sea) to clarify mtDNA
32 phylogeography and dispersal patterns within and phylogenetic relationships between these two

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1 species (O’Corry-Crowe & Westlake 1997; Westlake & O’Corry-Crowe 2002; O’Corry-Crowe et
2 al. 2003). We also generated multi-locus genotypes in 9 independent hypervariable microsatellite
3 loci (Allen et al. 1995; Coltman et al. 1996; Goodman 1997) that we previously screened in 766
4 harbour seals and 199 spotted seals (of which 38 spotted seals and 187 harbour seals were sampled
5 in an area of known overlap). A subset of 23 spotted seals and 47 harbour seals were also screened
6 for polymorphism in an extended set of 20 microsatellite loci to assess genetic assignment power
7 with respect to locus number (Table S1).

8

9 Satellite telemetry

10 The SDR tags transmitted radio signals to Service Argos receivers on board National Oceanic and
11 Atmospheric Administration polar-orbiting satellites. The signals were processed by Service Argos
12 to estimate locations of the tagged seals, and the precision (location quality) of the locations was
13 provided by Service Argos based on the number of signals received (Vincent et al. 2002; see
14 Appendix S1 in Supporting Information). The tags also transmit histogram files, which contain
15 information on dive depth, dive duration, and time at depth (see Appendix S1). These data were
16 recorded as number of dives or proportion of time spent in ten bins of differing depth or duration
17 within 6-hour intervals. For our analyses we derived mean and max dive depth, mean and max dive
18 duration, dive focus and focal depth from these dive bin data (see Appendix S1).

19

20 Our comparison of movements and dive behaviour for the two species was focussed on the
21 September-December period, when data were available from at least two individuals of both
22 species. This allowed a more direct comparison of movements and dive behaviour, and avoided
23 periods when the behaviour of individuals may be influenced by the approaching breeding season
24 or periods when spotted seals are more likely to be associated with sea ice offshore. During our
25 selected study period one seal (PV00B02) left the Bristol Bay study area and moved into Russian
26 waters (>1500 km; see Fig. 2). This individual was not included in subsequent analyses of
27 movements and dive behaviour as its journey into Russian waters no longer reflected a utilisation
28 distribution or distance from haul-out, and any differences between this and other individuals in
29 dive behaviour may simply be an artefact of different habitat characteristics encountered by the
30 individual seals.

31

32 Statistical analysis**33 Genetic analysis**

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1 We analysed molecular data using phylogenetic reconstruction and likelihood-based clustering and
2 assignment methods. Phylogenetic relationships among mtDNA sequences were inferred using
3 maximum parsimony analysis in PAUP 4.0 (Swofford 2002) and median joining networks, using
4 Network 4.6 (Fluxus technology Ltd. 2011). We used the model-based clustering algorithm,
5 STRUCTURE, (v.2.3.4, Pritchard et al. 2000) to assess nDNA subdivision among spotted and harbour
6 seals, assign tagged seals to species, and assess the likelihood of admixed ancestry for each animal;
7 the method uses a Bayesian approach to estimate the most likely number of population clusters, K ,
8 given the data. Both admixture and no-admixture models were applied. We used MCMC methods
9 to integrate over the parameter space and multiple ($n=10$) long runs with different starting
10 conditions were conducted and summary statistics monitored for convergence. The clear species
11 clustering meant that prior information on sample group (i.e. LOCPRIOR model; Hubisz et al.
12 2009) was not needed to resolve species structure.

13

14 Satellite telemetry and location error

15 There are a number of challenges associated with analysing Argos data, which include handling
16 location error, irregular time intervals, and dive data collected in discrete depth and duration bins.
17 In terms of location error, >50% of locations were associated with low quality codes (0, A, B, Z)
18 and simply discarding these data can severely reduce sample size and information content (Freitas
19 et al. 2008). Furthermore, locations with high quality codes (1, 2, 3) only have a ~68% probability
20 of being within the defined distances (Freitas et al. 2008). To eliminate improbable locations, yet
21 without discarding excessive amounts of data, we applied the Speed-Distance-Angle (SDA) filter in
22 R (argos filter package; Freitas 2012; R Core Team 2014), which first removes all locations with a
23 quality code Z. Locations with swim speeds >2.5m/s are then also removed (Dietz et al. 2013),
24 unless the location was within 5km of the previous one; this retains good quality locations in which
25 high swim speeds are purely due to locations being recorded in quick succession. Finally, we
26 discarded locations with unlikely turn angles, defined as all locations requiring turning angles
27 higher than 165° and 155° , if the track prior to the location was >2.5km and >5km, respectively
28 (Freitas et al. 2008). Overall, the SDA-filter discarded 1778 locations, ~18.6% of the dataset, the
29 majority of which had poorer quality codes; B=58.6%, A=18.0%, 0=14.2%, 1=6.2%, 2=2.1%, and
30 3=0.8%. The filtered data contained 7739 locations within the following quality codes: B=35.3%,
31 A=26.2%, 0=8.6%, 1=15.2%, 2=9.1%, and 3=5.6%.

32

33 Utilisation distribution and overall range

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1 The kernel Brownian bridge approach, which accounts for serial autocorrelation between
2 relocations, was used to estimate monthly UD of individual seals (adehabitatHR package; Bullard
3 1999; Calenge 2006; Horne et al. 2007). This approach takes into account the path between two
4 successive relocations, which may not be linear, and estimates the density probability that this path
5 passed through any point of the study area while accounting for a certain amount of inaccuracy.
6 Specifically, the Brownian bridge is estimated using two smoothing parameters, sig1 (related to the
7 speed of the animal) and sig2 (related to the inaccuracy of relocations). Since no declared
8 measurement error was provided for most of the low quality codes, and due to the inaccuracy of the
9 reported Argos error for locations with high quality codes, we assigned error measurements (sig2)
10 based on the 68th percentile estimated error from GPS double-tagging experiments in Costa *et al.*
11 2010 (3=0.5; 2=1; 1=1.2; 0=4.2; A=6.2; B=10.3km). Sig1 for individual seals was then estimated
12 using the liker function, which uses a maximum likelihood approach. From the kernel Brownian
13 bridge analysis we extracted the 50% and 90% monthly UD for all individuals and subtracted the
14 area of intersection with the Alaska landmass polygon. The frequency distribution of 50% and 90%
15 monthly UD were skewed towards smaller areas and were therefore log-transformed.

