Supplementary Information for

Perturbation drives changing metapopulation dynamics in a top marine predator

Emma L. Carroll1,2,3\*, Ailsa Hall3, Morten Tange Olsen4, Aubrie B. Onoufriou2,Oscar E. Gaggiotti2 and Debbie JF Russell3

1. School of Biological Sciences, University of Auckland, Auckland 1010, New Zealand

2. Scottish Oceans Institute and School of Biology, University of St Andrews, St Andrews, KY16 8LB, UK

3. Sea Mammal Research Unit, University of St Andrews, St Andrews, KY16 8LB, UK

4. Section for Evolutionary Genomics, GLOBE Institute, University of Copenhagen, Denmark

Emma Carroll

Email: [carrollemz@gmail.com](mailto:carrollemz@gmail.com)

**This PDF file includes:**

Supplementary text

Figure S1

Tables S1 to S7

SI References

Supplementary Information Text

**Supplementary Material: Microsatellite genotyping and analysis, details of satellite tracking tag deployment**

**Methods.**

*Microsatellite genotyping:* A total of 14 microsatellite loci were amplified in single reactions under conditions and reaction mixtures specified in Table S1. Amplicons were co-loaded for capillary electrophoresis on an ABI 3730. Alleles were sized using the *Geneious V7* microsatellite plugin (1) and all automated calling was confirmed visually (2). Linkage disequilibrium (LDE) and deviations from the Hardy-Weinberg equilibrium (HWE) were tested using *GENEPOP* (10,000 dememorization steps, 100 steps, 10,000 iterations per batch) at each haul-out site. Loci were considered to be out of HWE or in LDE if the calculated statistic was *p* < 0.005 (based on the conservative sequential Bonferroni calculation based on α = 0.05/11 = 0.0045) and found in more than three of the UK haul-out sites (only sites with *n* > 10 considered). Patterns found at multiple sampling sites were considered more likely to be indicative of genome-wide patterns than sample size related issues. Null alleles were investigated using program *CERVUS* (3).

*BayesAss*: In order to understand migration and genetic connectivity over recent time scales, we used program *BayesAss* (4). The program estimates immigration rates over the past two generations using gametic disequilibrium signal generated by immigrant individuals or their descendants. We conducted four *BayesAss* runs, each consisting of ten million iterations with initial burn-ins of one million iterations. Parameters were sampled every 1000 iterations and convergence was confirmed by visual checking in *TRACER v1.6* (5) and by confirming that the independent runs converged on similar values. We report median migration rates with 95% HPD interval from all runs and the mean assignment probabilities of individuals across the four runs. The patterns of connectivity, in terms of migration rates and ancestry of individuals, was used to infer connectivity over the past two generations. As samples were collected between 2003 and 2012 and the harbour seal is estimated to have a 14.8 year generation span (6), the approximate timings for the migration estimates are 1993 to 2007 (taking midpoint of the samples) for the past one generation, clearly spanning the recent decline (peri-perturbation), and 1977 to 1992 for the second generation, clearly preceding the recent decline (pre-perturbation).

*Tracking data:* We determined movement behaviour in non-pup seals (>1 year old) using Argos satellite relay data loggers (SRDLs) or GPS/GSM phone tags (developed and supplied by the SMRU Instrumentation Group) deployed between 2001 and 2017 on 334 harbour seals in eight of the SMUs (Tables 1 and S5: for details see Supplementary Material).

Telemetry tags were attached to the fur at the back of the neck using fast-setting two-part epoxy adhesive or Loctite® 422 Instant Adhesive. Locational data from the SRDLs are subject to location error, so we used a Kalman Filter to estimate locations (7) and any erroneous locations from the GPS/GSM phone tags were also removed (8). The duration of the telemetry tags is less than one year as the tags fall off during the annual moult in August. To minimise bias associated with variations in tag longevity, we excluded deployment durations of less than four weeks with tag durations ranging from 28 to 243 days (mean 95 days). The tags send data remotely and thus do not have to be recovered, such that there is no relationship between movements and data recovery. However, at-sea movements during the summer breeding season may be affected by breeding status, for example, there may be movement between regions associated with breeding. Breeding status of tagged individuals is not known so to ensure estimated movement rates were comparable between regions, we excluded data collected during the breeding season (June to July).

