Geographic realms	Location	Oceanographic features	Geographic / habitat break	Data for coastal/ offshore?	Materials used and quantities			Genetic markers		Genetic analysis		Morphological markers					Feeding Ecology			Parasite data	Behaviour			Overall Degree of Differentiation		
					Morphological	Biochemical	Genetic	mtDNA	nuclear	Phylogenetic	Population	Tail body length	Teeth	Coloration	Skulls	Other	Stable isotopes/ fatty acids	stomach contents	Other		Acoustic	Migratory	Other	Genetics	Habitat	Morphology
IO	Bangladesh			coastal			**Amaral et al., SC/66a/SM/18:** 17 samples compared against database			Median-joining network, Maximum likelihood								**Smith et al., SC-66a-SM19:** photo-ID 1,144 photo-identified Indo-Pacific bottlenose dolphins. gave abundance estimates of 1,701 - 2,239 between 2005 and 2009. Dorsal fins were highly variable, but extensively affected by fisheries interaction scarring and tissue loss						Reciprocal monophyly when compared with database		
IO	Pakistan, Oman		exposure of the Sunda and Sahul shelves during Pleistocene proposed	coastal	**Gray, 2017 PhD.** Skull morphology based on 26 cranial characters across 50 individuals (Hol-Ta: n = 29, 46-Ta: n = 4, Tt: n = 9, unknown: n = 8)		**Gray et al., 2018:** n=40 compared against database; mtDNA, Acton intron & a-Lactalbumin intron; **Moura et al., Pers.comms.:** 1 sample for RADseq phylogeny: basal within 'holotype' (South African) lineage	**mitogenome: Moura et al., 2015:** 4,301bp mtDNA	**Introns: Gray et al., 2018:** Acton intron & a-Lactalbumin intron;**RADseq: Moura et al., Pers.comm.:** 4Mb	Bayesian analysis, maximum parsimony, BEAST					Morphometrics data were consistent with the molecular phylogenetic assessment of the group, where there is clear separation between T. truncatus and T. aduncus, and Ad-Ta is differentiated from Hol-Ta, but those two sample sets group most closely together									non-overlapping PCA clusters	
IO	South Africa			coastal	**Hale et al., 2000:** 25 Body length/Skull length ratios truncatus vs aduncus length		**Natoli et al., 2004/ 2008:** mtDNA (N=38/ 50) and microsatellite DNA (n=107/ 142 compared against multiple populations and among populations within South Africa; **Moura et al., Pers.comm.:** RADseq phylogeny – differentiated lineage within T. aduncus lineage. **Hoebel et al., 1998:** mtDNAcr	**ssrDNA cr: Natoli et al., 2004/ 2008:** 297bp/516bp	**msat: Natoli et al., 2004/ 2008:** 9 loci;**RADseq: Moura et al., Pers.comm.:**4Mb	Minimum spanning network, Median-Joining Network, Neighbor Joining, Maximum Parsimony, Bayesian	FST, RhoST, PhiST, spatial autocorr.	**Hale et al., 2000:** truncatus vs aduncus length				**Hale et al., 2000:** truncatus vs aduncus - body length to skull ratios									Distinguish aduncus from truncatus - note that compared against Australian samples as well and consistent for skull length/ body length ratios.
IO	Tanzania, Zanzibar			coastal			**Samsbal et al., 2018:** n= 45	**mtDNA cr: Samsbal et al., 2019:** 534bp		Median Joining Network, Maximum Parsimony,	PhiST													Differentiated from Australasia, not from South Africa		
IO	Western Australia			coastal / offshore			**Allen et al., 2016:** n=144Population structure in NW Australia, species delination between offshore and inshore Tursiops;**Kriitzen et al., 2004:** n=302Population structure within Shark Bay;**Cormac 2015:** n=37 genomes plus n=119 previously publishedMitogenomics of Tursiops in Australasian and Indonesian waters	**mtDNA cr: Allen et al., 2016:** 410bp;**Kriitzen et al., 2004:** 35 bps;**Cormac:** mitogenome	**msat:Allen et al., 2016:** 19 loci;**Kriitzen et al., 2004:** 11 loci	Bayesian; Maximum Likelihood	FST, Structure, IMA and migrate-n modelling, AMOVA, PhiST, RhoST	**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography		**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography									Fine-scale population differentiation among nearshore habitat (3 identified, eit T. aduncus), differentiated from offshore (T. truncatus); Cormac - in Shark Bay T. aduncus but ~40% have T. truncatus haplotypes.	nearshore/ offshore	
WSP	Eastern Australia			coastal	**Hale et al., 2000:** 25 Body length/Skull length ratios truncatus vs aduncus length		**Möller & Beheregaray, 2001:** n=57 Population structure in SW Australia**Anmanon et al. 2012:** Population structure in Moreton Bay (QLD)**Moura et al., pers.comm.**	**mtDNA cr: Möller & Beheregaray, 2001:** 368bp;**Möller et al., 2008:** 420bp**Anmanon et al. 2012:** 402bpMoura et al: 500bp Clicyb b;**Möller et al., 2008:** 1000bp	**msat:Möller et al., 2008:** 6 loci;**Anmanon et al., 2012:** 20 loci;**RADseq: T. truncatus, Moura et al., (pers. comm.):**-4Mb data	Maximum Parsimony, Neighbor-joining network; Bayesian	FST; structure	**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography; **Hale et al., 2000** truncatus vs aduncus length		**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography	**Hale et al., 2000** truncatus vs aduncus length									**Möller & Beheregaray, 2001:** differentiation between T. truncatus and T. australis; **Möller et al., 2007:** fine-scale differentiation (within bay and between in and outside the bay) – microsat FST up to 0.14 (in w outside Port Stephens Bay). **Anamaon et al., 2012:** differentiation within and with comparisons outside Moreton Bay – FST up to 0.05. RADseq phylogeny gives well-defined lineage within T. aduncus clusters	inshore/ offshore; Embayment/ coastal	Distinguish aduncus from truncatus - note that compared against Australian samples as well and consistent for skull length/ body length ratios.