16

17 We analysed the 50% and 90% monthly UD separately using generalised linear mixed models
18 (nlme package; Pinheiro et al. 2014), which included the null model, single parameter models
19 including species, month, sex, mass, a species-month interaction, as well as two, three and four
20 parameter additive models. The frequency distributions of monthly UD were skewed towards
21 smaller areas, and these data were therefore log-transformed. Model selection was carried out using
22 AIC_c scores and AIC_c weights. Model averaging (AICcmodavg package; Mazerolle 2015) of the
23 top models that accounted for 95% of the AIC_c weight was used to extract the β -estimates and their
24 95% confidence intervals of individual parameters. We considered β -estimates with confidence
25 intervals that did not (or only marginally) overlap zero to have a significant effect.

26

27 Distance from haul-out

28 To explore differences in movement, we extracted the linear distances between last haul-out
29 location and 1) each at-sea location in the subsequent at-sea period, and 2) the single at-sea location
30 at the maximum distance away. All distances were analysed using generalised linear mixed
31 modelling (Pinheiro et al. 2014) and model averaging (as described above). To account for auto-
32 correlation in distances from haul-out (i.e., if one location is far away from the haul-out site chances
33 are that subsequent locations also are far away) the corAR1 function was applied. Furthermore, the
34 frequency distribution of distances from haul-out was skewed towards shorter distances, and these

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1 data were therefore log-transformed. We ran a null model, single parameter models of species, sex,
2 mass and month, as well as two and three parameter additive models.

3

4 **Dive behaviour**

5 The total number of dives within each bin (as described above) were multiplied by the median
6 depth or duration value for each bin, and then divided by the sum of all dives to calculate mean dive
7 depths and durations (Folkow & Blix 1999; see Appendix S1). Maximum depths and dive durations
8 were based on the upper value of the bin in which the maximum depth or duration was recorded
9 during any 6-hour interval. Dive focus was calculated as the sum over all depth bins of the
10 proportion of dives that fell within each bin; a finite correction factor was included that allowed this
11 index to be used for small sample sizes (Frost *et al.* 2001):

12

13

$$Dive\ focus = \sum_{i=1}^{10} \left\{ \frac{[n_i(n_i-1)]}{[N(N-1)]} \right\}$$

14

15 where n_i is the number of dives in depth bin i , and N is the total number of dives. Dive focus >0.50
16 indicates that dives within a 6-hour period were primarily to one particular depth bin. Dive focus
17 values were constrained between 0 and 1, thus a logit transformation was used in the GLMM. The
18 focal depth was defined as the dominant dive bin within which dive focus was >0.50 . The different
19 dive behaviours were analysed using GLMM and model averaging, as described above. We used
20 the corCAR(~time | ID) function to account for autocorrelation and unequal time spacing between
21 6-hour intervals among repeated measures of individual seals. We ran a null model as well as single
22 and additive models including a combination the parameters species, month, sex, mass, and a
23 species-month interaction.

24

25 **Results**

26 **Genetic analyses**

27 Earlier phylogenetic studies determined that harbour and spotted seals were reciprocally
28 monophyletic for mtDNA (O’Corry-Crowe & Westlake 1997). Of the 20 seals tagged in our study,
29 14 had mtDNA haplotypes characteristic of harbour seals whereas 6 had maternal lineages
30 characteristic of spotted seals (Table 1b). To assess whether the mtDNA ‘miss-assignments’
31 represented (1) misidentifications in the field, (2) incomplete mtDNA lineage sorting, or (3)
32 hybridization, we compared our findings to reference datasets of 766 North Pacific harbour seals

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1 and 199 spotted seals from across the species' ranges that had complete or near complete genetic
2 profiles for both mtDNA and the nine microsatellite loci screened in both species (Table 1b).
3 Defining known harbour and spotted seals as animals sampled in areas of allopatry, we confirmed
4 that mtDNA is reciprocally monophyletic across these two species. Bayesian cluster analysis, even
5 allowing for admixture (MCMC burn-in of 50,000, followed by 1×10^6 reps, no LOCPRIOR), also
6 clearly differentiated two discrete genetic clusters ($K=2$, $\text{Pr}(2/X) \approx 1.0$) based on the nDNA data
7 that are consistent with harbour and spotted seals. Furthermore, no evidence of mixed ancestry that
8 may indicate recent hybridization has been documented at the nuclear loci to date. All reference
9 seals had high ($Q > 0.81$) assignment probabilities to one species.

10

11 In all cases, the nuclear DNA agreed with the mtDNA data in species assignment: All six tagged
12 seals found to possess a spotted seal mtDNA lineage were unambiguously assigned to the spotted
13 seal genetic cluster (allowing for admixture, $Q > 0.9$, Table 1b). Furthermore, all seals with harbour
14 seal mtDNA were assigned to *P. vitulina* for nDNA (Table 1b). Whereas the nine-locus
15 microsatellite data set yielded very strong assignments to one species or the other (Table 1b), we
16 were concerned that the number of independent loci screened may not be sufficient for
17 unambiguous assignments or estimation of mixed ancestries. Therefore, we ran a subset of 70 seals,
18 including the six tagged seals assigned to *P. largha*, for a total of twenty independent microsatellite
19 loci (Table 1c). Apart from slightly higher ancestry likelihoods for the most likely species, the
20 results were similar to the analysis that used the lower number of loci (Table 1c).

21

22 Utilisation distributions and distance from haul-out

23 Overall there was substantial individual variation in utilisation distributions and movement patterns
24 (Figs. 1, 2). However, the largest UD's (both 50% and 90% utilisation distributions) and longest
25 distances travelled between haul-outs to at-sea locations were recorded for spotted seals (Figs. 1, 2);
26 these also exhibited the greatest variation.

27

28 For the generalised linear mixed models (GLMM) of the 50 and 90% monthly UD's the top model in
29 both cases accounted for most of the weight and did not include species as a parameter (see Table
30 S2). Model averaging did not reveal any species difference in the size of the 50 or 90% monthly
31 UD's, but there were significant differences in the size of UD's across months, with UD's in
32 September being the smallest, and UD's in December being the largest. There was also a negative
33 relationship between monthly UD and mass, and monthly UD's were larger for males compared to
34 females (Table 2). The area of overlap between the species' 50% UD covered 35% of the harbour

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1 seal 50% UD and 36% of the spotted seal 50% UD (Fig. 3), while the area of overlap between the
2 species' 90% UD covered 69% of the harbour seal 90% UD and 36% of the spotted seal 90% UD
3 (Fig. 3).