**Results.**

*Microsatellite genotyping:* No significant LDE was observed and no loci showed significant deviation from the HWE at more than three sampling sites. No loci showed null alleles across sampling sites. The final dataset therefore comprised 269 individuals that were genotyped at an average of 11.5 loci. Given their small sample sizes, the West England and Wales Management Unit was removed (n = 2) and the samples from France (n = 3) and the Dutch Wadden Sea (n = 9) were combined to represent the Southern European region. Samples from animals captured in Loch Sheildaig (n = 6) were included in the broader West Scotland dataset but significance testing for *FST* analyses are not reported due to the uncertainty associated with the small sample size.

*BayesAss:* See main manuscript.

*Tracking data:* See main manuscript

Fig. S1. Plot of the isolation by distance analysis, comparing FST and log of at-sea distance between haul out sites.

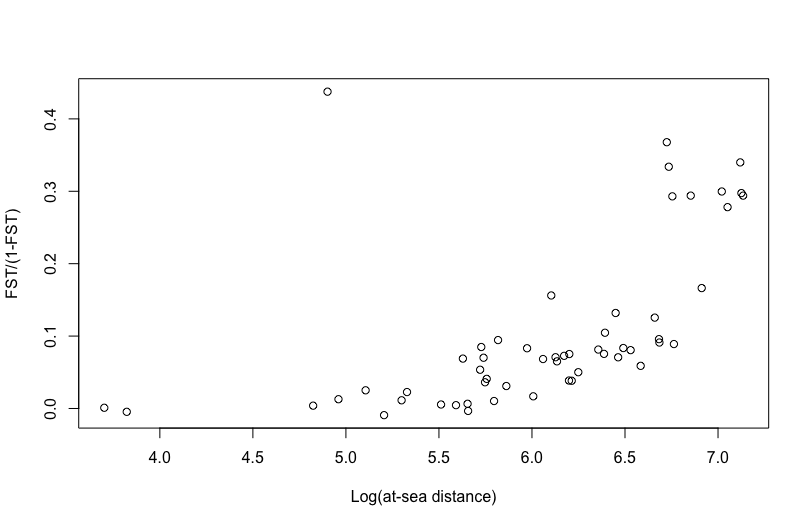


Table S1. Pairwise FST values for the Seal Management Units (SMU) and local populations (LP) of UK harbour seals, with sample size (n) and metapopulation membership (M: northern (N) or southern (S)) for each partition listed. West Scotland SMU (WS) southern (WS-S) and central subunits (WS-C) are also considered here. The bottom quadrant shows pairwise FST values per sampling location Loch Sheildaig n=6; results not reported due to small sample size (but included in NW group analyses). For acronyms, see Table 1. P-values of comparisons represented by astrixes: \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | NW (n = 90) | | |  | MFNCO (n = 79) | |  |  |  |  |  |
|  |  |  | NIR | ISJ | LIS | SKY | WIS | ORK | PF | MF | SH | ESC | SEE | EUR |
| M | LP | n | 20 | 30 | 22 | 17 | 15 | 34 | 13 | 32 | 14 | 28 | 24 | 12 |
| N |  | NIR |  |  | 0.023\* | |  |  | 0.053\*\*\* |  | 0.082\*\*\* | 0.143\*\*\* | 0.254\*\*\* | 0.214\*\*\* |
| N | NW | WS-S (Islay) | 0.022\* |  |  |  |  |  |  |  |  |  |  |  |
|  |  | WS-S (Lismore) | 0.005 | 0.000 |  |  |  |  | 0.040\*\*\* |  | 0.066\*\*\* | 0.085\*\*\* | 0.217\*\*\* | 0.174\*\*\* |  |
|  |  | WS-C (Skye) | 0.037\* | 0.000 | 0.005 |  |  |  |  |  |  |  |  |  |
|  |  | WI | 0.017 | 0.011 | 0.000 | 0.004 |  |  |  |  |  |  |  |  |
| N | MFNCO | NCO  (Orkney) | 0.056\*\*\* | 0.048\*\*\* | 0.037\*\*\* | 0.039\*\*\* | 0.030\* |  |  |  |  |  |  |  |
|  |  | NCO  (Pentland Firth) | 0.075\*\*\* | 0.068\*\*\* | 0.061\*\*\* | 0.065\*\*\* | 0.035\* | 0.001 |  |  | 0.032\*\*\* | 0.072\*\*\* | 0.227\*\*\* | 0.180\*\*\* |