WSP	Southern Australia & Tasmania			coastal/ offshore	**Hale et al., 2000:** 25 Body length/Skull length ratios truncatus vs aduncus;**Ross & Cockcroft, 1990:** n=103 skulls **Charlton-Robb et al., 2011:** n=44 skulls**Jedensjö et al. 2017:** n=347 skulls	**Charlton-Robb et al., 2011:** n=35description of 'T. australis'., genetic comparison to other Delphinids, morphological comparison to other Tursiops **Möller et al., 2008;** n=102Genetic structure of 'bottlenose dolphins' in southern Australia., comparison to T. aduncus, T. truncatus, D. delphis **Moura et al., (pers. comm.)**	**mtDNAcr:Charlton-Robb et al., 2011:** 418bpCytb: **Charlton-Robb et al., 2011:** 1086bps	**msat: Möller et al., 2008:** 6 loci;**RADseq:Moura et al., (pers. comm.):** 4Mb data	Bayesian, Maximum likelihood; Maximum Parsimony	Factorial correspondence, Structure	**Charlton-Robb et al., 2011:** (T. australis); **Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography; **Hale et al., 2000** truncatus vs aduncus length	**Charlton-Robb et al., 2011**	**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography	**Charlton-Robb et al., 2011:** metrics, geo-morph - putative T. australis; clustering, DFA; **Jedensjö et al., 2017:** n=347 skulls**Kemper, 2004:** truncatus vs aduncus - some overlap - aduncus more		**Kemper, 2004:** truncatus vs aduncus - some overlap - aduncus more									Differentiation between putative T. australis and T. truncatus/ T. aduncus; Population differentiation along southern coast - Jedensjo thesis (for both truncatus and especially aduncus)**Cornuz thesis:** microsat and mitogenome data show structure for T. truncatus, not strongly geographically defined**Moura et al. (pers. comm):**T.australis a well-defined lineage within T. aduncus lineage		**Charlton-Robb et al., 2011:** Differentiation between putative T. australis and T. truncatus/ T. aduncus **Jedensjo et al. 2017:** Grouping between T. australis and T. truncatus **Kemper, 2004:** truncatus vs aduncus
WSP	North of Australia			coastal	**Hale et al., 2000:** 25 Body length/Skull length ratios truncatus vs aduncus		**Cornuz 2015;** 37 genomes plus 108 previously publishedMitogenomics of Tursiops in Australasian and Indonesian waters	mitogenomes		Bayesian; BEAST		**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography; **Hale et al., 2000:** truncatus vs aduncus length		**Ross & Cockcroft, 1990:** differentiation between T. truncatus & T. aduncus, and by geography; **Hale et al., 2000:** truncatus vs aduncus length									Cluster with western lineage - perhaps ancestral		
WSP	Solomon Islands, New Caledonia			coastal			**Oremus et al. 2015:**Tursiops in New Caledonia and Solomon Island	**mtDNA cr:**700bp		Maximum Likelihood														Differentiated T. aduncus and T. truncatus forms; truncatus in broad global lineage.		
