# Post-glacial colonization of northern coastal habitat by bottlenose dolphins: A marine leading-edge expansion?

Electronic Supplementary Material

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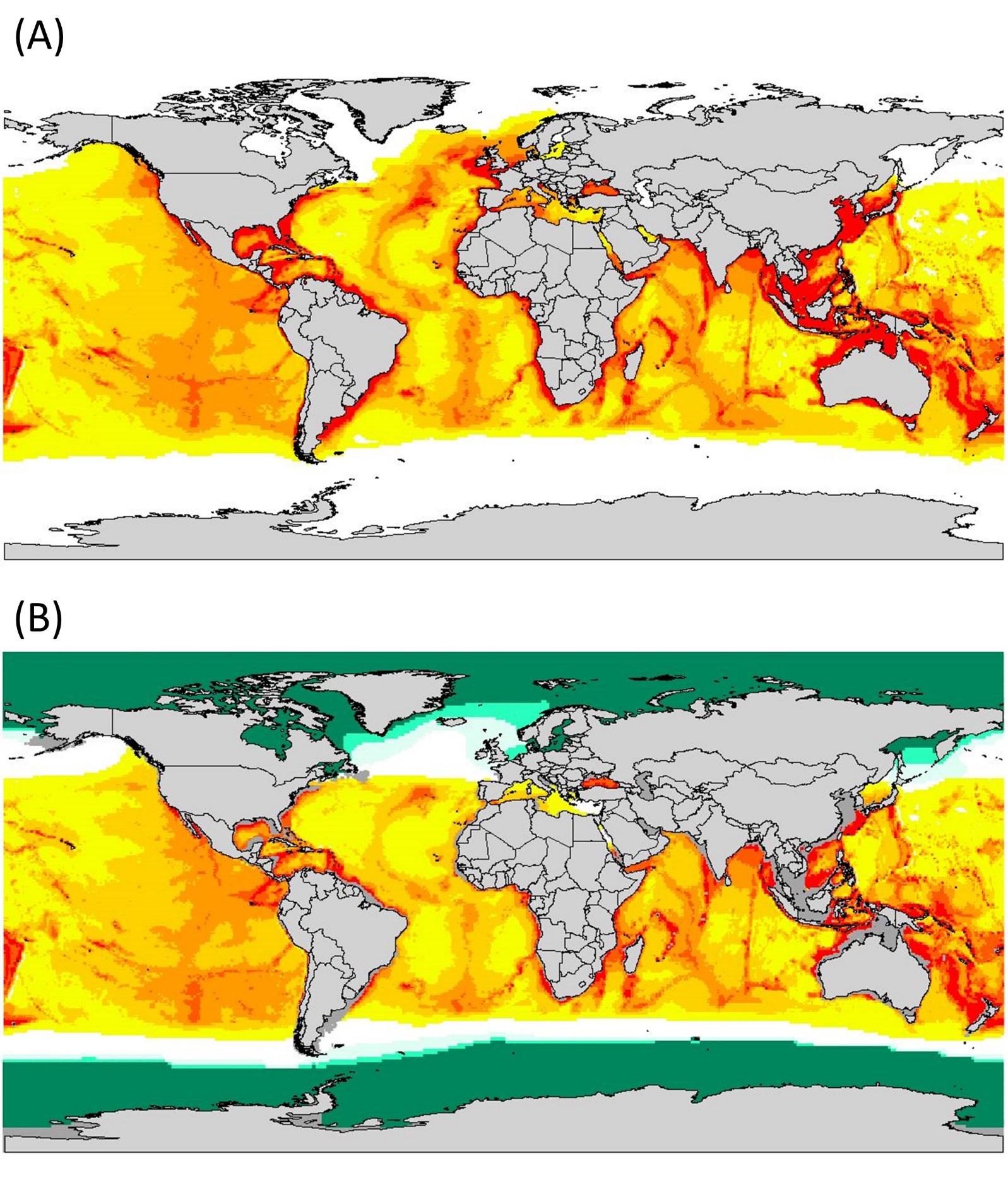
## **Appendix S1.** Whole mtDNA sequences/mitochondrial haplotypes downloaded from GenBank and used in the phylogenetic and coalescent analyses. Only the protein coding regions from these sequences were used in the estimation of time-calibrated phylogenies for delphinids and for the genus *Tursiops*. The numbers in brackets in the *Tursiops* spp*.* table indicate the number of samples found with the haplotype.