4

5 Neither of the analyses of linear distances from haul-out to subsequent at-sea locations and
6 maximum distance to haul-out during an at-sea bout (GLMM) showed evidence of a species-
7 specific difference (Table S2; Table 3). Instead, linear distance to haul-out generally increased
8 across months, and were larger for males compared to females. For maximum distance to haul-out,
9 distances in October and December were significantly larger than in September. Both linear
10 distance and maximum distance were larger for lighter individuals compared to heavier ones (Table
11 3).

12

13 **Dive behaviour**

14 As with movement patterns, we recorded a wide range of dive behaviours in both harbour and
15 spotted seals. The analysis of dive focus (GLMM) revealed six top models with $\Delta AIC_c < 2$, which
16 accounted for 0.95 of the AIC_c weight (see Table S3). Although both species were very focussed in
17 their dives (>0.50), harbour seals were significantly more focussed compared to spotted seals
18 (Table 3; Fig. 4). Furthermore, males appeared less focussed in their dives compared to females
19 (Table 3; Fig. 4). For focal depth the GLMM revealed seven top models with $\Delta AIC_c < 3$,
20 accounting for 0.96 of the AIC_c weight (see Table S3). Model averaging indicated that focal depth
21 increased across months, and that there was a species-specific differences in focal depth in
22 November. Males also had a deeper focal depth compared to females (Table 3).

23

24 For mean dive depth, there were seven models within $\Delta AIC_c < 3$, which accounted for 0.97 of the
25 AIC_c weight (Table S3). Again, model averaging did not reveal any species or sex-specific
26 differences in mean dive depth; however, as above, mean dive depth increased across months and
27 there was a species-specific differences in focal depth in November (Table 3; see similar results for
28 maximum dive depth in Table S3 and Table 3). For mean dive duration there were six models with
29 $\Delta AIC_c < 5$, accounting for 0.96 of the AIC_c weight (Table S3). Again, model averaging did not
30 reveal a significant species difference in mean dive duration, despite species being a parameter in
31 the top model, however, there was a general increase in mean dive duration across months (Table 3;
32 see results for maximum dive duration in Table S3 and Table 3).

33

34 **Discussion**

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1 All of the twenty seals captured in Bristol Bay were initially identified as harbour seals during field
2 operations, but the long-distance movement by PV00BB02 was not typical of the species, and thus
3 prompted further investigation. Genetic analysis revealed that six of the twenty seals caught were
4 actually spotted seals. These findings not only emphasize the strong morphological similarity of
5 these two phocids, but also reveal their tendency to haul-out together at a number of discrete coastal
6 sites in late summer, autumn, and early winter. Satellite tracking documented individual variation in
7 ranging patterns and dive behaviour, gender and size-specific differences in habitat utilisation, and a
8 temporal trend towards longer-range movements and longer, deeper dives from late summer to
9 early winter. Interestingly, this study did not reveal dramatic species differences in movement and
10 dive behaviour in this area of seasonal sympatry, apart from a subtle difference in dive focus. We
11 did, however, find that some spotted seals tended towards more expansive movements further from
12 shore. These generally consisted of just a few trips, hence the non-uniform kernels, and were most
13 likely outweighed by the higher frequency of shorter movements. Nevertheless this may reflect
14 subtle differences in foraging strategy between the two species at a time of year when they co-occur
15 in the southeast Bering Sea, and highlight what may be greater flexibility and range in spotted seal
16 movements compared to that of harbour seals. More substantial species differences may occur in
17 the late winter or early spring when the sea ice reaches Bristol Bay or when spotted seals may travel
18 further offshore to locate breeding habitat around the sea ice. During both winters sea ice did not
19 reach Bristol Bay until December/January (National Snow & Ice Data Center); thus the behaviour
20 of individual seals was unlikely to be significantly affected by this seasonal phenomenon during our
21 study period (apart from PV00BB02 which may have been associated with sea ice in Russian
22 waters).

23

24 The at-sea movements and dive behaviour of harbour seals have been widely studied across the
25 temperate regions of the northern hemisphere (e.g. Bjørge et al. 1995; Frost et al. 2001; Boness et
26 al. 1994; Tollit et al. 1998; Thompson et al. 1998; Eguchi & Harvey 2005), and concur with results
27 of our study, whereby individuals typically remained within 70 km of haul-out sites, dive durations
28 were 2-4 minutes, and dive depths were <25 m (dependent on bathymetry). However, substantially
29 greater dive depths and durations of up to 480m and 35 minutes have also been recorded (Eguchi &
30 Harvey 2005). Current information on spotted seal movements has been obtained primarily from
31 more northerly areas (Chukchi and Bering seas), which are highly influenced by seasonal sea ice.
32 Seals first haul out on sea ice in October or November, and remain associated with the sea ice
33 through June (Boveng et al. 2009; Lowry et al. 1998; Lowry et al. 2000). Spotted seals tagged in the
34 Chukchi Sea during a time period similar to our study often undertook long-distance trips to sea

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1 (~1000km) lasting more than 30 days (Lowry et al. 1998), similar to the behaviour of PV00BB02 in
2 this study. In the northern Bering Sea between August and October, spotted seals remained closer to
3 shore south of the sea ice edge, while later in the winter (January onwards) seals were typically
4 located further offshore either on or north of the edge of the sea ice (Lowry et al. 2000).

5
6 Despite the fact that the two species could not be visually distinguished in the field and exhibited
7 many similarities in movement and dive behaviour, the genetic analysis did not reveal any evidence
8 of hybridization. The small sample size of animals in this study, however, cannot exclude the
9 possibility of inter-breeding between these sibling species. However, the absence of documented
10 mixed ancestry in the much larger reference sample sets that were genotyped for both species is
11 noteworthy. Differences in breeding season and in preferred breeding habitat likely limit
12 opportunities for inter-breeding. Age-specific segregation has been observed in spotted seals in
13 Japan whereby immature seals are typically found at the southern edge of their distribution (Mizuno
14 et al. 2001). The possibility of hybridization may thus be reduced further if the Alaskan spotted seal
15 population was segregated by age. In fact, most spotted seals in our study were likely juveniles,
16 based on their mass at capture (range 30.2-50.0 kg; mean 38.7 kg; Boveng et al. 2009).