WSP	New Zealand			coastal			**Terrano-Pinto et al., 2008:** n=195 from north and south island including fiordland populations	**mtDNA cr:** 647bp		Neighbour joining	FST, PhiST													T. truncatus - two ecotypes, inshore and offshore - PHist = 0.302		
WNP	China, Korea, Japan, Taiwan, Philipines	Kuroshio current appears to separate coastal and offshore populations off Japan, the location of Kuroshio shifts 5-10 over years.	Island-associated populations of T aduncus, multiple islands off Japan and off Jeju island, South Korea, which is near northern range limit for T ad(u); Density gap between coastal and offshore animals off Japan where Kuroslio current is.		**Wang et al., 2020:** n=57 (40 T ttu, 17 T ads; from China waters) for gross morphology; **Kim et al., 2010:** 1 skull from Jeju island, South Korea; **Kurihara & Oda, 2006:** n=27 skulls from Japanese waters; **Shirakihara et al., 2003:** 2 carcasses from Amakusa-Shimoshima Island off Japan.		**Wang et al., 1999:** n=47, aduncus from China, Taiwan and Indonesia; truncatus from Taiwan, N. Africa, Hong Kong, Brazil; **Kita et al., 2013:** 165 Truncatus from Taiji fishery (Eastern Japan). mtDNA 402 bp. Concluded "more similar to oceanic T ttu"**Chen et al., 2017:** Ttr=42 samples, Tar7 samples compared with published data	**mtDNA cr:Wang et al., 1999:** 388 bps, 7 fixed differences between aduncus and truncatus, sequence divergence 6.4%; **Chen et al., 2017:** 388 bps, n=42 Ttr from Japan, Taiwan and Philippines, n=7 Ta From Taiwan and Japan, found mtDNA differentiation between Tt in Eastern Japan, South East China, North East China, HI, and Palmyra when combined with published data.	**msat:Chen et al., 2017P:** n=20 loci, n=66; evidence for three clusters: western (West coast of Japan, western and northern Taiwan and Miyazaki), East cluster - East Taiwan and Taiji, and Philliipines (but only n=2 Taij),	**Wang et al., 1999:** Maximum likelihood;Minimum-spanning network**Chen et al., 2017:** Median-joining network	**Chen et al., 2017:** Factorial correspondence;Bayesian (Geneland)		**Kurihara & Oda, 2006:** Japan waters, found that aduncus generally has more teeth but ranges were overlapping		**Kim et al., 2010:** n=1 skull compared to measures for Ta and Tt; all measures within range of Tt; **Kurihara & Oda, 2006:** found separation in cranial characters in skulls from Japanese animals - identified two morphological groups corresponding to Ta (island-associated) and Tt;**Shirakihara et al., 2003:** 2 specimens from Amakusa-Shimoshima Island, most skull measures within range of Ta and outside range of Tt.			**Wang et al., 2020:** external gross morphology based on dead animals; n=40 Tt and n=17 Ta. Discriminant scores based on 8 characters non-overlapping; rostrum length as absolute measure or as proportion of total body length or snout-to-eye length non-overlapping		**Kim et al., pers.comm:** lighting data indicates Tt found in waters along both sides of Korean Peninsula and bycatch off Jeju but unpublished data						**Wang et al., 1999:** 7 fixed differences, sequence divergence of 6.4% **Chen et al., 2017:** mtDNA differentiation between 6 Japan, SE China, Hol Chima, and Palmyra, musts suggest clusters of Tt west coast of Japan and western and northern Taiwan, East Taiwan & Taiji, and Philipines (but small sample size)		**Wang et al., 2020:** gross morphology: non-overlapping distributions of rostral length characters, discriminant scores based on 8 characters non-overlapping**Kurihara & Oda, 2006:** identified two morphological groups - skulls from Amami, Amakusa-Shimoshima, and Mikuri islands corresponding to Ta other from Japan waters corresponded to Tt**Shirakihara et al., 2003:** confirmed 2 specimens from Amakusa-Shimoshima had cranial measures within range of Ta.
MED&BS	Black Sea	Enclosed basin connected to the Med only by small strait/ not older than 10K-8K years/ low salinity, colder waters/depth variable up to 2000 mt. Northern area shallow with enclosed basin (Azov Sea)	Dardanelles/ Bosphorus Strait system; 4km strait into Sea of Azov.	**Gol'din & Gladilin, 2015:** Some evidence of possible offshore and inshore populations (Crimea)	**Visad et al., 2008:** 27 samples.**Gol'din & Gladilin, 2015:** 64 samples		**Natoli et al., 2005:** 16 samples**Visad et al., 2008:** 43 samples**Moura et al., 2013:** 10 samples	**mtDNAcr: Natoli et al., 2005:** 16 samples; 630bp**Visad et al., 2008:** 43 samples; 442bps **mitogenome:** Moura et al., 2013 n=10	**msat: Natoli et al., 2005:**16 samples; 9 loci	**Natoli et al., 2005:** Minimum-spanning network**Visad et al., 2008:** Network parsimony reconstruction, TCS 1.1.0; **Moura et al., 2013** BEAST analysis for node estimation age calculation and LAGER	**Natoli et al., 2005:** FST, Structure, PhiST**Visad et al., 2008:** PhiST,	**Visad et al., 2008:** 27 individuals. 194-244 cm **Gol'din & Gladilin, 2015:** (C'rimea) 64 individuals, 49 with known sex, newborns. Adults: 169' (201-260cm, average 240.2cm; 104♀ (241-276cm, average 255.5cm)		**Visad et al., 2008:** 27 skulls measured. Mean adult skull length of 452.3 mm (maximum length = 503 mm); 26 cranial measurements (following Perrin et al., 1975); PCA analysis.		**Gladilina et al., 2014:** 11 stomachs Compared with data from 1918, wider number of species and shift towards smaller species and similar to those found in Mediterranean		**Birkun, 2002:** Parasite data Available from the 1960's and 1990's: no protozoa infection and external macroparasites. 6 species internal macro parasites		Tursiops in the Black Sea is considered coastal, however the occurrence of this species in deeper waters should be assessed. Some info in **Birkun, 2002** and **Gol'din & Gladilin, 2015**		Differentiation between Tt pelagic and Tt Med supported by teh and nuclear markers analysis, from multiple authors, although incomplete lineage sorting based on mtDNA	Drastic difference from the neighboring Med, in term of salinity and temperature, with obvious geographic barrierWithin BS different habitats from oceanic to shallow waters.	Evidence of smaller total body size, by two independent works. Hypothesis of a bigger (offshore) and smaller (inshore) form.