|  |  | MF | 0.084\*\*\* | 0.070\*\*\* | 0.075\*\*\* | 0.077\*\*\* | 0.064\*\*\* | 0.013 | 0.006 |  |  |  |  |  |
| N |  | SH | 0.082\*\*\* | 0.077\*\*\* | 0.066\*\*\* | 0.066\*\*\* | 0.070\*\*\* | 0.025\*\* | 0.010 | 0.051\*\*\* |  | 0.135\*\*\* | 0.227\*\*\* | 0.152\*\*\* |
| N |  | ESC | 0.143\*\*\* | 0.087\*\*\* | 0.112\*\*\* | 0.095\*\*\* | 0.117\*\*\* | 0.086\*\*\* | 0.078\*\*\* | 0.065\*\*\* | 0.135\*\*\* |  | 0.304\*\*\* | 0.235\*\*\* |
| S |  | SEE | 0.254\*\*\* | 0.229\*\*\* | 0.227\*\*\* | 0.231\*\*\* | 0.218\*\*\* | 0.227\*\*\* | 0.250\*\*\* | 0.269\*\*\* | 0.227\*\*\* | 0.304\*\*\* |  | 0.018\*\*\* |
| S |  | EUR | 0.214\*\*\* | 0.175\*\*\* | 0.179\*\*\* | 0.173\*\*\* | 0.167\*\*\* | 0.184\*\*\* | 0.181\*\*\* | 0.203\*\*\* | 0.152\*\*\* | 0.235\*\*\* | 0.018\*\*\* |  |

Table S2. Median estimates (and 95% HPD intervals) of the fraction of individuals in population i that are migrants derived from population j (per generation) from across four BayesAss analyses for all SMUs and both metapopulations.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | *i sink* | | | | | | |
| *j - source* | NIR | NW:  WI+WS | MFNCO  NCO/MF | SH | ESC | SEE | EUR |
| NIR | 0.676  (0.667, 0.703 | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.011  (<0.001, 0.046 | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.066) |
| NW:  WI+WS | 0.243  (0.182, 0.299) | 0.932  (0.879, 0.976) | 0.018  (<0.001, 0.070) | 0.064  (<0.001, 0.136) | 0.024  (<0.001, 0.086) | 0.015  (<0.001, 0.054) | 0.016  (<0.001, 0.062) |
| MFNCO  NCO/MF | 0.022  (<0.001, 0.069) | 0.042  (0.006, 0.095) | 0.947  (0.885, 0.985) | 0.187  (0.103, 0.268) | 0.131  (0.033, 0.230) | 0.019  (<0.001, 0.062) | 0.020  (<0.001, 0.069) |
| SH | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.682  (0.667, 0.713) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.066) |
| ESC | 0.010  (<0.001, 0.040 | 0.005  (<0.001, 0.022) | 0.009  (<0.001, 0.030) | 0.012  (<0.001, 0.048) | 0.791  (0.705, 0.891) | 0.009  (<0.001, 0.038) | 0.018  (<0.001, 0.065) |
| SEE | 0.007  (<0.001, 0.036) | 0.003  (<0.001, 0.013) | 0.008  (<0.001, 0.026) | 0.012  (<0.001, 0.047) | 0.012  (<0.001, 0.042) | 0.914  (0.854, 0.967) | 0.193  (0.121, 0.264) |
| EUR | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.015) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.045) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.689  (0.667, 0.730) |