17
18 Although we developed our study retrospectively after documenting the long distance movement of
19 PV00BB02, our data represent a rare opportunity to investigate the ecological separation of two
20 parapatric sibling species, and to consider the potential consequences of changes in range overlap
21 that may result from climate change. In comparison, studies of other sympatric pinnipeds, such as
22 Steller sea lions and northern fur seals, have shown very distinct ecological separation occupying
23 clearly different niches; i.e., near-shore benthic forager versus offshore pelagic forager (Waite et al.
24 2012). Furthermore, ecological separation within a single species (e.g. northern fur seal; Robson et
25 al. 2004) has also been shown to be more dramatic than the differences between harbour and
26 spotted seals in our study. Harbour and spotted seals in Bristol Bay currently appear to haul-out
27 together and, overall, have very similar ecologies during this period. Nevertheless, introgression is
28 likely rare as there may be little overlap during the breeding season when spotted seals most likely
29 are located further offshore along the edge of the sea-ice. From the data that were available during
30 late winter (i.e. after December) one of three spotted seals did conduct longer-distance movements,
31 although it returned to Bristol Bay. In other regions, spotted seals have been observed to spend part
32 of the year feeding in one area before returning to breeding grounds elsewhere (Won & Yoo 2004),
33 which again would reduce the possibility of inter-breeding if this was the case for the spotted seals
34 in Bristol Bay.

Ecological separation of two sibling species

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2 Isolating mechanisms that maintain species integrity among sibling species typically involve
3 allopatry, phenotypic divergence or both (Mayr 1970). In allopatric species, the extent of
4 phenotypic divergence may be limited if both species occupy similar but geographically isolated
5 niches. In contrast, closely related species whose ranges overlap substantially often occupy distinct
6 niches and display greater phenotypic divergence (Lack 1983; Schluter et al. 1985; Grant & Grant
7 2006). Where the range of two similar species overlap The degree of phenotypic divergence or
8 character displacement, including morphology, breeding behaviour or ecological differences, is
9 driven by the level of inter-specific competition, which is expected to be more intense in areas of
10 range overlap (Brown & Wilson 1956; Grant & Grant 2006). Thus, environmental changes that
11 alter the degree of range and niche overlap among closely related species might be expected to also
12 alter the ecological and reproductive relationship which may result in increased divergence on the
13 one hand or a breakdown of species barriers on the other. Such environmental change may also
14 increase species extinction risk as the competitive exclusion of one species by another becomes
15 more widespread due to an increase in the extent of range and niche overlap. Under such a scenario,
16 a more temperate subarctic might be expected to favour harbour seals. Extinction probabilities of
17 one species in such a manner, however, could be offset by its ability to adapt.

18

19 In this study, we documented two morphologically similar species that are currently maintaining
20 genetic distinctness despite an apparent limited niche separation during the season of sympatry (late
21 summer to early winter). This contrasts with extensive niche separation at other locations and at
22 other times of the year, including the separation of breeding season and habitat (sea-ice vs. coastal
23 areas). In the Arctic and subarctic, changes to the cryosphere are already altering species
24 distributions, behaviour and ecology (see Gilg et al. 2012). Such climate-induced changes in the
25 environment will likely influence the spatial and temporal extent of range and ecological overlap of
26 spotted and harbour seals. We contend this may alter the delicate balance between current isolating
27 mechanisms, including competitive exclusion, asynchronous breeding, and genetic introgression
28 with consequences for species integrity and fitness. Predicting the effects of climate change on
29 biodiversity is one of the most pressing eco-evolutionary challenges (Thomas et al. 2004), and
30 requires a detailed understanding of species' ecology and habitat use; an understanding hindered
31 when co-occurring sibling species are not visually distinguishable.

32

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1 **Figure 1.** Kernel Brownian bridge 50% (dark grey) and 90% utilisation distribution (light grey) for
2 individual harbour seals.

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4 **Figure 2.** Kernel Brownian bridge 50% (dark grey) and 90% utilisation distribution (light grey) for
5 individual spotted seals.

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7 **Figure 3.** Kernel Brownian bridge a) 90% and b) 50% utilisation distributions for all harbour seals
8 (medium grey) and spotted seals (light grey) with the areas of overlap indicated in dark grey.

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10 **Figure 4.** Species- and sex-specific predicted estimates of dive focus (95% CI) from the top model
11 for an individual of average mass.

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Ecological separation of two sibling species

1 **Table 1.** a) Field measurements, tag performance and b-c) genetic determination of the 20 seals
2 captured in Bristol Bay, Alaska, 2000-2001. Six seals (shaded entries) were identified as spotted
3 seals based on a summary of mtDNA and microsatellite assignment-based testing of harbour and
4 spotted seals in Alaskan, Russian and Japanese waters where field and genetic determinations do
5 not agree. Specifically, b) nuclear analysis based on a set of nine microsatellite loci screened in 766
6 harbour and 199 spotted seals and c) nuclear analysis based on a set of 20 microsatellite loci
7 screened in 47 harbour seals and 23 spotted seals.

8

9 **Table 2.** Presents β -estimates of model parameters for the utilisation distribution analyses with 95%
10 confidence intervals. Confidence intervals that do not overlap zero signify a significant
11 effect/difference and are highlighted in bold.

12

13 **Table 3.** Presents β -estimates of model parameters for the movement and dive behaviour analyses
14 with 95% confidence intervals. Confidence intervals that do not overlap zero signify a significant
15 effect/difference and are highlighted in bold.