MED&BS	Mediterranean	Enclosed basin with different habitats. Inside, partially enclosed seas (Adriatic, Aegean).	Strait of Gibraltar considered as physical boundary.Almeria Oran Front divides Oran Sea from western Mediterranean, identified as likely habitat/population break.Sicily Channel shallow plateau divides east from west		**Visad et al., 2008:** 27 samples**Sharir et al., 2011:** Bicamphes for total length and 82 skulls		**Natoli et al., 2005:** 74 samples**Visad et al., 2008:** 31 samples**Moura et al., 2013:** 10 samples**Gaspari et al., 2015:** 192 samples	**mtDNA cr: Natoli et al., 2005:** 62 samples; 630bp**Visad et al., 2008:** 63 samples; 442bps **Gaspari et al., 2015:** 192 samples for 820bpsmitogenome: **Moura et al., 2013:** 10 samples	**msat: Natoli et al., 2005:** 74 samples; 9 loci;**Gaspari et al., 2015:** 192 samples for 12 loci	**Natoli et al., 2005:** Minimum-spanning network**Visad et al., 2008:** network parsimony reconstruction, TCS 1.1.0; **Moura et al., 2013:** BEAST analysis for node estimation age calculation and LAGER	**Natoli et al., 2005:** Structure, FST, PhiST**Visad et al., 2008:** PhiST**Gaspari et al., 2015:** Structure, FST	**Visad et al., 2008:** 27 individuals 220–315 cm and 246–320 cm for the Mediterranean and Atlantic respectively **Sharir et al., 2011:** 26 exotMed vs 64 westMed. Significat difference between the means		**Visad et al., 2008:** 27 skulls measured. 26 cranial measurements (according to Perrin et al., 1975), mean lengths of 526.3 mm and 537.4 mm in the Mediterranean and the Atlantic Ocean. PCA analysis**Sharir et al., 2011:** CWL of 42 from exotMed vs 40 from westMed. Significantly smaller.			**Blanco-et al., 2001:** 6 stomach contents from Western Med.Different main prey compared ENA Tursiops			Mixt: strong population structure between BS/Med/ENA but no mtDNA lineage sorting (Natoli et al. 2005 & Moura et al 2013).Likely colonization from the west towards the east.	A variety of different habitats from Scotland throughout the Black Sea. Habitat boundaries appear to coincide with population boundaries	**Visad et al., 2008:** Evidence of not overlapping cluster PCA analysis of 26 cranial measurements.Within Med dwarfism suggested in the eastern Med population (Israel) supporting evidences of population differentiation. Different populations in different basins
ENA	Eastern North Atlantic	Warm Gulf Stream coming form the Western side of the basin and keeping water warmer than average (temperature at same latitude. Canary current heading south. Estuaries and oceanic islands = specific coastal habitats	Coastal areas of shallow waters or estuaries likely habitats released after the last Glacial Maxima	Yes: coastal populations present in many areas (Moray Firth, Shannon estuary etc.) and pelagic population**Van Waerebeek 2016:** evidence of Tursiops turnicatus occurrence in pelagic and coastal waters is reported along all the African west coastline.	**Louis et al., 2014:** coastal= 12 samples and pelagic = 27 samples (females = 20; males= 18; undetermined = 1)		Louis et al., 2014a: 381 samples**Louis et al., 2014b:** 355 samples from different regions from Scotland to Mediterranean.**Quaroli et al., 2007:** 86 samples from Azores & 28 from Madeira**Möller et al., 2011:** 98 samples from North, center and South Ireland**Nicholas et al., 2007:** 58 archeological samples**Hoebel et al., 1998:** 2 samples from Senegal compared with broad dataset.	**mtDNAcr: Louis et al., 2014b:** 681bps**Louis et al., 2014a:** 388 samples 681bps**Quaroli et al., 2007:** 609bp**Möller et al., 2011:** 544bp **Nichols et al., 2007:** 171bp**Hoebel et al., 1998:** 297bp	**msat:** Louis etal. 2014b: 25 loci; 355 samples**Louis et al., 2014a:** 355, 25 msat loci;**Quaroli et al 2007:** 86 samples from Azores & 28 from Madeira 10 msat**Möller et al., 2011:** 15 loci;**Nichols et al., 2007:** 5 loci;**Hoebel et al., 1998:** 5 loci	**Louis etal 2014b:** DYANA;**Hoebel et al., 1998:** Neighbour joining	**Louis et al., 2014a:** Structure & TESS: 4 populations identified: MedEpelagic, coastal north and south. Most FST, mtDNA FST & PhiST.**Möller et al., 2011 and Fernandez et al 2011:** Fine scale pop analysis in Irelan and Iberia.