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DEPARTMENT OF COMMERCE

National Oceanic and Atmospheric Administration

Docket No. 141015853-4853-01

RIN 0648-XD563

Endangered and Threatened Wildlife and Plants; Notice of 12-Month Finding on a Petition to List the Harbor Porpoise (Phocoena phocoena) in the Baltic Sea as an Endangered or Threatened Distinct Population Segment (DPS) Under the Endangered Species Act (ESA).

AGENCY: National Marine Fisheries Service (NMFS), National Oceanic and Atmospheric Administration (NOAA), Commerce.

ACTION: Notice of 12-month Finding.

SUMMARY: We, NMFS, announce a 12-month finding on a petition to list the harbor porpoise (Phocoena phocoena) in the Baltic Sea as an endangered or threatened distinct population segment (DPS) under the Endangered Species Act of 1973, as amended. We conducted a DPS analysis based on our joint U.S. Fish and Wildlife Service and NMFS DPS Policy. Based on the best available scientific and commercial information, we find that the harbor porpoise population in the Baltic Sea is not a DPS because it does not meet the criterion for significance outlined by our DPS Policy. Thus, we find this population is not warranted for listing.

DATES: This finding was made on [insert date of publication in the FEDERAL REGISTER].

ADDRESSES: Information used to make this finding is available for public inspection by appointment during normal business hours at NMFS, Office of Protected Resources, 1315 East

West Highway, Silver Spring, MD 20910. The petition and a list of the references we used can also be found at <http://www.nmfs.noaa.gov/pr/species/petition81.htm>.

FOR FURTHER INFORMATION CONTACT: Heather Coll, NMFS, Office of Protected Resources, (301) 427-8455.

#### SUPPLEMENTARY INFORMATION:

##### Background

On July 15, 2013, we received a petition from the WildEarth Guardians to list 81 marine species or subpopulations as threatened or endangered under the Endangered Species Act (ESA). We found that the petitioned actions may be warranted for 24 species and 3 subpopulations, announced the initiation of status reviews, and solicited information from the public for each of the 24 species and 3 subpopulations (78 FR 63941, October 25, 2013; 78 FR 66675, November 6, 2013; 78 FR 69376, November 19, 2013; 79 FR 9880, February 21, 2014; and 79 FR 10104, February 24, 2014). We completed comprehensive status reviews under the ESA for six foreign marine species and evaluated whether one foreign marine subpopulation met our DPS Policy criteria in response to the petition (79 FR 74954; December 16, 2014).

This notice addresses the finding for one of the petitioned subpopulations: a putative Baltic Sea harbor porpoise (*Phocoena phocoena*) subpopulation (79 FR 9880; February 21, 2014). The remaining species and subpopulation will be addressed in subsequent findings.

We are responsible for determining whether species are threatened or endangered under the ESA (16 U.S.C. 1531 et seq.). To make this determination, we first consider whether a group of organisms constitutes a “species” under the ESA, then whether the status of the species qualifies it for listing as either threatened or endangered. Section 3 of the ESA defines a “species” as “any subspecies of fish or wildlife or plants, and any distinct population segment of

any species of vertebrate fish or wildlife which interbreeds when mature.” On February 7, 1996, NMFS and the U.S. Fish and Wildlife Service (USFWS; together, the Services) adopted a policy describing what constitutes a DPS of a taxonomic species or subspecies (the DPS Policy; 61 FR 4722). The DPS Policy identified two elements that must be considered when identifying a DPS: (1) the discreteness of the population segment in relation to the remainder of the species (or subspecies) to which it belongs; and (2) the significance of the population segment to the remainder of the species (or subspecies) to which it belongs. As stated in the joint DPS Policy, Congress expressed its expectation that the Services would exercise authority with regard to DPSs sparingly and only when the biological evidence indicates such action is warranted. Listing determinations under the ESA must be based on the best available scientific and commercial information.

Under the DPS Policy, a population segment of a vertebrate species may be considered discrete if it satisfies either one of the following conditions:

(1) It is markedly separated from other populations of the same taxon as a consequence of physical, physiological, ecological, or behavioral factors. Quantitative measures of genetic or morphological discontinuity may provide evidence of this separation.

(2) It is delimited by international governmental boundaries within which differences in control of exploitation, management of habitat, conservation status, or regulatory mechanisms exist that are significant in light of section 4(a)(1)(D) of the Act.

If a population segment is considered discrete under one or more of the above conditions, we will evaluate its biological and ecological significance. The significance consideration may include the following:

(1) Persistence of the discrete population segment in an ecological setting unusual or

unique for the taxon,

(2) Evidence that loss of the discrete population segment would result in a significant gap in the range of a taxon,

(3) Evidence that the discrete population segment represents the only surviving natural occurrence of a taxon that may be more abundant elsewhere as an introduced population outside its historic range, or

(4) Evidence that the discrete population segment differs markedly from other populations of the species in its genetic characteristics.