|  |  |  |
| --- | --- | --- |
| Delphinid phylogeny: | |  |
| Species | **Accession number** | **Reference** |
| *Cephalorhynchus heavisidii* | JN632624 | Hassanin *et al.*, 2012 |
| *Orcaella brevirostris* | JF289177 | Vilstrup *et al.*, 2011 |
| *Orcaella heinsohni* | JF339977 | Vilstrup *et al.*, 2011 |
| *Peponocephala electra* | JF289175 | Vilstrup *et al.*, 2011 |
| *Feresa attenuata* | JF289171 | Vilstrup *et al.*, 2011 |
| *Globicephala melas* | JF339972 | Vilstrup *et al.*, 2011 |
| *Globicephala macrorhynchus* | JF339976 | Vilstrup *et al.*, 2011 |
| *Pseudorca crassidens* | JF289173 | Vilstrup *et al.*, 2011 |
| *Grampus griseus* | EU557095 | Xiong *et al.*, 2009 |
| *Stenella attenuata* | EU557096 | Xiong *et al.*, 2009 |
| *Stenella coeruleoalba* | EU557097 | Xiong *et al.*, 2009 |
| *Delphinus capensis* | EU557094 | Xiong *et al.*, 2009 |
| *Sousa chinensis* | EU557091 | Xiong *et al.*, 2009 |
| *Tursiops truncatus* | EU557093 | Xiong *et al.*, 2009 |
| *Lagenorhynchus albirostris* | NC005278 | Arnason *et al.*, 2004 |
| *Orcinus orca*, resident ecotype | GU187192 | Morin *et al.*, 2010 |
| *Orcinus orca*, transient ecotype | GU187173 | Morin *et al.*, 2010 |
| *Steno bredanensis* | JF339982 | Vilstrup *et al.*, 2011 |

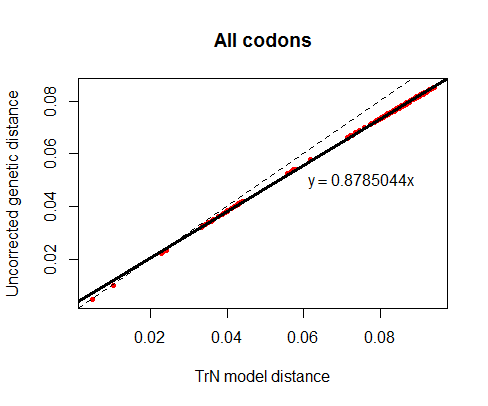
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genus *Tursiops* phylogeny: | | | | | |
| Species | **Haplotype name** | **Accession#** | **GenBank reference** | **Ecotype or population/sampling location** | **Ecotype reference** |
| *T. truncatus* | EMED3 | KF570315 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED4 | KF570316 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED5 | KF570317 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED1 | KF570318 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED2 | KF570319 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED10 | KF570320 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED6 | KF570321 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED9 | KF570322 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED7 | KF570323 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus* | EMED8 | KF570324 | Moura *et al.*, 2013 | Coastal/Eastern Mediterranean | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA2 | KF570325 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA3 | KF570326 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA1 | KF570327 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA6 | KF570328 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA7 | KF570329 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA5 | KF570330 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA4 | KF570331 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA8 | KF570332 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA9 | KF570333 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus ponticus* | BSEA10 | KF570334 | Moura *et al.*, 2013 | Coastal/Black Sea | Natoli *et al.*, 2005 |
| *T. truncatus* | WNAC11 | KF570370 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC13 | KF570371 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC14 | KF570372 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC16 | KF570373 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC19 | KF570374 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC22 | KF570375 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC23 | KF570376 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC25 | KF570377 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. truncatus* | WNAC8 | KF570378 | Moura *et al.*, 2013 | Coastal/Northwest Atlantic | Hoelzel *et al.*, 1998 |
| *T. aduncus* | IPTA1 | KF570335 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA2 | KF570336 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA3 | KF570337 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA4 | KF570338 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA5 | KF570339 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA6 | KF570340 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA7 | KF570341 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA8 | KF570344 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA9 | KF570343 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | IPTA10 | KF570342 | Moura *et al.*, 2013 | Coastal/Eastern Australia | Wang *et al.*, 1999; Möller & Beheregaray, 2001 |
| *T. aduncus* | SA101 | KF570353 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA102 | KF570354 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA115 | KF570355 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA116 | KF570356 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA120 | KF570357 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA133 | KF570358 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA26 | KF570359 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA95 | KF570360 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA98 | KF570361 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. aduncus* | SA99 | KF570362 | Moura *et al.*, 2013 | Coastal/South Africa | Natoli *et al.*, 2004 |
| *T. australis* | SABD1 | KF570364 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD2 | KF570365 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD3 | KF570366 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD4 | KF570369 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD5 | KF570367 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD6 | KF570368 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. australis* | SABD7 | KF570363 | Moura *et al.*, 2013 | Coastal/southern Australia | Charlton-Robb *et al.*, 2006; Möller *et al.*, 2008 |
| *T. truncatus* | ENAC1 (N=5) | KT601188 | This study | Coastal North/Shannon Estuary, West Ireland, West Scotland | Mirimin *et al.*, 2011; Louis *et al.*, 2014; Islas-Villanueva, 2010; Nykänen *et al.*, 2018 |
|  |  |  |  |  |  |
| *T. truncatus* | ENAC2 (N=1) | KT601189 | This study | Coastal North/West Ireland | Mirimin *et al.*, 2011; Nykänen *et al.*, 2018 |
| *T. truncatus* | ENAC3 (N=1) | KT601190 | This study | Coastal North/West Ireland | Mirimin *et al.*, 2011; Nykänen *et al.*, 2018 |
| *T. truncatus* | ENAC4 (N=6) | KT601191 | This study | Coastal North/Shannon Estuary, West Ireland, East Scotland, France, Wales | Mirimin *et al.*, 2011; Louis *et al.*, 2014; Islas-Villanueva, 2010; Nykänen *et al.*, 2018 |
| *T. truncatus* | ENAC5 (N=1) | KT601192 | This study | Coastal North/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAC6 (N=2) | KT601193 | This study | Coastal South/France, England | Louis *et al.*, 2014 |
| *T. truncatus* | ENAC7 (N=1) | KT601194 | This study | Coastal South/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAC8 (N=1) | KT601195 | This study | Coastal North/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAC9 (N=1) | KT601196 | This study | Coastal South/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP1 (N=1) | KT601197 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP2 (N=1) | KT601198 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP3 (N=1) | KT601199 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP4 (N=1) | KT601200 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP5 (N=1) | KT601201 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP6 (N=1) | KT601202 | This study | Pelagic NEA/France | Louis *et al.*, 2014 |
| *T. truncatus* | ENAP7 (N=1) | KT601203 | This study | Pelagic NEA/Ireland | Mirimin *et al.*, 2011; Nykänen *et al.*, 2018 |
| *T. truncatus* | ENAP8 (N=1) | KT601204 | This study | Pelagic NEA/Ireland | Mirimin *et al.*, 2011; Nykänen *et al.*, 2018 |
| *T. truncatus* | ENAP9 (N=1) | KT601205 | This study | Pelagic NEA/Wales | Islas-Villanueva, 2010 |
| *T. truncatus* | ENAP10 (N=1) | KT601206 | This study | Pelagic NEA/Wales | Islas-Villanueva, 2010 |
| *T. truncatus* | ENAP11 (N=1) | KT601207 | This study | Pelagic NEA/Wales | Louis *et al.*, 2014; Islas-Villanueva, 2010 |