**Quaroli et al., 2007:** STRUCTURE FST, PhiST**Nichols et al., 2007:** FST, PhiST, Structure							**Louis et al., 2014b:** 40 samples: coastal=14, pelagic= 26. No difference in the C13 but difference in S34 and N15**Fernandes et al., 2011:** 43 samples from Galicia, differences between North and South Galicia		**Louis et al., 2014b:** 39 samples (12 coastal, 27 pelagic)						Clear strong differentiation between coastal and pelagic. Coastal populations suggested to have originated from pelagic in the last Glacial Maxima 10-220 yrBP. Divergence between pelagic Atlantic and West Mediterranean populations occurred later (7260 yrBP). Coastal north and south likely to be recently originated or results of fragmentation of metapopulation. Within pelagic, no differentiation even across long distances (see **Quaroli et al., 2007**). Fine population structure across the range in coastal estuaries habitats and evidences of extinct populations that have not been replaced at least in the last 100 years **(Nichols et al., 2007)**. No data for the Atlantic North African coast except for occurrence and 2 samples of Tt from Senegal that fall in the broad turnicatus lineage.	Clear niche separation between coastal and pelagic both from Stable isotopes and stomach contents. Oceanic deep waters environment likely to define pelagic population widely homogeneous throughout the Atlantic (no difference between Azores samples and pelagic ENA)	No significant difference between coastal and pelagic.
ESA	Eastern South Atlantic			**Van Waerebeek, 2016:** evidence of Tursiops occurrence in pelagic and coastal waters is reported along all the African west coastline.			**Hoebel et al., 1998:** 4 samples from Namibia	**Hoebel et al., 1998:** 297bp	**Hoebel et al., 1998:** 5 loci	**Hoebel et al., 1998:** Neighbour joining													Only analyzed samples are 4 Tt from Namibia that fall in the broad Tt lineage.		
WNA	Western North Atlantic	Multiple habitats: deep offshore temperate waters, continental shelf and nearshore coastal waters, bays, sounds and estuarine waters, Western North Atlantic, Gulf of Mexico, Caribbean	**Rosel & Wilcox, 2016 SC/66b/SM/16:** Estuarine/nearshore and shelf waters versus continental slope and deeper, Cites Kenney 2000**Vollmer & Rosel, 2017:** Habitat break in north central Gulf of Mexico for shelf and offshore populations	Yes, morphological (cranial and vertebral morphometrics; body size) and genetic data.	**Costa et al., 2016 SC/66b/SM11:** 101 skulls (44 offshore; 57 coastal adult skulls based on a prior identification); 24 vertebra counts, of those 16 measured. Compared with 78 skulls from WSA (coastal and offshore)**Mead and Potter, 1995:** 33 offshore, 72 coastal. Three basic measurements, condylobasal length,zygomatic width and internal nares width	**Duffield, 1987, Duffield et al., 1983:** present differences in hematological parameters	**Rosel et al., 2009:** 481 samples. mtDNA control region, microsatellite**Rosel & Wilcox, 2016 SC66b/SM/16:** 766 samples. mtDNA control region, microsatellite**Vollmer & Rosel, 2017:** 563 samples, mtDNA control region, microsatellites, SNPs**Hingston et al., 2020** mtDNA control region, AFLP markers	**mtDNA cr: Rosel et al., 2009:** 451, 354 bp; **Rosel & Wilcox, 2016 SC66b/SM/16:** 766 samples, 354 bps, fixed nucleotide differences**Vollmer & Rosel 2017:** 540 individuals for 354bps	**msat: Rosel et al., 2009:** 431 samples for 18 loci;**Rosel & Wilcox, 2016 SC66b/SM/16:** 766 samples, 18 microsatellite loci: distinct allele frequency distributions, high number of private alleles;**MME complex** (genes DQB and DRB) sequences: Morphotypic specific alleles see n 18 for DQB and 14 for DRB)**SNPs: Vollmer & Rosel, 2017:** 52 SNPs on 563 samples;**AFLP- Kingston et al., 2009:** 418 polymorphic AFLP markers total. n= 5 offshores and n=15 coastals	**Rosel et al., 2009:** Bayesian analysis: two well supported clusters offshore /coastal**Kingston et al., 2009:** AFLP tree reciprocal monophyly for coastal and offshore animals. mtDNA tree unresolved	**Rosel et al., 2009:** Structure, FST, Migrate, mismatch distribution. Distinct coastal populations; No evidence of male dispersal. Gulf of Mexico most distinct.**Vollmer & Rosel, 2017:** Structure, DPCA, FST, PhiST, Migrate		**Mead and Potter, 1995:** Modal length of offshores (n=23) 260cm, modal length of coastals (n=72) = 250-260cm. But total length did overlap to some degree**Costa et al., 2016 SM/66b/SM11:** Offshores in wNA significant longer than coastals in WNA			**Costa et al., 2016 SC/66b/ SM11:** 101 skulls (44 offshore, 57 coastal based on a priori identification). 