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	ID	Sex	Mass (kg)	Capture date	Days w/ locations	Locations (N)	Field ID	mtDNA	Microsatellites			
									No. loci screened	No. loci scored	Assignment (<i>Q</i> value)	
										<i>P. largha</i>	<i>P. vitulina</i>	
a)	PV00BB02	F	30.7	12/09/2000	47	265	<i>P. vitulina</i>	<i>P. largha</i>	9	7	.967	.033
	PV00BB03	M	30.2	12/09/2000	23	136	<i>P. vitulina</i>	<i>P. largha</i>	9	7	.956	.044
	PV00BB04	M	46.7	12/09/2000	50	249	<i>P. vitulina</i>	<i>P. largha</i>	9	7	.950	.050
	PV00BB06	F	41.4	12/09/2000	38	120	<i>P. vitulina</i>	<i>P. largha</i>	9	7	.903	.097
	PV00BB10	M	45.2	13/09/2000	15	44	<i>P. vitulina</i>	<i>P. vitulina</i>	9	7	.002	.998
	PV00BB11	F	33.1	13/09/2000	16	45	<i>P. vitulina</i>	<i>P. largha</i>	9	7	.954	.046
	PV00BB12	F	51.9	13/09/2000	49	171	<i>P. vitulina</i>	<i>P. vitulina</i>	9	7	.002	.998
	PV00BB13	F	31.7	13/09/2000	65	390	<i>P. vitulina</i>	<i>P. vitulina</i>	9	7	.004	.996
	PV00BB15	F	46.2	13/09/2000	54	203	<i>P. vitulina</i>	<i>P. vitulina</i>	9	9	.023	.977
	PV00BB18	M	49.0	14/09/2000	46	169	<i>P. vitulina</i>	<i>P. vitulina</i>	9	9	.001	.999
	PV01BB05	F	52.7	04/09/2001	102	473	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.001	.999
	PV01BB07	F	65.0	06/09/2001	108	739	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.001	.999
	PV01BB11	F	64.1	06/09/2001	7	42	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.001	.999
	PV01BB23	F	53.3	07/09/2001	92	378	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.002	.998
	PV01BB24	F	53.5	07/09/2001	81	299	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.002	.998
	PV01BB28	F	36.4	07/09/2001	114	1136	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.001	.999
	PV01BB35	F	50.0	08/09/2001	97	495	<i>P. vitulina</i>	<i>P. largha</i>	9	9	.996	.004
	PV01BB41	M	72.9	09/09/2001	87	511	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.002	.998
	PV01BB48	M	71.9	09/09/2001	112	1016	<i>P. vitulina</i>	<i>P. vitulina</i>	9	7	.001	.999
	PV01BB49	F	63.1	09/09/2001	111	858	<i>P. vitulina</i>	<i>P. vitulina</i>	9	8	.002	.998
c)	PV00BB02							<i>P. largha</i>	20	20	.997	.003
	PV00BB03							<i>P. largha</i>	20	20	.995	.005
	PV00BB04							<i>P. largha</i>	20	20	.998	.002
	PV00BB06							<i>P. largha</i>	20	20	.995	.002
	PV00BB11							<i>P. largha</i>	20	20	.998	.002
	PV01BB35							<i>P. largha</i>	20	20	.998	.002

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Ecological separation of two sibling species

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<i>Model parameters</i>	<i>50% UDs</i>		<i>90% UDs</i>	
	β	<i>95% CI</i>	β	<i>95% CI</i>
Species (<i>P.vitulina</i>)	-0.77	(-1.82 / 0.29)	-0.75	(-1.78 / 0.28)
Month (Oct)	0.62	(0.32 / 0.92)	0.46	(0.18 / 0.73)
Month (Nov)	0.51	(0.21 / 0.82)	0.40	(0.12 / 0.68)
Month (Dec)	1.02	(0.71 / 1.34)	0.80	(0.51 / 1.09)
Sex (male)	0.91	(0.10 / 1.71)	1.30	(0.50 / 2.10)
Mass	-0.04	(-0.07 / -0.01)	-0.05	(-0.08 / -0.01)

Ecological separation of two sibling species

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Model parameters	Dist. from haul-out		Max dist. from haul-out		Dive focus		Focal depth	
	β	95% CI	β	95% CI	β	95% CI	β	95% CI
Species (<i>P.vitulina</i>)	-0.38	(-1.06 / 0.31)	-0.03	(-0.49 / 0.44)	0.04	(0.01 / 0.07)	0.33	(-8.46 / 9.12)
Month (Oct)	0.39	(0.21 / 0.57)	0.43	(0.05 / 0.81)	0.01	(0.00 / 0.02)	5.17	(2.44 / 7.91)
Month (Nov)	0.60	(0.39 / 0.81)	0.37	(-0.04 / 0.77)	0.00	(-0.01 / 0.01)	4.54	(1.73 / 7.34)
Month (Dec)	0.85	(0.63 / 1.07)	0.49	(0.03 / 0.96)	0.01	(0.00 / 0.02)	12.28	(9.48 / 15.07)
Sex (male)	0.68	(0.12 / 1.24)	0.24	(-0.14 / 0.62)	-0.04	(-0.07 / -0.02)	7.89	(0.60 / 15.19)
Mass	-0.02	(-0.04 / 0.00)	-0.02	(-0.03 / 0.00)	0.00	(0.00 / 0.00)	-0.18	(-0.45 / 0.10)
Species(Vit):Month(Oct)	-0.08	(-0.49 / 0.34)	-0.72	(-1.68 / 0.23)	0.01	(-0.01 / 0.04)	-2.18	(-9.42 / 5.06)
Species(Vit):Month(Nov)	-0.15	(-0.69 / 0.40)	0.21	(-0.08 / 1.23)	-0.01	(-0.04 / 0.03)	-9.51	(-17.46 / -1.56)
Species(Vit):Month(Dec)	0.09	(-0.53 / 0.70)	0.22	(-0.86 / 1.30)	0.03	(0.00 / 0.07)	-2.56	(-10.86 / 5.73)
Model parameters	Mean dive depth		Max dive depth		Mean dive duration		Max dive duration	
	β	95% CI	β	95% CI	β	95% CI	β	95% CI
Species (<i>P.vitulina</i>)	1.39	(-3.66 / 6.44)	-1.71	(-9.64 / 6.22)	0.29	(-0.14 / 0.72)	1.22	(-0.12 / 2.56)
Month (Oct)	3.49	(2.14 / 4.85)	5.20	(3.12 / 7.27)	0.16	(0.06 / 0.26)	0.17	(-0.13 / 0.48)
Month (Nov)	3.39	(1.99 / 4.80)	5.62	(3.46 / 7.78)	0.28	(0.17 / 0.38)	0.16	(-0.15 / 0.48)
Month (Dec)	8.86	(7.46 / 10.25)	12.65	(10.49 / 14.80)	0.73	(0.62 / 0.83)	0.27	(-0.04 / 0.58)
Sex (male)	2.95	(-1.66 / 7.56)	7.58	(0.57 / 14.58)	-0.09	(-0.50 / 0.31)	-0.44	(-1.76 / 0.89)
Mass	2.92	(-0.69 / 7.53)	-0.01	(-0.37 / 0.17)	0.01	(0.00 / 0.03)	0.03	(-0.02 / 0.09)
Species(Vit):Month(Oct)	-0.82	(-4.10 / 2.47)	-2.55	(-7.52 / 2.43)	-0.11	(-0.36 / 0.14)	0.73	(-0.02 / 1.48)
Species(Vit):Month(Nov)	-4.59	(-8.33 / -0.86)	-8.83	(-14.48 / -3.17)	-0.15	(-0.43 / 0.12)	0.30	(-0.53 / 1.13)
Species(Vit):Month(Dec)	-0.05	(-3.80 / 3.70)	-5.24	(-10.93 / 0.46)	0.20	(-0.07 / 0.48)	0.30	(-0.53 / 1.13)

Ecological separation of two sibling species

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2 **Supporting information**

3 Additional Supporting Information may be found in the online version of this article:

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5 **Appendix S1.** Additional information on satellite telemetry.