### Species Description

The harbor porpoise, Phocoena phocoena, is a widely distributed cetacean found in temperate and subarctic coastal and offshore waters of the northern hemisphere and is usually seen in groups of two to five animals (Reeves et al., 2002). Although it is sometimes found in offshore waters, it is primarily considered a coastal species limited to continental shelf waters (Perrin et al., 2002; Hammond et al., 2008), possibly due to feeding preference and reproduction. It is also commonly found in bays, estuaries, harbors, and fjords (Powell et al., 2002).

Harbor porpoises are easy to identify because they are smaller than most other cetaceans in the northern hemisphere. Males can reach up to 1.57 m in length and 61 kg in weight, while females reach up to 1.68 m and 76 kg (Reeves et al., 2002). They reach maximum girth just ahead of the dorsal fin, which gives them a robust body and short back (Reeves et al., 2002). They are medium to dark gray with a white belly and throat, a short blunt beak, and a medium-sized triangular dorsal fin. Their maximum life span is thought to be 24 years (Reeves et al., 2002). Data from the Baltic Sea indicates that females are larger than males in all age classes (Benke et al., 1997).

Despite their small size, harbor porpoises are highly mobile animals. Satellite tagging studies show that harbor porpoises have an average swim speed of 0.6-2.3 km/h, can swim distances of up to 58 km/day, and have large home ranges (Read and Westgate, 1997; Sveegaard et al., 2011). This movement likely has implications for reproduction, foraging behavior, bioenergetics, environmental preferences, and population structure.

Sexual maturity is generally reached at about 3 to 4 years, with a large proportion of mature females producing a calf every year (Read and Hohn, 1995; Koschinski, 2002; Reeves et al., 2002). Gestation lasts 10 – 11 months (Reeves et al., 2002). Mean conception date is reported as 6 July  $\pm$  9.5 days in the Bay of Fundy and Gulf of Maine and 25 July  $\pm$  20.3 days in the Kattegat and Skagerrak seas in the Baltic region (Borjesson and Read, 2003). Timing of conception was found to be significantly earlier in the Baltic Sea (18 August  $\pm$  11.8 days) than in the North Sea, but did not differ between the Kattegat and Skagerrak (Borjesson and Read, 2003). The North Atlantic harbor porpoise sex ratio has been reported as biased toward males throughout life (Lockyer, 2003). The sex ratio found in Danish waters in the Baltic region is 55:45, male:female (Clausen and Andersen, 1988; Sorensen and Kinze, 1994).

It is thought that shallow water areas are important for harbor porpoise calving, nursing, or breeding (Kinze, 1990; Hammond et al., 1995). Calving areas in the Baltic region have been identified inside the 20-meter depth contour in the northern part of the Little Belt, Great Belt, Sejro Bight, waters north of Fyn, archipelago south of Fyn, and Smalandsfarvandet (Kinze, 1990). The significantly higher proportion of calves off Sylt and Amrum in the North Sea indicates that these coastal waters are used as a preferred calving ground for North Sea harbor porpoises (Kremer et al., 1990; Sonntag et al., 1999). North Sea harbor porpoises have also been found in high densities during summer at the tip of Jylland in the northern part of the Danish

North Sea, 30km from the Danish coast at Horns Rev, and also in the German Bight (Teilmann et al., 2008), suggesting possible calving areas or even foraging areas.

Harbor porpoises' small size, high mobility, and relatively fast reproduction cycle require a great deal of energy (Read, 1999; Koopman et al., 2002; MacLeod et al., 2007). For this reason, they feed on high lipid content fishes (Perin et al., 2002), though preferred prey species can vary regionally based upon availability (Koschinski, 2002; Perrin et al., 2002; Hammond et al., 2008). Harbor porpoises are solitary feeders and do not cooperatively forage (Reeves et al., 2002). Herring, sprat, and cod have been reported as the most important schooling fish prey items in the Baltic Sea (Koschinski, 2002), and harbor porpoises in Polish Baltic waters have been reported to feed on herring, sprat, and gobies (Malinga et al., 1997). Harbor porpoises in the Baltic Sea feed opportunistically on certain species found in their local area (Koschinski, 2002), and this may be the explanation for significant differences in species preference when compared to harbor porpoises in other areas, such as the North Sea (Benke et al., 1998). Harbor porpoises in the Kattegat and Skagerrak seas are reported to feed on Atlantic herring as juveniles and Atlantic hagfish as adults (Boerjesson et al., 2003).

Long-distance migrations of Baltic harbor porpoises were thought to occur in the past (Mohl-Hansen, 1954; Wolk, 1969; Andersen, 1982; Gaskin, 1984). This assumption of a massive seasonal migration has since been challenged in the literature (Kinze, 2008; Andersen and Clausen, 1993), and modern telemetry research in the Baltic region has shown there to be more of a seasonal net movement rather than complete seasonal migration (Read and Westgate, 1997; Teilmann et al., 2008; Sveegaard et al., 2011).