19 measurements. PCA and DFA analyses. Two well divided groups. When compared with WSA skulls: three groups (WNA coastal, WSA offshore &WNA offshore, WSA coastal)**Mead and Potter, 1995:** No overlap in three skull measurements for coastal and offshore animals in wNA		**Costa et al., 2016 SC/66b/ SM11:** 24 vertebra counts, of those 16 fully measured. PCA analysis. Two clear divided groups.Offshores (n=23): 63-65 vertbrae; Coastals (n=9): 59-60 vertebrae		**Barnes et al., 2009:** n=60 and three isotopes. **Knoff, 2004:** n=267 dolphins from wNA and three isotopes	**Mead and Potter, 1995:** 16 offshore stomaches and 117 coastal stomachs. Different feeding habits with different prey species observed		**Mead and Potter, 1995:** Offshores individuals infected with Phyllobothrium, Monorchiagrne and the nematode Crassicauda. Crassicauda lesions in76% of 38 offshore skulls, 1.6% of 183 coastal skulls analyzed. Coastal individuals infected with trematode Braunina**Costa et al., 2016 SM/66b/SM11:** 57% of offshore skulls have Crassicauda scars while only 3.5% of coastal skulls have scars		Clear differentiation between WNA offshore and coastal ecotype in mtDNA, microsatellites and AFLP markers. Also clear population structure within coastal ecotype across the range. Nuclear AFLP markers separate the coastal and offshore form in the WNA in a phylogenetic (Bayesian) analysis. They show reciprocal monophyly	Offshore habitat seems similar across the range. Coastal habitat characteristics vary among areas. This is likely driving the fine population structure observed. Stable isotopes indicate habitat partitioning between offshore and coastal forms	Clear evidence of morphological differentiation between coastal and offshore populations with the latter being bigger. Differentiation confirmed by both skulls measurements and vertebra counts, total body length

WSA	Western South Atlantic	Tropical, subtropical, and temperate coastal and offshore waters. Mainly driven by the warm, southerly flowing Brazil current, but also influenced by the colder northerly flowing Malvinas Current, with the two mixing around the northern border of Argentina	Geographic range of papers reviewed: North and northeast Brazil to Tierra del Fuego. Habitat discontinuities invoked: currents and water temperature, coastal v. offshore, coastal v. estuarine, continental shelf width	Yes. morphological (coloration, dorsal fin shape, skull) and genetic evidence of offshore (truncatus-type) and inshore (gephyrus-type) forms	**Barreto 2000:** n=68 (max. adult skulls 14 from north and 54 from south)**Wickert et al., 2016:** 135 adult skulls**Costa et al., 2016:** 78 adult skulls**Wickert et al., 2016:** 139 samples in the final analysis		**Barreto 2000:** 16 samples, 338bp of control region**Fruet et al., 2014:** 134 samples (coastal)**Costa et al., 2015:** 41 (coastal)**Fruet et al., 2016:** 124 coastal and 65 offshore **Oliveira et al., 2016:** 109 samples	**mtDNA** or**Barreto 2000:** n=16, 338bp; **Fruet et al., 2014:** 124 samples, 417bp; **Costa et al., 2015:** 41 samples, 316bp; **Fruet et al., 2017:** 45 samples, 417bp; **Oliveira et al., 2016:** 109 samples, 316bp	**msat: Fruet et al., 2014:** 124 samples, 15 loci; **Costa et al., 2015:** 37 samples, 5 loci;**Fruet et al., 2017:** 68 samples, 11 loci;**Oliveira et al., 2016:** 102 samples, 7 loci		**Fruet et al., 2014;Costa et al., 2015Fruet et al., 2017Oliveira et al., 2016:**All did FST and PhiST	**Ott et al., 2016:** 87 - 284 From Otts (literature review);**Costa et al., 2016** has table with measurements of body lengths from four geographic regions. Coastal form in WSA significantly longer than offshores from WSA	**Costa et al., 2016:** 16-26 total tooth range, significant but small difference in # of teeth in mandible**Wickert et al., 2016:** no significant difference in tooth counts between offshore and coastal**Barreto, 2000:** suggests difference in # of teeth in N and S animals	**Ott et al., 2016:** literature review of Brazilian and Argentinian color patterns**Costa et al., 2016:** suggests difference in coloration between offshore and coastal**Fruet et al., 2017:** suggests difference between offshore and coastals	**Costa et al., 2016:** 100 mature, 79 used in full PCA, DFA; t-test, MANOVA, 21 measurements **Wahl et al., 2016:** 135 from WSA (also has 31 ENP, 23 ENA, and 20 ESA), 20 geometric morphometrics (63 landmarks, 13 semilandmarks), PCA, DFA**Ott et al., 2016:** 486-621cm from (literature review) **Barreto, 2000:** 81(?) samples, 58 measurements and 17 meristic measures**Wickert et al., 2016:** 280 skulls (total n= 144 truncatus:136 gephyrus; 139 complete adult skulls for PCA; 14 characters, 29 measurements, PCA, CVA	**Costa et al., 