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7 **Table S1.** Microsatellite loci used in this study.

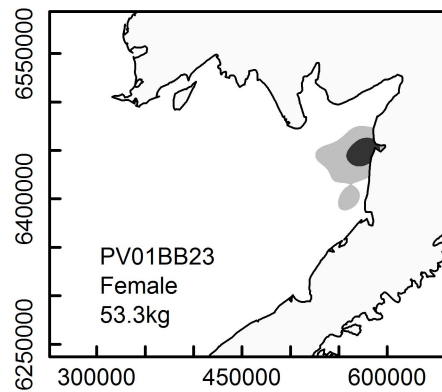
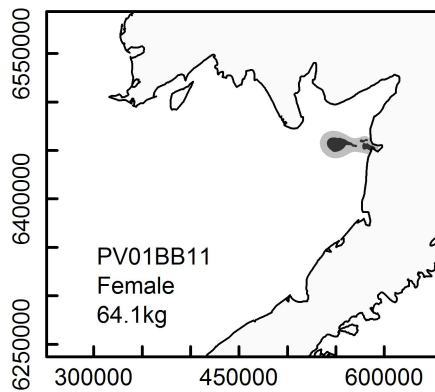
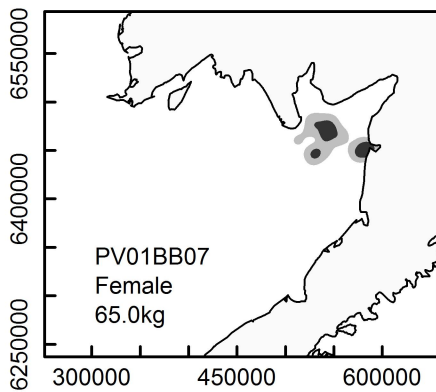
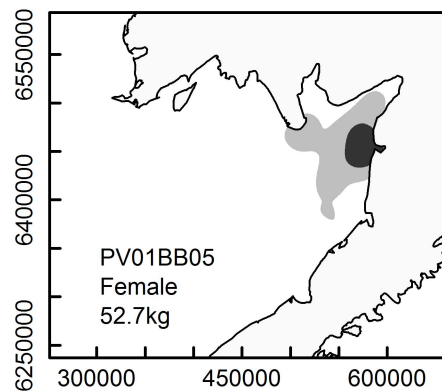
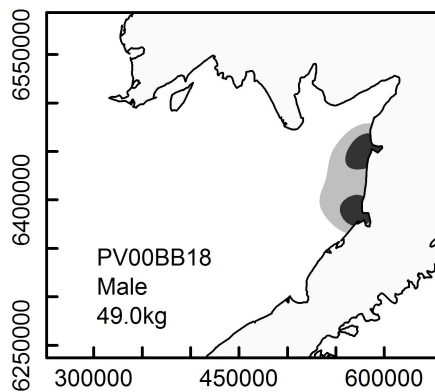
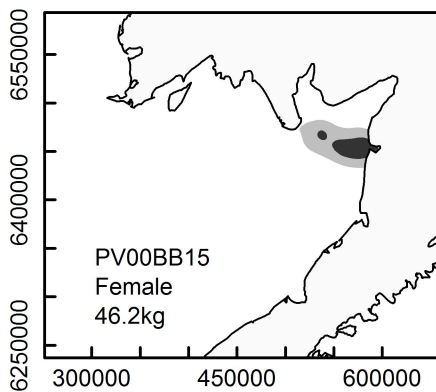
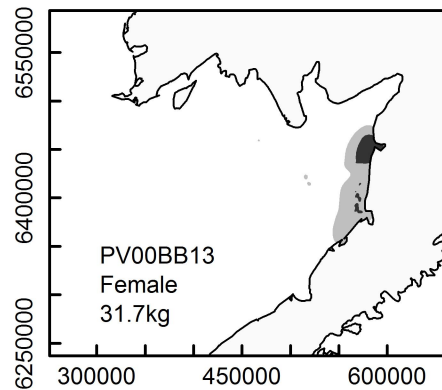
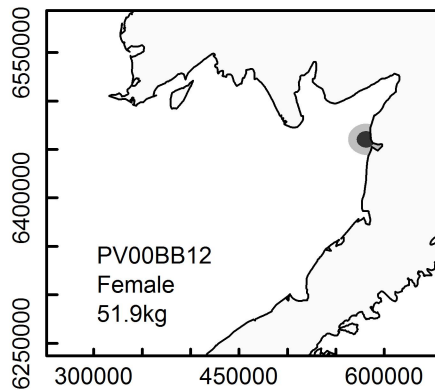
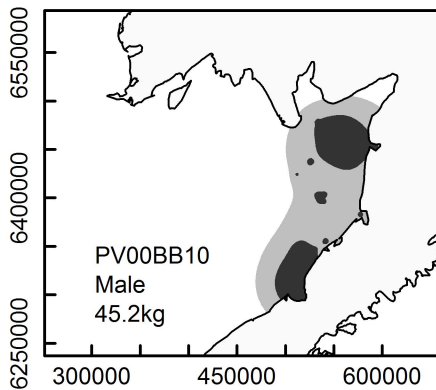
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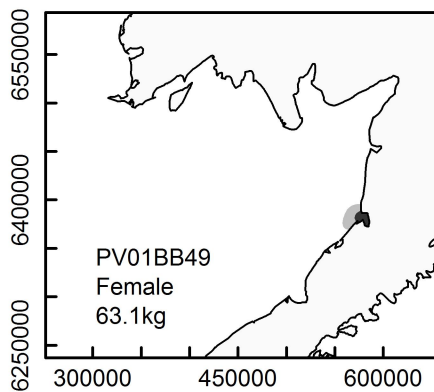
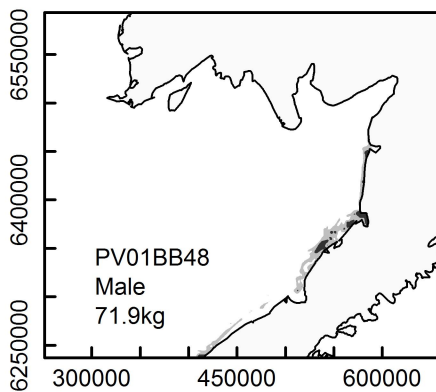
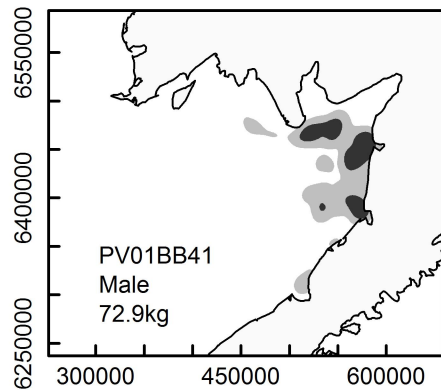
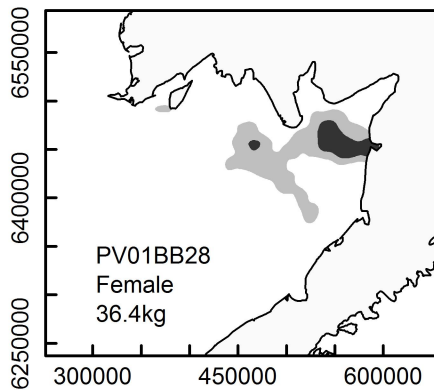
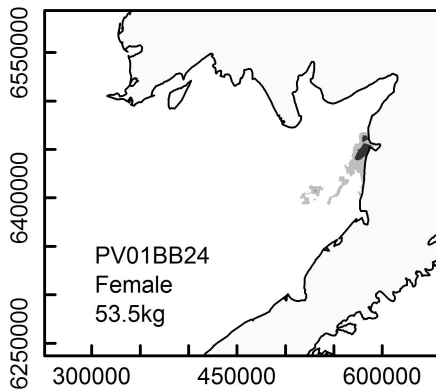
9 **Table S2.** Model selection for movement analyses.