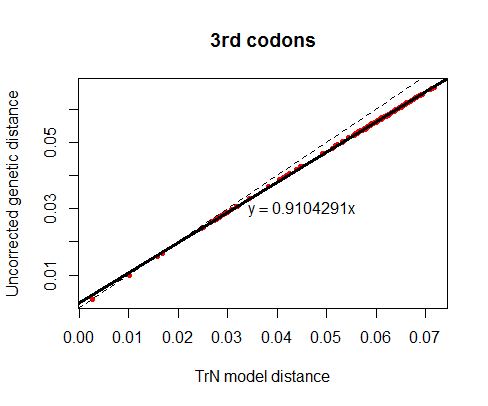
## Appendix S2. Best partitioning schemes for nucleotide substitution models used in the construction of the delphinid and *Tursiops* sp. time-calibrated phylogenies.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Delphinids: All codon model | | | | |
| **Partition** | | **Best model** | | **Subset partitions** |
| p1 | | HKY+I+G | | atp6, atp8, cox2, cox3, cytb, nd1, nd2, nd3, nd4, nd4l, nd5 |
| p2 | | HKY+I+G | | cox1 |
| p3 | | HKY+I+G | | nd6 |
|  |  | |  | |
| Delphinids: Third codon only model | | | | |
| **Partition** | | **Best model** | | **Subset partitions** |
| p1 | | TrN+I+G | | atp6, cox3, cytb, nd1, nd2, nd3, nd4, nd4l, nd5 |
| p2 | | TrN+G | | atp8, cox1, cox2 |
| p3 | | TrN+G | | nd6 |
|  |  | |  | |
| *Tursiops* sp: All codon model | | | | |
| **Partition** | | **Best model** | | **Subset partitions** |
| p1 | | HKY+I | | atp6, atp8, cox2, cox3, cytb, nd1, nd2, nd3, nd4, nd4l, nd5 |
| p2 | | HKY+G | | cox1 |
| p3 | | HKY+I | | nd6 |
|  |  | |  | |
| *Tursiops* sp: Third codon only model | | | | |
| **Partition** | | **Best model** | | **Subset partitions** |
| p1 | | TrN+G | | cox3, cytb, nd1, nd2, nd4, nd4l, nd5 |
| p2 | | TrN+I | | atp6, atp8, cox1, cox2, nd3 |
| p3 | | TrN | | nd6 |