**Table S3:** BayesAss: Median estimates (and 95% HPD intervals) of the fraction of individuals in population *i* that are migrants derived from population *j* (per generation) for each of the four runs of the program, for the entire dataset.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *i* | | | | | | | |
| 1. |  | NIR 0 | WSC/WIS | NCO/MF | SH | ESC | SEE | EUR |
| *j* | NIR | 0.675  (0.667, 0.703) | 0.002  (<0.001, 0.011) | 0.003  (<0.001, 0.011) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.019  (<0.001, 0.066) |
| WSC/WIS | 0.247  (0.183, 0.301) | 0.933  (0.883, 0.976) | 0.020  (<0.001, 0.099) | 0.064  (<0.001, 0.136) | 0.025  (<0.001, 0.090) | 0.015  (<0.001, 0.055) | 0.017  (<0.001, 0.063) |
| NCO/MF | 0.021  (<0.001, 0.067) | 0.043  (0.006, 0.091) | 0.945  (0.863, 0.986) | 0.187  (0.100, 0.267) | 0.124  (0.033, 0.224) | 0.019  (<0.001, 0.062) | 0.019  (<0.001, 0.068) |
| SH | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.680  (0.667, 0.713) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.065) |
| ESC | 0.010  (<0.001, 0.041) | 0.005  (<0.001, 0.020) | 0.009  (<0.001, 0.029) | 0.012  (<0.001, 0.048) | 0.795  (0.708, 0.891) | 0.009  (<0.001, 0.038) | 0.018  (<0.001, 0.065) |
| SEE | 0.009  (<0.001, 0.036) | 0.003  (<0.001, 0.013) | 0.008  (<0.001, 0.025\_ | 0.012  (<0.001, 0.047) | 0.012  (<0.001, 0.042) | 0.914  (0.850, 0.966) | 0.193  (0.122, 0.263) |
| EUR | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.031) | 0.684  (0.667, 0.730) |
|  |  |  |  |  |  |  |  |  |
| 2. | i | NIR | WSC/WIS | NCO/MF | SH | ESC | SEE | EUR |
| *j* | NIR  0 | 0.680  (0.667, 0.703) | 0.003  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.066) |
| WSC/WIS  1 | 0.243  (0.182, 0.299) | 0.930  (0.882, 0.973) | 0.018  (<0.001, 0.061) | 0.062  (<0.001, 0.136) | 0.023  (<0.001, 0.084) | 0.015  (<0.001, 0.055) | 0.016  (<0.001, 0.062) |
| NCO/MF  2 | 0.023  (<0.001, 0.068) | 0.046  (0.006, 0.092) | 0.947  (0.898, 0.983) | 0.187  (0.104, 0.268) | 0.131  (0.029, 0.231) | 0.019  (<0.001, 0.062) | 0.019  (<0.001, 0.068) |
| SH  3 | 0.009  (<0.001, 0.037) | 0.003  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.678  (0.667, 0.713) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.031) | 0.018  (<0.001, 0.065) |
| ESC  4 | 0.010  (<0.001, 0.040) | 0.006  (<0.001, 0.024) | 0.010  (<0.001, 0.031) | 0.012  (<0.001, 0.047) | 0.791  (0.702, 0.900) | 0.010  (<0.001, 0.039) | 0.018  (<0.001, 0.065) |
| SEE  5 | 0.009  (<0.001, 0.036) | 0.003  (<0.001, 0.013) | 0.008  (<0.001, 0.024) | 0.011  (<0.001, 0.047) | 0.012  (<0.001, 0.041) | 0.913  (0.853, 0.967) | 0.193  (0.117, 0.261) |
| EUR  6 | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.007  (<0.001, 0.032) | 0.684  (0.667, 0.730) |
|  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |
| 3. |  | NIR | WSC/WIS | NCO/MF | SH | ESC | SEE | EUR |
| *j* | NIR | 0.676  (0.667, 0.703) | 0.003  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.067) |
| WSC/WIS | 0.245  (0.180,0.298) | 0.933  (0.880, 0.978) | 0.017  (<0.001, 0.065) | 0.066  (0.002, 0.140) | 0.024  (<0.001, 0.086) | 0.014  (<0.001, 0.052) | 0.016  (<0.001, 0.061) |
| NCO/MF | 0.022  (<0.001, 0.069) | 0.045  (0.004, 0.098) | 0.948  (0.892, 0.985) | 0.184  (0.099,0.263) | 0.128  (0.028, 0.223) | 0.018  (<0.001, 0.060) | 0.019  (<0.001, 0.068) |
| SHT | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.678  (0.667, 0.713) | 0.007  (<0.001, 0.029) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.067) |
| ESC | 0.010  (<0.001, 0.041) | 0.006  (<0.001, 0.022) | 0.009  (<0.001, 0.030) | 0.012  (<0.001, 0.049) | 0.797  (0.708, 0.894) | 0.009  (<0.001, 0.037) | 0.019  (<0.001, 0.067) |
| SEE | 0.009  (<0.001, 0.036) | 0.003  (<0.001, 0.013) | 0.008  (<0.001, 0.025) | 0.012  (<0.001, 0.047) | 0.012  (<0.001, 0.043) | 0.916  (0.857, 0.968) | 0.193  (0.122, 0.265) |
| EUR | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001,0.032) | 0.684  (0.667, 0.730) |
|  |  |  |  |  |  |  |  |  |
| 4 |  | NIR | WSC/WIS | NCO/MF | SH | ESC | SEE | EUR |
| *j* | NIR | 0.676  (0.667, 0.703) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.046) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.065) |
| WSC/WIS | 0.242  (0.182, 0.300) | 0.929  (0.876, 0.974) | 0.017  (<0.001, 0.061) | 0.062  (<0.001, 0.133) | 0.023  (<0.001, 0.084) | 0.015  (<0.001, 0.054) | 0.016  (<0.001, 0.062) |
| NCO/MF | 0.022  (<0.001, 0.070) | 0.048  (0.009, 0.101) | 0.948  (0.898, 0.984) | 0.188  (0.104, 0.268) | 0.139  (0.039, 0.231) | 0.020  (<0.001, 0.063) | 0.021  (<0.001, 0.070) |
| SH | 0.009  (<0.001, 0.037) | 0.003  (<0.001, 0.010) | 0.003  (<0.001, 0.011) | 0.678  (0.667, 0.713) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.018  (<0.001, 0.066) |
| ES | 0.010  (<0.001, 0.040) | 0.005  (<0.001, 0.021) | 0.008  (<0.001, 0.029) | 0.012  (<0.001, 0.048) | 0.783  (0.702, 0.884) | 0.009  (<0.001, 0.037) | 0.017  (<0.001, 0.065) |
| SEE | 0.009  (<0.001, 0.036) | 0.003  (<0.001, 0.013) | 0.010  (<0.001, 0.028) | 0.011  (<0.001, 0.047) | 0.012  (<0.001, 0.041) | 0.913  (0.853, 0.965) | 0.192  (0.121, 0.264) |
| EUR | 0.009  (<0.001, 0.036) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.012) | 0.011  (<0.001, 0.047) | 0.007  (<0.001, 0.028) | 0.008  (<0.001, 0.032) | 0.684  (0.667, 0.731) |