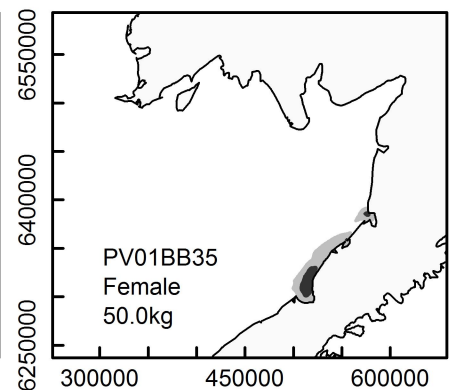
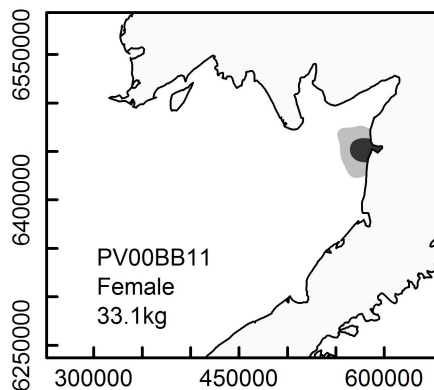
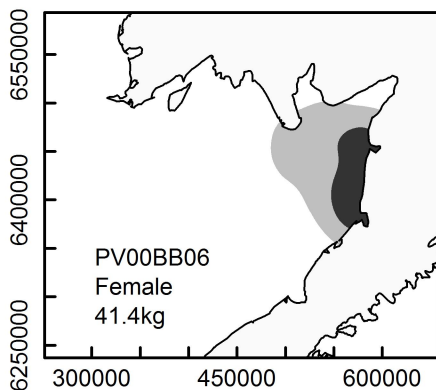
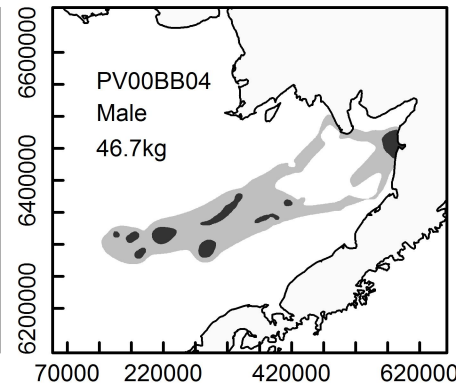
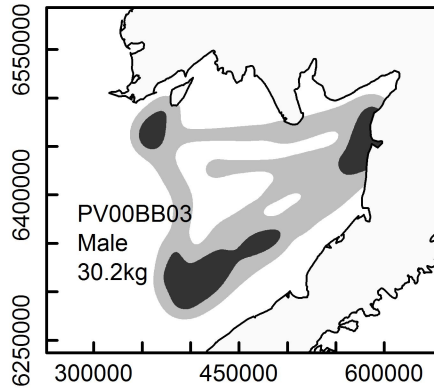
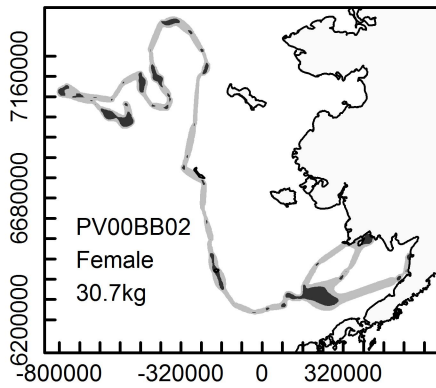
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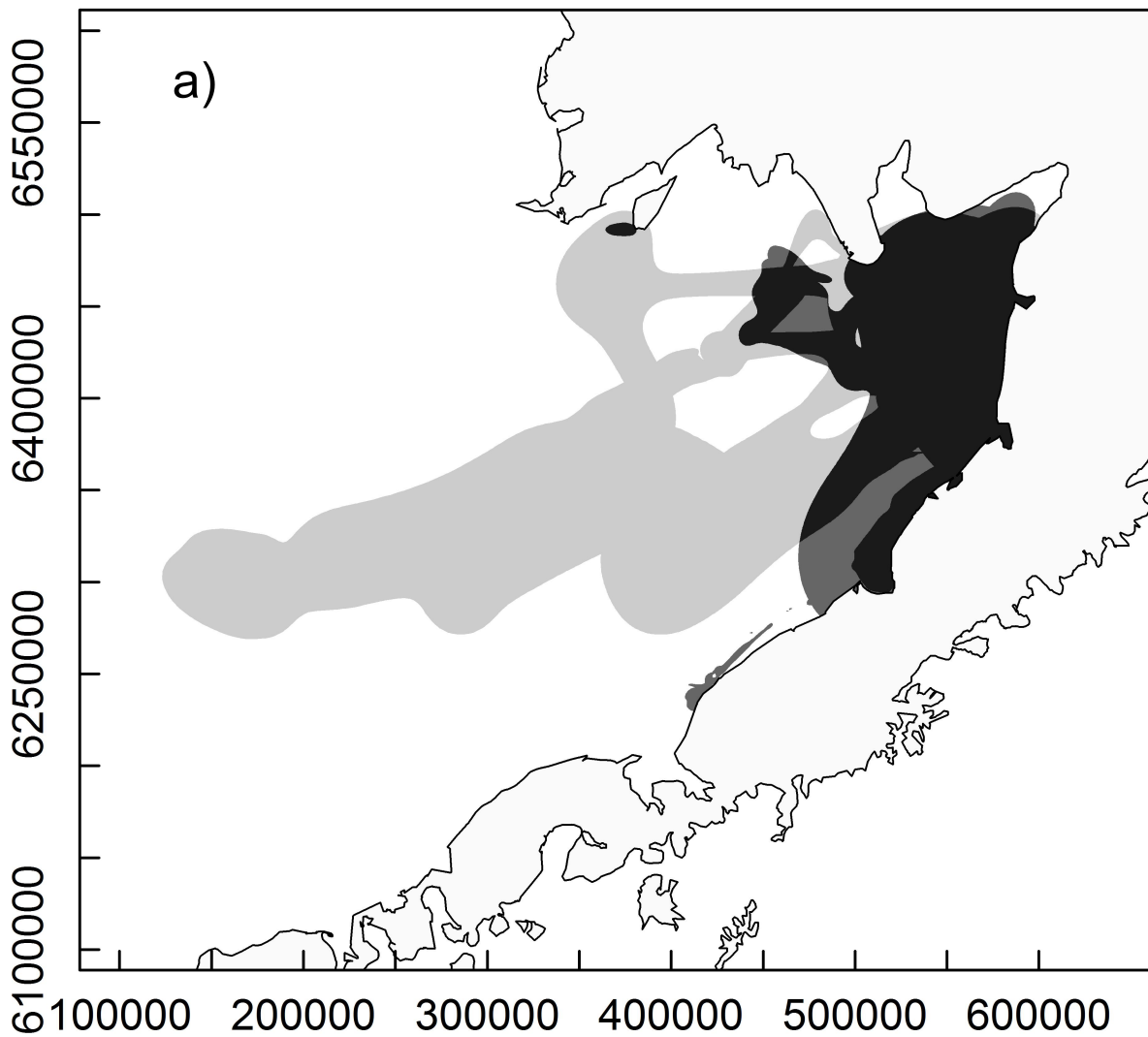
11 **Table S3.** Model selection for dive behaviour analyses.