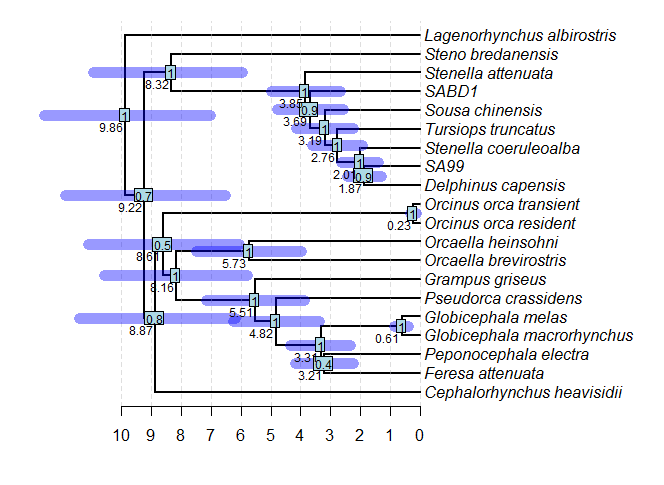
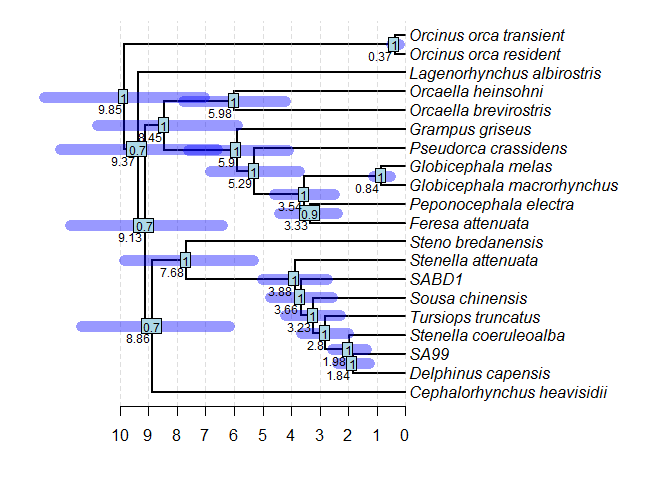


## Appendix S3. AquaMaps world-wide suitable habitat map for *T. truncatus* for (a) the present day, and (b) the Last Glacial Maximum. White to red colors represent least to most suitable habitat, respectively, and land is shown in light gray. Dark green color in Fig. (b) represents areas with permanent ice sheet and light green color areas with >50% sea ice concentration.





## Appendix S4. Uncorrected and TrN model-corrected genetic distances in the aligment consisting of 13 protein coding mtDNA genes of 20 delphinids. Red dots are the data values and the solid line represents their correlation. Dashed line represents linear regression with a slope of 1.



(A)

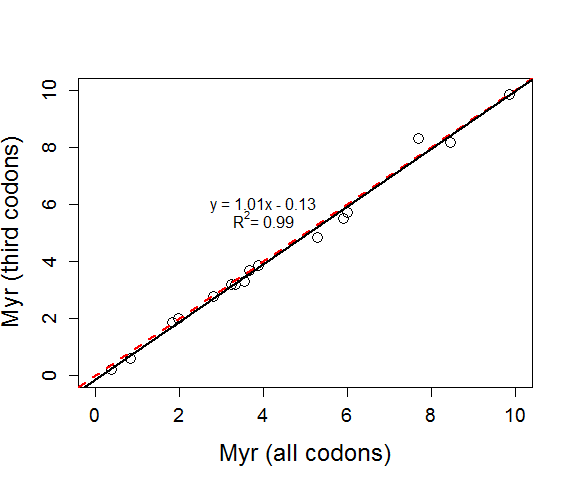
(B)

Myr

Myr



## Appendix S5. Time-calibrated phylogenetic tree for delphinids inferred with StarBEAST2 strict clock model using 13 mitochondrial genes and including (A) all codon positions, and (B) only the third codon positions. The numbers in rectangles are node posterior probabilities, numbers below nodes the mean TMRCA, and the bars represent 95% HPDI in TMRCA. SABD1 and SA99 are the most divergent *Tursiops* haplotypes representing *T. australis* and *T. aduncus* haplotypes from South Australia and South Africa, respectively. Illustrations by Uko Gorter (http://ukogorter.com).



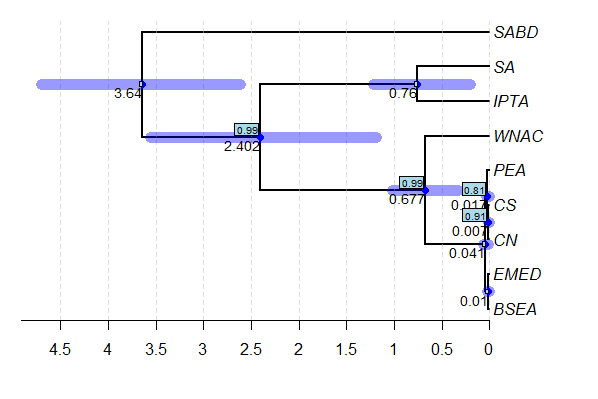
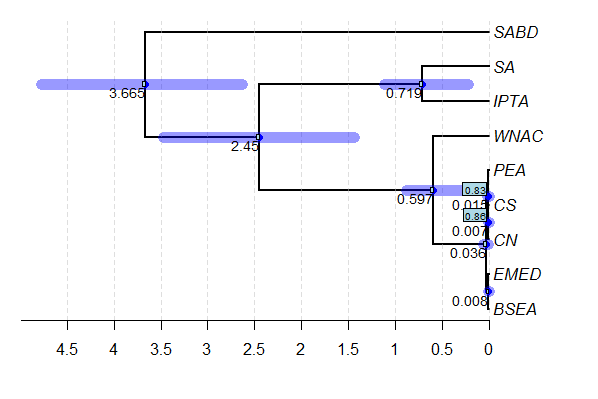
## Appendix S6. Correlation of TMRCA (mean) of the common nodes inferred from two different BEAST2 models of delphinid time-calibrated phylogeny, a model including all codon positions and a model using only the third codon positions. The solid black line is fitted to the data, and the dashed red line represents perfect linear correlation with a slope of 1.