Table S4: Location and sample size of telemetry tags deployed.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Seal Management Unit - SubUnit | Area | Longitude | Latitude | nnon-pups | npups |
| West Scotland - south | Islay & Jura | -6.096 | 55.831 | 33 | 0 |
| West Scotland - south | Lismore | -5.526 | 56.501 | 0 | 24 |
| West Scotland - central | Shieldaig | -5.658 | 57.522 | 1 | 0 |
| West Scotland - central | Skye | -6.300 | 57.365 | 27 | 0 |
| Western Isles | Sound of Harris | -7.144 | 57.729 | 10 | 0 |
| Western Isles | Eriskay & Sound of Barra | -7.360 | 57.051 | 10 | 0 |
| North Coast & Orkney | Northern Orkney (Eday, Eynhallow, Rousay, Sanday, Stronsay) | -2.796 | 59.200 | 19 | 22 |
| North Coast & Orkney | Pentland Firth & /Southern Orkney | -3.114 | 58.738 | 34 | 0 |
| Shetland | Southern Shetland (Mousa & Cunnigsburgh) | -1.210 | 60.022 | 5 | 0 |
| Shetland | Yell Sound | -1.258 | 60.551 | 9 | 0 |
| Moray Firth | Dornoch Firth & Loch Fleet | -4.023 | 57.901 | 39 | 0 |
| Southeast Scotland | Firth of Tay and Eden Estuary SAC | -2.824 | 56.367 | 32 | 0 |
| Southeast Scotland | Kinghorn Rocks | -3.170 | 56.069 | 1 | 0 |
| Northern Ireland | Strangford Lough | -5.583 | 54.483 | 31 | 0 |
| Southeast England | Thames, Hadley Sands | 0.708 | 51.532 | 5 | 0 |
| Southeast England | Thames, Margate Sands | 1.377 | 51.389 | 14 | 0 |
| Southeast England | The Wash | 0.329 | 52.914 | 64 | 0 |
| Grand Total |  |  |  | 334 | 46 |