2016Fruet et al., 2017**	**Costa et al., 2016:** 35 vertebral columns, measurements and counts, (truncatus) 62-68, (gephyrus) 57-58 **Wickert et al., 2016:** 62-64 (truncatus), 57-59 (gephyrus)		**Ott et al., 2016:** (literature review)			**Costa et al., 2016:** No significant difference in Crassicauda scars between truncatus and gephyrus**Ott et al., 2016** (literature review)	**Ott et al., 2016:** (literature review) coastal and offshore differ. But very little information here. See also **Fruet, 2017** workshop report	**Coscarella, 2016 SC/66b/SM06:** 15y photoID catalog from central Argentina (San Matias Gulf/Nuevo Gulf)		**Costa et al., 2015:** coastal, S. Brazil - 3 nuclear clusters, significant difference between northern (Laguna) and southern regions**Fruet et al., 2017:** coastal vs. offshore S. Brasil, Uruguay - msat F_{ST} = 0.35 significant, mtDNA $FST/PHiST = 0.2$ significant, offshore and coastal vs. WSA, Argentina = 0.37 (msat FST) & 0.4 (mtDNA FST, PhiST) significant; No shared haplotypes between the 2 ecotypes in Brasil, but no reciprocal monophyly either**Oliveira et al., 2016:** Saint Paul's rocks, NE Brasil, mid-southern Brasil (SC/RG) distinct groups, mtDNA FST/PhiST = 0.3, msat FST = 0.06. But Structure analysis (with location priors) indicates a number of admixed individuals of the two subspecies for some animals that had been identified to subspecies based on skull morphology	**Wahl et al., 2016:** Unclear the amount of sympatry between truncatus (offshore) and gephyrus (coastal) forms between 25.6S and 31S**Wickert et al., 2016:** gephyrus type more restricted in range - coastal waters of southern Brasil, Uruguay, northern Argentina**Costa et al., 2016:** suggest coastal shelf habitat and warmer water for gephyrus. gephyrus range suggested to be limited in south by cold Malvinas current	**Barreto, 2000:** Significant difference North and South of Santa Catarina State, explained by different current preferences. i.e. proposing N/S split of the two forms as subspecies**Costa et al., 2016:** Concludes subspecies for offshore and coastal clusters w/distinct characteristics, offshore: shorter skulls, more vertebrae, no PCA overlap for skulls or skeletons. Offshore individuals are smaller and have more, smaller vertebrae. Suggests panspatric coastal/offshore distributions for truncatus and gephyrus**Wahl et al., 2016:** diagnostic differences in maxillae shape between truncatus and gephyrus - conclude valid PSC species; But 2D geomorphometric analysis of truncatus versus gephyrus had overlap of the two groups for all three views (dorsal, ventral, lateral)**Wickert et al., 2016:** No PCA overlap between truncatus and gephyrus, 6 diagnostic characters. Concludes species-level differences for truncatus versus gephyrus based on Phylogenetic Species concept: 1 diagnostic character of skull separated them, plus vertebral count
ENP	US and Mexico west coasts, Gulf of California	Narrow continental shelf in ENP, broad shelf in Gulf of Mexico; coastal dolphins generally <1km from shore, offshore >4km from shore (overlap possible in some areas?)		**Perrin et al., 2011:** Coastal and offshore populations identified; **Lowther-Thieleking et al., 2015:** difference between main coast and Gulf of California. Coastal population in oceanic islands (Hawaii)	**Perrin et al., 2011:** 139 skulls; study expanded from Walker 1981; **Moreno et al., 2017:** 133 dorsal fins	**Segura et al., pers.comm.:** 60 samples for stable isotopes	**Lowther-Thieleking et al., 2015:** 64 coastal and 69 offshore samples, mtDNA and microsats; **Segura et al., pers. comm:** 250 samples for mtDNA, n=246 microsatellites	**mtDNA** or**Lowther-Thieleking et al., 2015:** 402 bp differentiation between coastal and offshore South California Bight (SCB). Also SCB differs from coastal and offshore and Gulf of California coastal and offshore; 1 shared haplotype between coastal and offshore SCB. **Segura et al., 2006 & pers.comm.:** 480bp significant differences between most strata representing offshore v. coastal ecotype; also some differences between strata within ecotype	**msat Lowther-Thieleking et al., 2015:**15 loci; significant differentiation between CA offshore and CA coastal. **Segura et al., pers.comm.:** 8 loci; genetic differentiation between most strata of coastal v. offshore; general separation in assignment and ordination analysis		**Lowther et al., 2015:** FST, PhiST, median joining network, Structure. **Segura et al., 2006 & pers.comm.:** FST, PhiST, Structure, PCA	