## Appendix S7. The mean and Effective Sample Size (ESS) values for the different parameters in one run of the BEAST2 time-calibrated models for delphinids. The models were run with all codon positions and including only the third codon positions, both using a a strict clock.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| All codon model | | |  | 3rd codon model | | |
| Statistic | Mean | ESS |  | Statistic | Mean | ESS |
| posterior | -43897.3 | 3276 |  | posterior | -23151.4 | 3249 |
| likelihood | -43827.2 | 3563 |  | likelihood | -23044.3 | 2441 |
| prior | -70.1 | 4348 |  | prior | -107.1 | 2539 |
| treeLikelihood.atp6 | -2864.1 | 7353 |  | treeLikelihood.atp6\_pos3 | -1434.6 | 2265 |
| treeLikelihood.atp8 | -780.8 | 884 |  | treeLikelihood.atp8\_pos3 | -391.8 | 1680 |
| treeLikelihood.cox1 | -5340.5 | 5820 |  | treeLikelihood.cox1\_pos3 | -3005.5 | 4141 |
| treeLikelihood.cox2 | -2531.2 | 4681 |  | treeLikelihood.cox2\_pos3 | -1357.1 | 3078 |
| treeLikelihood.cox3 | -2835.7 | 3671 |  | treeLikelihood.cox3\_pos3 | -1512.6 | 3019 |
| treeLikelihood.cytb | -4482.6 | 1557 |  | treeLikelihood.cytb\_pos3 | -2308.9 | 4368 |
| treeLikelihood.nd1 | -3564.9 | 8629 |  | treeLikelihood.nd1\_pos3 | -1873.1 | 6392 |
| treeLikelihood.nd2 | -4189.5 | 8262 |  | treeLikelihood.nd2\_pos3 | -2158.3 | 5069 |
| treeLikelihood.nd3 | -1489.3 | 805 |  | treeLikelihood.nd3\_pos3 | -758.1 | 5288 |
| treeLikelihood.nd4 | -5244.0 | 6490 |  | treeLikelihood.nd4\_pos3 | -2743.8 | 6143 |
| treeLikelihood.nd4l | -1186.3 | 3252 |  | treeLikelihood.nd4l\_pos3 | -573.4 | 3952 |
| treeLikelihood.nd5 | -7345.2 | 2111 |  | treeLikelihood.nd5\_pos3 | -3841.3 | 4088 |
| treeLikelihood.nd6 | -1973.2 | 3415 |  | treeLikelihood.nd6\_pos3 | -1085.9 | 1878 |
| TreeHeight | 9.873 | 9001 |  | TreeHeight | 9.871 | 9001 |
| kappa.1 | 43.627 | 5131 |  | kappa1.1 | 164.484 | 810 |
| kappa.2 | 56.998 | 4669 |  | kappa1.2 | 107.570 | 1247 |
| kappa.3 | 40.449 | 4330 |  | kappa1.3 | 49.071 | 1730 |
| gammaShape.1 | 1.050 | 151 |  | kappa2.1 | 60.929 | 1424 |
| gammaShape.2 | 0.628 | 426 |  | kappa2.2 | 58.129 | 1581 |
| gammaShape.3 | 0.687 | 472 |  | kappa2.3 | 87.791 | 791 |
| proportionInvariant.1 | 0.537 | 152 |  | proportionInvariant.1 | 0.077 | 2727 |
| proportionInvariant.2 | 0.518 | 360 |  | gammaShape.1 | 3.515 | 3157 |
| proportionInvariant.3 | 0.475 | 386 |  | gammaShape.2 | 1.163 | 5270 |
| clockRate | 0.007 | 9001 |  | gammaShape.3 | 1.304 | 4056 |
| CalibratedYuleModel | -41.426 | 9001 |  | clockRate | 0.017 | 8298 |
| birthRateY | 0.075 | 9001 |  | CalibratedYuleModel | -41.325 | 8441 |
| logP(mrca(root)) | -1.804 | 9001 |  | birthRateY | 0.082 | 8318 |
| mrcatime(root) | 9.873 | 9001 |  | logP(mrca(root)) | -1.780 | 8528 |
|  |  |  |  | mrcatime(root) | 9.871 | 9001 |
|  |  |  |  | freqParameter.11 | 0.436 | 1135 |
|  |  |  |  | freqParameter.12 | 0.333 | 1254 |
|  |  |  |  | freqParameter.13 | 0.024 | 567 |
|  |  |  |  | freqParameter.14 | 0.207 | 1890 |
|  |  |  |  | freqParameter.21 | 0.421 | 1625 |
|  |  |  |  | freqParameter.22 | 0.267 | 1903 |
|  |  |  |  | freqParameter.23 | 0.050 | 987 |
|  |  |  |  | freqParameter.24 | 0.261 | 1812 |
|  |  |  |  | freqParameter.31 | 0.221 | 1674 |
|  |  |  |  | freqParameter.32 | 0.032 | 579 |
|  |  |  |  | freqParameter.33 | 0.239 | 1726 |
|  |  |  |  | freqParameter.34 | 0.508 | 1289 |