Table S5. Movement patterns of UK harbour seals (non-pups), as a proportion of the seals tagged in each Seal Management Unit (SMU) or SMU SubUnit (Tagging location) that moved to the SMU or SMU subunit indicated in the Location visited, during the tagging period. Sample size (*n*) represents the number of seals fitted with a location telemetry device in each SMU or SMU subunit (Tagging location), and Locations visited is the proportion of those tagged seals that moved from tagging location to another SMU or SMU SubUnit. Italicised values the proportion of tagged animals did not move out of the SMU in which the seal was tagged. Local population (LP) membership of each SMU is also listed.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| LP | Tagging location | | |  |  | Locations visited | | | | | | | | | | |  | |  | |  |
|  | SMU | Subunit | *n* | SW  Scotland |  | West Scotland | | |  | WI | NCO | SH | MF | ESC | SEE | NIR | | Ireland | | EUR | |
|  |  | South | Central | North |  |  |  |  |  |  |  |  | |  | |  | |
| NIR | NIR |  | 31 | - |  | - | - | - |  | - | - | - | - | - | - | *1* | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| NW | WI |  | 20 | - |  | - | 0.15 | - |  | *0.75* | - | - | - | - | - | - | | 0.05 | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| NW | WS | South | 33 | 0.24 |  | *0.7* | 0.03 | - |  | 0.03 | - | - | - | - | - | - | | - | | - | |
| Central | 28 | - |  | 0.04 | *0.93* | - |  | 0.04 | - | - | - | - | - | - | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| MFNCO | NCO |  | 53 | - |  | - | - | - |  | - | *0.96* | 0.02 | 0.02 | - | - | - | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| SH | SH |  | 14 | - |  | - | - | - |  | - | - | *1* | - | - | - | - | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| MFNCO | MF |  | 39 | - |  | - | - | - |  | - | 0.1 | - | *0.9* | - | - | - | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| ESC | ESC |  | 33 | - |  | - | - | - |  | - | - | - | - | *1* | - | - | | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  | |  | |
| - | SEE |  | 83 | - |  | - | - | - |  | - | - | - | - | - | *0.98* | - | | - | | 0.02 | |

**Table S6:** Median estimates (and 95% HPD intervals) of the fraction of individuals in population *i* that are migrants derived from population *j* (per generation) from across four *BayesAss* analyses for the northern metapopulation.

|  |
| --- |
|  |
|  | *i* | | | | |
| *j* | NIR | NW:  WI+WS | MFNCO:  NCO + MF | SH | ESC |
| NIR | 0.676  (0.667, 0.706) | 0.003  (<0.001, 0.014) | 0.003  (<0.001, 0.013) | 0.013  (<0.001, 0.051) | 0.007  (<0.001, 0.030) |
| NW:  WI+WS+SW | 0.262  (0.196, 0.314) | 0.911  (0.851, 0.968) | 0.021  (<0.001, 0.079) | 0.077  (<0.001, 0.160) | 0.024  (<0.001, 0.088) |
| MFNCO:  NCO/MF | 0.025  (<0.001, 0.079) | 0.003  (<0.001, 0.016) | 0.947  (0.883, 0.989) | 0.197  (0.108, 0.287) | 0.087  (<0.001, 0.178) |
| SH | 0.009  (<0.001, 0.040) | 0.002  (<0.001, 0.010) | 0.003  (<0.001, 0.015) | 0.680  (0.667, 0.720) | 0.007  (<0.001, 0.030) |
| ESC | 0.012  (<0.001, 0.048) | 0.013  (<0.001, 0.049) | 0.017  (<0.001, 0.052) | 0.014  (<0.001, 0.058) | 0.859  (0.764, 0.947) |

**Table S7:** Microsatellite loci used in this work, with citation, AT (Optimal Annealing Temp (°C)) and whether it was used in previous work (9).