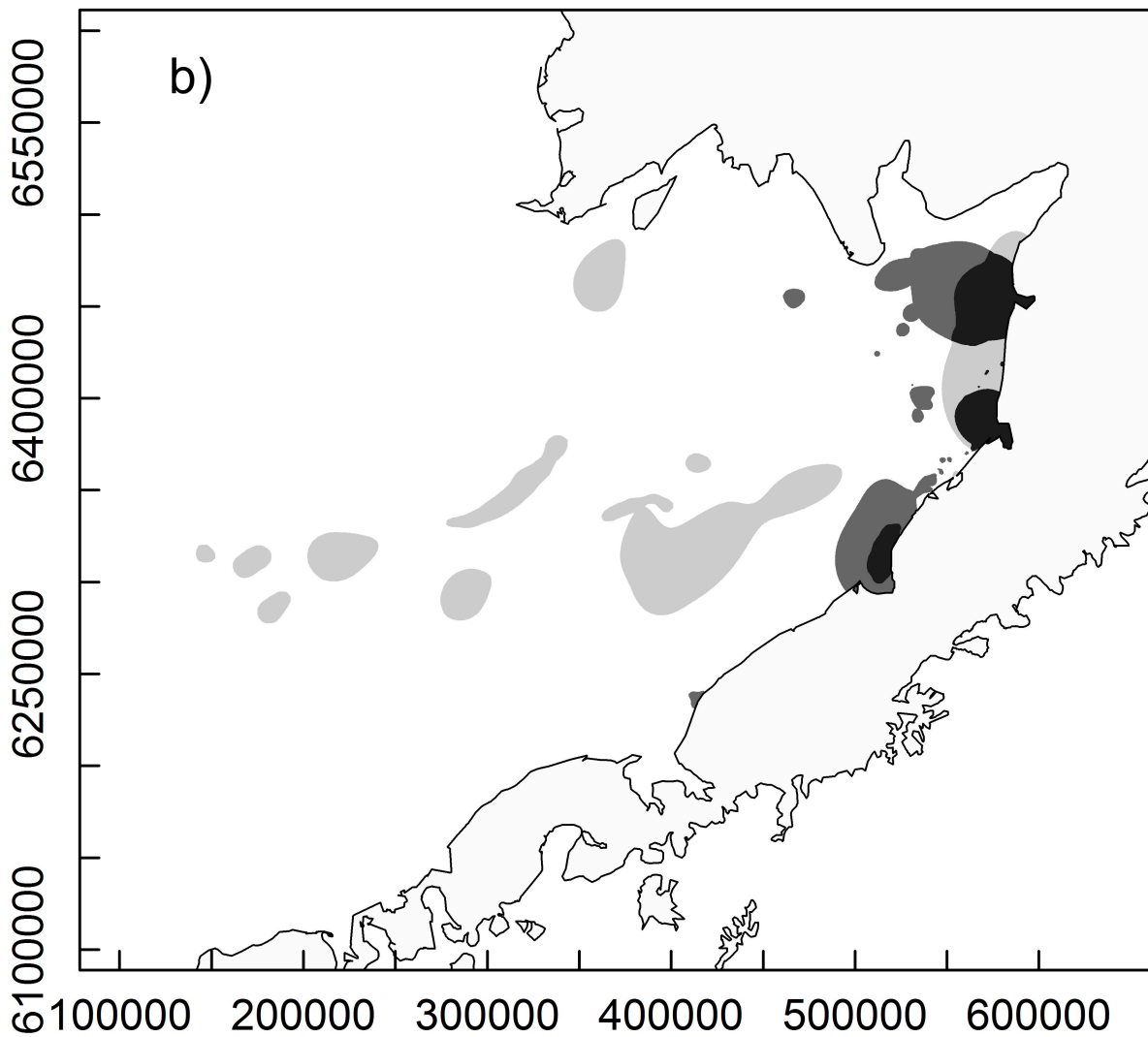
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□ *P.vitulina* ■ *P.largha*