## Appendix S8. The mean and Effective Sample Size (ESS) for the different parameters in one run of the StarBEAST2 time-calibrated models for genus *Tursiops.* The models were run with all codon positions and including only the third codon positions, both using a a strict clock.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| All codon model | | |  | 3rd codon model | | |
| Parameter | Mean | ESS |  | Parameter | Mean | ESS |
| posterior | -22073.5 | 3304 |  | posterior | -8807.4 | 3636 |
| likelihood | -22162.6 | 7438 |  | likelihood | -8899.4 | 7238 |
| prior | -11.517 | 2572 |  | prior | -34.2 | 2577 |
| speciescoalescent | 100.6 | 4074 |  | speciescoalescent | 126.3 | 4545 |
| TreeHeight.Species | 3.649 | 8899 |  | TreeHeight.Species | 3.670 | 8290 |
| TreeHeight.t:all\_codon\_tree | 3.845 | 8854 |  | TreeHeight.t:tree | 3.807 | 8786 |
| TreeLength.Species | 11.209 | 4928 |  | TreeLength.Species | 11.195 | 6404 |
| treeLikelihood.atp6 | -1441.9 | 7567 |  | treeLikelihood.atp6\_pos3 | -582.6 | 7775 |
| treeLikelihood.atp8 | -355.4 | 7044 |  | treeLikelihood.atp8\_pos3 | -167.0 | 6756 |
| treeLikelihood.cox1 | -2845.1 | 8184 |  | treeLikelihood.cox1\_pos3 | -1162.9 | 7452 |
| treeLikelihood.cox2 | -1318.7 | 6659 |  | treeLikelihood.cox2\_pos3 | -529.5 | 6822 |
| treeLikelihood.cox3 | -1496.3 | 7264 |  | treeLikelihood.cox3\_pos3 | -576.7 | 8002 |
| treeLikelihood.cytb | -2299.1 | 7455 |  | treeLikelihood.cytb\_pos3 | -910.2 | 7293 |
| treeLikelihood.nd1 | -1862.7 | 8559 |  | treeLikelihood.nd1\_pos3 | -700.8 | 6585 |
| treeLikelihood.nd2 | -1984.9 | 5407 |  | treeLikelihood.nd2\_pos3 | -782.9 | 7265 |
| treeLikelihood.nd3 | -702.8 | 7521 |  | treeLikelihood.nd3\_pos3 | -313.1 | 7454 |
| treeLikelihood.nd4 | -2609.5 | 7964 |  | treeLikelihood.nd4\_pos3 | -1028.2 | 7101 |
| treeLikelihood.nd4l | -623.0 | 7060 |  | treeLikelihood.nd4l\_pos3 | -252.8 | 7906 |
| treeLikelihood.nd5 | -3620.9 | 6398 |  | treeLikelihood.nd5\_pos3 | -1464.3 | 7281 |
| treeLikelihood.nd6 | -1002.3 | 7114 |  | treeLikelihood.nd6\_pos3 | -428.5 | 7983 |
| strictClockRate.c:strict | 0.007 | 7827 |  | strictClockRate.c:strict | 0.017 | 8973 |
| kappa.s:p1 | 47.112 | 8833 |  | kappa1.s:p1 | 226.7 | 7327 |
| kappa.s:p2 | 77.472 | 8927 |  | kappa1.s:p2 | 112.7 | 7354 |
| kappa.s:p3 | 40.724 | 8911 |  | kappa1.s:p3 | 19.867 | 8251 |
| gammaShape.s:p2 | 0.081 | 8630 |  | kappa2.s:p1 | 65.249 | 7476 |
| CalibratedYuleModel.t:Species | -3.202 | 2930 |  | kappa2.s:p2 | 47.706 | 7245 |
| cySpeciationRate.t:Species | 2.120 | 329 |  | kappa2.s:p3 | 52.082 | 8382 |
| proportionInvariant.s:p1 | 0.779 | 8795 |  | gammaShape.s:p1 | 1.322 | 8858 |
| proportionInvariant.s:p3 | 0.774 | 8997 |  | proportionInvariant.s:p2 | 0.408 | 8445 |
| logP(mrca(root\_species)) | -0.782 | 9001 |  | CalibratedYuleModel.t:Species | -3.150 | 2014 |
| mrcatime(root\_species) | 3.649 | 8899 |  | cySpeciationRate.t:Species | 2.042 | 325 |
| lwcrPopScale.Species | 0.090 | 2039 |  | logP(mrca(root\_species)) | -0.829 | 9001 |
|  |  |  |  | mrcatime(root\_species) | 3.670 | 8290 |
|  |  |  |  | lwcrPopScale.Species | 0.065 | 2575 |