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | Reference | AT | Previous |
| HG6.1 | (10) | 60 | No |
| Hg6.3 | (10) | 60 | Yes |
| Hgdii | (10) | 60 | Yes |
| Lc26 | (11) | 60 | Yes |
| Lc28 | (11) | 56 | Yes |
| Lw11 | (11) | 56 | Yes |
| Lw20 | (11) | 60 | No |
| Pvc19 | (12) | 54 | No |
| Pvc78 | (12) | 54 | Yes |
| Sgpv10 | (13) | 54 | Yes |
| Sgpv11 | (13) | 56 | Yes |
| SGPv3 | (14) | 60 | No |
| SGPv9 | (14) | 60 | No |
| TBPV2 | (15) | 54 | No |

**SI References**

1. M. Kearse, *et al.*, Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**, 1647–1649 (2012).

2. A. Bonin, *et al.*, How to track and assess genotyping errors in population genetics studies. *Mol. Ecol.* **13**, 3261–3273 (2004).

3. S. Kalinowski, M. Taper, T. Marshall, Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Mol. Ecol.* **9**, 801–888 (2007).

4. G. A. Wilson, B. Rannala, Bayesian inference of recent migration rates using multilocus genotypes. *Genetics* **163**, 1177–1191 (2003).

5. A. Rambaut, M. Suchard, D. Xie, A. Drummond, Tracer v1.6, Available from http://beast.bio.ed.ac.uk/Tracer (2014).

6. M. Pacifici, L. Santini, M. Di Marco, D. Baisero, Generation length for mammals. *Nat. Conserv.* **5**, 87–94 (2013).

7. E. L. Jones, *et al.*, Patterns of space use in sympatric marine colonial predators reveal scales of spatial partitioning. *Mar. Ecol. Prog. Ser.* **534**, 235–249 (2015).

8. D. J. F. Russell, *et al.*, Intrinsic and extrinsic drivers of activity budgets in sympatric grey and harbour seals. *Oikos* **124**, 1462–1472 (2015).

9. M. T. Olsen, *et al.*, Genetic population structure of harbour seals in the United Kingdom and neighbouring waters. *Aquat. Conserv. Mar. Freshw. Ecosyst.* **27**, 839–845 (2017).

10. P. J. Allen, W. Amos, P. P. Pomeroy, Microsatellite variation in grey seals (*Halichoerus grypus*) shows evidence of genetic differentiation between two British breeding colonies. *Mol. Ecol.* **4**, 653–662 (1995).

11. C. Davis, S. Gelatt, D. Siniff, C. Strobeck, Dinucleotide microsatellite markers from the Antarctic seals and their use in other Pinnipeds. *Mol. Ecol. Notes* **2**, 203–208 (2002).

12. D. Coltman, W. Don Bowen, J. Wright, PCR primers for harbour seal (Phoca vitulina concolour) microsatellites amplify polymorphic loci in other pinniped species. *Mol. Ecol.* **5**, 161–163 (1996).

13. S. Goodman, Patterns of extensive genetic differentiation and variation among European Harbor seals (*Phoca vitulina vitulina*) revealed using ... *Mol. Biol. Evol.* **15**, 104–118 (1998).

14. S. Goodman, “Molecular population genetics of the harbour seal (Phoca vitulina) with reference to the 1988 distemper virus epizootic,” Cambridge University. (1995).

15. T. Pastor, J. Garza, P. Allen, W. Amos, A. Aguilar, Low Genetic Variability in the Highly Endangered Mediterranean Monk Seal. *J. Hered.* **95**, 291–300 (2004).