**Walker, 1981:** sexually mature males in offshore populations have smaller body length than coastal dolphins from CA and Mexico (no sexually mature female in coastal). But sample sizes inadequate to assess and within offshore SCB sample there was selection for smaller animals during live-capture efforts	**Perrin et al., 2011:** 61 coastal, 26 offshore, differences in upper and lower tooth counts between coastal and offshore;**Walker, 1981:** tooth width best character to separate coastal from both (SCB and ETP) offshore		**Perrin et al., 2011:** (builds on Walker 1981) mature 24 coastal, 21 offshore, 22 of 28 measurements differed between coastal and offshore, most differences were in characters associated with feeding. offshore skulls larger in 10 of 30 measures, diagnosability of adult skulls based on cranial characters = 90.4%**Walker, 1981:** cranial measures were more similar among the offshore ETP and the offshore SCB dolphins than either was to the CA and Mexico coastal dolphins	**Mortea et al., 2017:** 30 each from Pacific, Gulf of California and Gulf of Mexico. Variation in dorsal fin shape but appeared clinal			**Walker, 1981:** different prey composition SCB coastal v ETP offshore. Coastal - croakers and perches, offshore - epipelagic fish and cephalopods		**Walker, 1981:** Differences in the incidence of 5 common marine mammal parasites between coastal and offshore				Significant differentiation between offshore and coastal at both mtDNA and msats		**Perrin et al., 2011:** PCA ellipses non-overlapping for coastal vs offshore; diagnosability of adult skulls based on cranial characters = 96.4%; P<0.05 for dorsal fins between 3 areas (Pacific coast, Gulf of California, Gulf of Mexico)
TNP	Colombia, Ecuador, Peru, Chile	Humboldt Current flows north along the western coast of South America, and extend 500-1,000 km (310-620 mi) offshore. The current extends from southern Chile to northern Peru where cold, upwelled waters intersect warm tropical waters to form the Equatorial Front. Three notably productive upwelling subsystems are produced by this current: 1 seasonal upwelling in Chile, 1) upwelling "shadow" (less productive, but still large) in northern Chile and Southern Peru, and 3) year-round upwelling in Peru.		yes	**Van Waerebeek et al., 1990:** skulls: 15 offshore, 4 coastal; tooth width averages: 7 inshore, 22 offshore**Félix et al., 2017** Ecuador: 139 coastal, 34 offshore; Peru: 9 coastal, 51 offshore; Chile (Profil) 25 coastal**Santillan et al., 2005:** Ecuador=12, Peru=39		**Sanino et al., 2008:** samples from Chile offshore (8), Peru offshore (12), Peru inshore (3), Profil-Chile (8); **Bayas-Rea et al., 2017:**Ecuador: 31 biopsy (inner Gulf of Guayaquil), 1 biopsy (Galapagos), 22 stranded specimens (outer coast), Gulf of Guayaquil	**Sanino et al., 2008:** 331 bp control region; **Bayas-Rea et al., 2017:**1227 bp from 7 mtDNA loci		**Sanino et al., 2008:** phylogenetic tree not specify protocol.	**Sanino et al., 2008** no analysis**Bayas-Rea et al., 2017** only inner Gulf of Guayaquil compared: no resolution between sites, inner estuary somewhat distinct mtDNA sequences		**Van Waerebeek, 1990:** average tooth width inshore (n=7) 8.65-9.6, offshore (n=22)4.55-8.55		**Van Waerebeek, 1990:** number too small for statistical analysis of skulls**Santillan et al., 2005:** PCA: very weak support for difference between Ecuador, Peru inshore, Peru offshore (note IWC paper only, never published)	**Félix et al., 2017:** Profil and offshore - tall, falcate fins; coastal - short, triangular fins; some evidence for difference between offshores					**Santillan et al., 2005:** Cirrencaxada lesions Ecuador (0%), Peru/inshore (6.8%), Peru/offshore (52.3%)**Van Bressem et al., 2007, 2015:** Lobomycosis-like disease (Paracoccidioides brasiliensis) found in coastal but not in offshore specimens (Peru, Columbia, Ecuador); pale dermititis in coastal but not offshore specimens (Peru)		**Van Waerebeek, 1990:** coastal group size average ~6.5, offshore group size average ~25		Peru/inshore no shared haplotypes; Peru/offshore 1 shared haplotype; Chile/inshore no shared haplotypes; Chile/offshore 1 shared haplotype; **Bayas-Rea et al., 2017:** single clade for all inner/some outer Gulf of Guayaquil (GG) plus published Peru sequence, another clade for single Galapagos plus one inner GG within worldwide clade of published T truncatus sequences. only inner Gulf of Guayaquil compared. No resolution between sites, inner estuary somewhat distinct from mtDNA sequences		