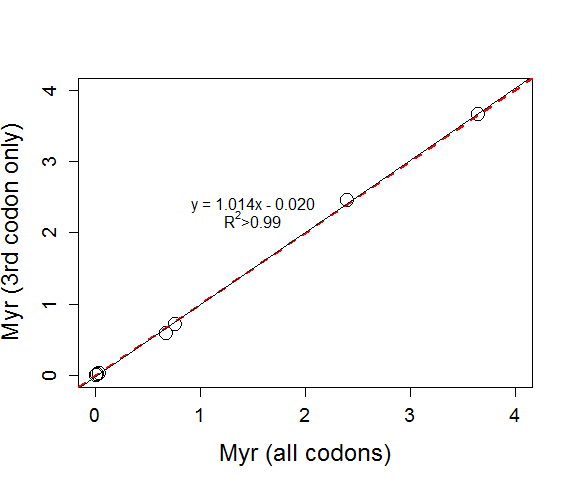
Myr

Myr

(A)

(B)

## Appendix S9. Time-calibrated phylogenetic species tree for genus *Tursiops* inferred with StarBEAST2 using (A) all codon positions, and (B) only the third codon positions, from 13 mitochondrial protein coding genes. The numbers below nodes are mean divergence times, and the boxed numbers node posterior probabilities, if <1.0. The bars represent 95% HPDI. The tips represent current species/populations and their sampling locations: SABD – *T. australis*, South Australia, SA – *T.* *aduncus*, South Africa, IPTA – *T. aduncus*, Southeast Australia, WNAC – *T. truncatus*, coastal Northwest Atlantic, PEA – *T. truncatus*, pelagic Northeast Atlantic, CS – *T. truncatus*, Coastal South (Northeast Atlantic), CN – *T. truncatus*, Coastal North (Northeast Atlantic), EMED – *T. truncatus*, Eastern Mediterranean Sea, BSEA – *T. truncatus ponticus*, Black Sea.

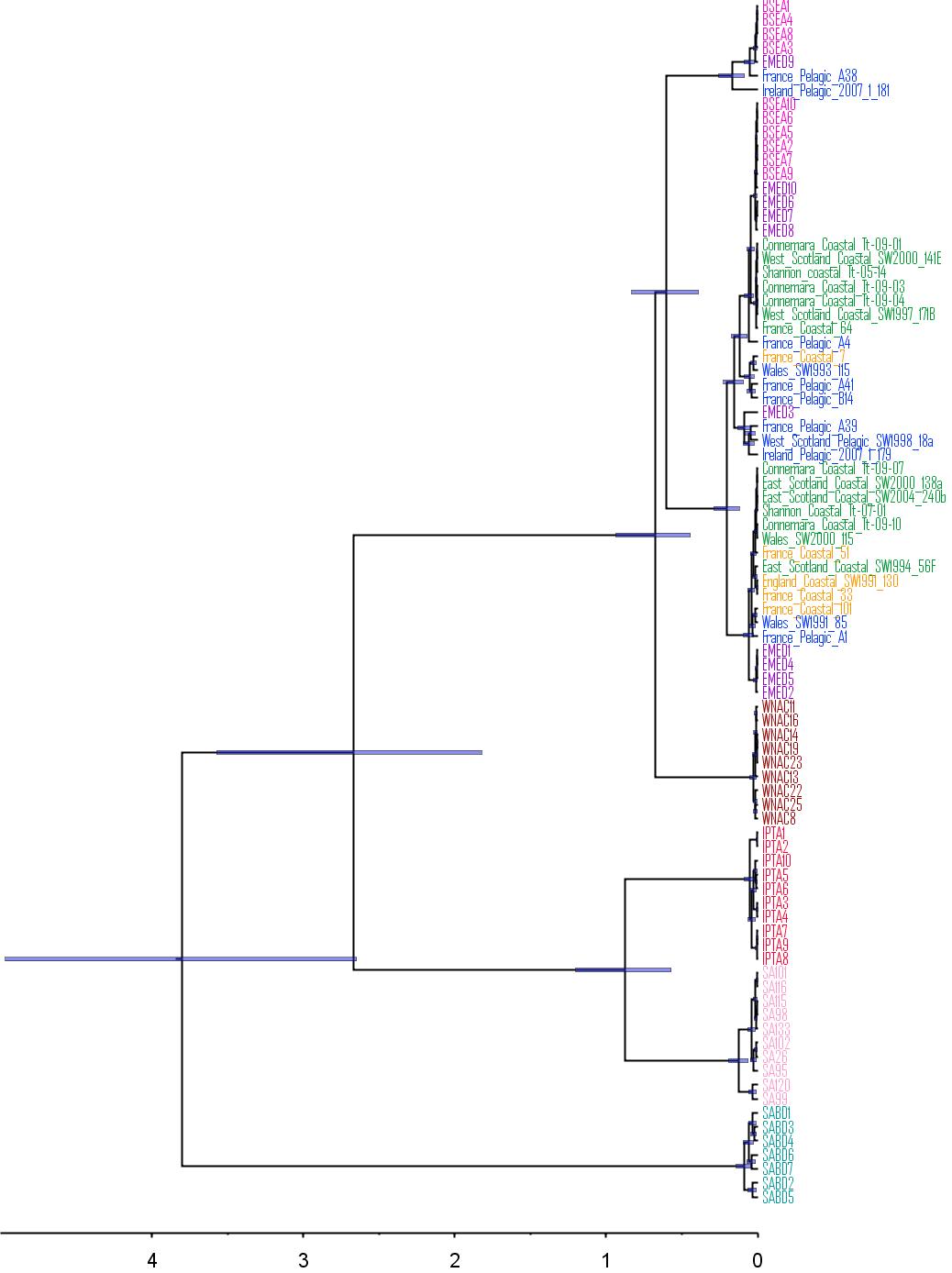


## Appendix S10. Correlation of average TMRCA of the common nodes in *Tursiops* gene trees inferred using two different StarBEAST2 models, a model including all codon positions and a model using only the third codon positions. The solid black line is fitted to the data, and the dashed red line represents perfect linear correlation with a slope of 1.

## Appendix S11. Effective population sizes (*N*e) for each branch in the phylogenetic tree presented in Fig. 3 of the main article.

|  |  |  |
| --- | --- | --- |
|  | *N*e | |
| Branch | Start | End |
| PEA | 11614 | 20829 |
| CS | 6571 | 11838 |
| CN | 224 | 13300 |
| EMED | 3424 | 15510 |
| BSEA | 548 | 5214 |
| PEA-CS-CN | 18057 | 23786 |
| CS-CN | 12171 | 6795 |
| EMED-BSEA | 17686 | 3971 |
| Root | 14276 | 35743 |

Start/end: Effective population size (*N*e) adjusted by the generation time, 21 years, at the start (older) and the end (more recent time) of the branch



1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

1.0

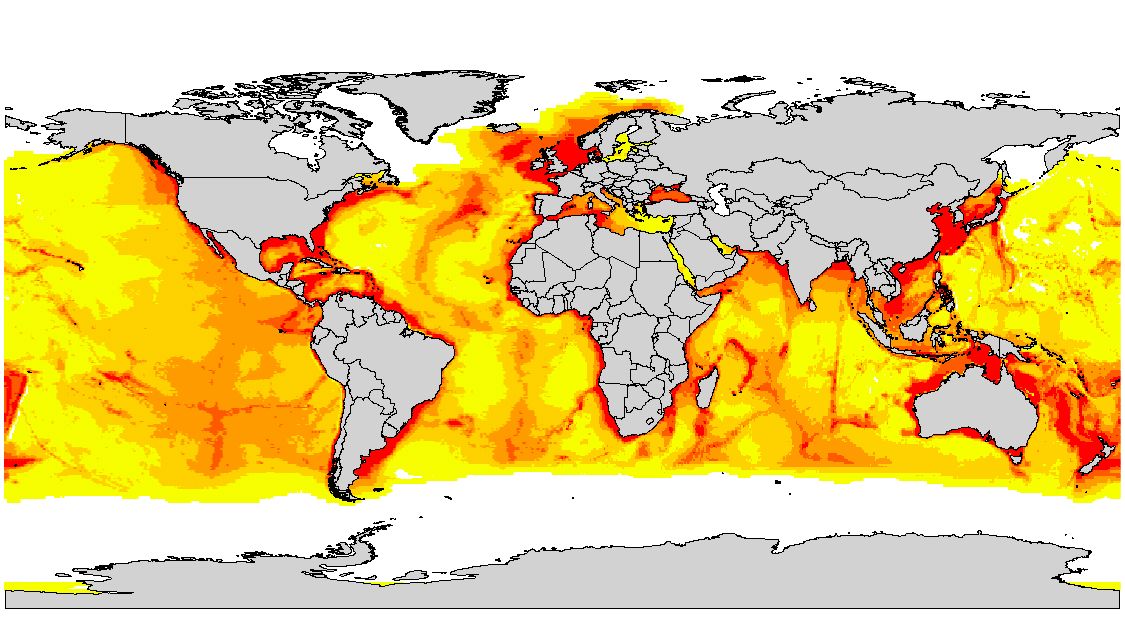
1.0

1.0

0.91

Myr

## Appendix S12. Time-calibrated consensus gene tree of genus *Tursiops* inferred with StarBEAST2 using third codon positions from 13 mitochondrial genes. The tips of the tree are individual samples that have been coloured according to their species/population assignment based on nuclear markers. Pink – *T. truncatus ponticus,* Black Sea, purple – *T. truncatus,* Eastern Mediterranean, blue – *T. truncatus,* pelagic Atlantic, green – *T. truncatus,* Coastal North, orange – *T. truncatus,* Coastal South, burgundy – *T. truncatus,* Coastal NW Atlantic, red – *T. aduncus*, Southeast Australia, pink – *T.* *aduncus*, South Africa, turquoise – *T. australis*, South Australia. The numbers above nodes are node posterior probabilities for the main clades and the bars represent 95% HPDI.



## Appendix S13. AquaMaps suitable habitat map for *T. truncatus* for the year 2100. White to red colours represent least to most suitable habitat, respectively. Land is shown in light grey.

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