Environmental conditions may drive some of their net movement. Decreasing access to food or air and ice entrapments could occur when the Baltic Sea almost completely freezes

during harsh winters, causing reports of mass deaths of harbor porpoises (Teilmann and Lowry, 1996). There are severe ice conditions reported in the southeastern Baltic Sea, but they are not consistent (Seina and Palusuo, 1996). There have been several winters with almost complete ice coverage in the Baltic Sea, which would have forced harbor porpoises from the Baltic Sea into the Belt Sea (Teilmann and Lowry, 1996; Koslowski and Schmelzer, 2007).

Environmental preferences for ideal foraging and reproduction conditions could also drive their movement. Telemetry studies of harbor porpoises in the Baltic region show that they concentrate in some areas (Read and Westgate, 1997; Teilmann *et al.*, 2008; Sveegaard *et al.*, 2011). Sveegaard *et al.* (2011) collected satellite telemetry data to identify key habitat use in the Baltic region by tagging harbor porpoises from a Skagerrak group (northern Kattegat, Skagerrak, North Sea) and an Inner Danish Waters group (southern Kattegat, Belts Seas, western Baltic Sea). They found that harbor porpoises in the region are not evenly distributed, and reported nine high density areas for the region, with clear seasonal movement for all animals tracked. Porpoises from the Inner Danish Waters group move south in winter, whereas porpoises from the Skagerrak group move west to the North Sea; during the spring and summer reproductive period, the Skagerrak group stays close to one particular area, while the Inner Danish Waters group spreads out over the entire range of their distribution. No difference was found in home range size in relation to sex for the Inner Danish Waters group, but males of the Skagerrak group had larger home ranges than the females. A more recent abundance study by Viquerat *et al.* (2014) confirmed that harbor porpoises in the Baltic region are not evenly distributed and reported them to concentrate in high density areas.

There is also other evidence that harbor porpoises move across water bodies in the Baltic region. Stable isotope analysis of prey items from the Baltic and Kattegat/Skagerrak Seas has

shown that harbor porpoises move between the Baltic and Kattegat/Skagerrak Seas, although the magnitude of these movements is not well known (Angerbjoern et al., 2006). An extensive review of sighting surveys and tagging has indicated extensive movement of animals within and between Inner Danish Waters and the Skagerrak/North Sea (Lockyer and Kinze, 2003).

#### DPS Analysis

The petitioner did not define the geographic boundaries of its petitioned Baltic Sea subpopulation. Therefore, we used the best available data from the region to determine whether any boundaries exist that could be used to define a DPS within the Baltic region. Here we review the best available information, including information on physical, physiological, ecological, and behavioral factors, to identify a Baltic Sea subpopulation and determine whether it is a DPS, as defined in our Policy.

The harbor porpoise is comprised of three subspecies in the northern hemisphere, which are assumed to be reproductively segregated by ocean basin: the North Pacific (Phocoena phocoena vomerina, Gill, 1865), North Atlantic (P. phocoena phocoena, L., 1758), and Black Sea/Sea of Azov (P. phocoena relicta, Abel, 1905) (Gaskin, 1984; Rosel et al., 1995). Within the North Atlantic subspecies, some authors have classified the Eastern and Western Atlantic harbor porpoises as populations based on migration distance (Gaskin, 1984; IWC, Sub-Committee on Small Cetaceans, 1996). More recently, genetic studies also differentiate harbor porpoises from the Eastern and Western Atlantic (Rosel et al., 1999; Tolley et al., 2001); however, an analysis using mitochondrial DNA has shown that movement of harbor porpoises across the Atlantic does occur at a low level (Rosel et al., 1999). Harbor porpoises in the Western Atlantic exhibit higher genetic diversity than those in the Eastern Atlantic (Tolley et al., 1999). Finer-level genetic

patterns of population structure remain to be resolved for the Eastern Atlantic population (Tolley et al., 2004).

The coastal nature of harbor porpoises led to an assumption of depth-restricted movement and a widespread acceptance of the proposal of thirteen populations in the North Atlantic (Tolley et al., 1999) (Figure 1): (1) Gulf of Maine/Bay of Fundy; (2) Gulf of St. Lawrence; (3) Newfoundland and Labrador; (4) West Greenland; (5) Iceland; (6) Faroe Islands; (7) Norway and Barents Sea; (8) North Sea; (9) Kattegat and adjacent waters; (10) Baltic Sea; (11) Ireland and Western British Isles; (12) Iberia and Bay of Biscay; and (13) Northwest Africa (Gaskin, 1984; Yurick and Gaskin, 1987; IWC, Sub-Committee on Small Cetaceans, 1996; Rosel et al., 1999; Andersen, 2003). Regional genetic and other studies have attempted to detail a finer subpopulation structure in the Eastern and Western Atlantic and test the assumption of the above divisions.

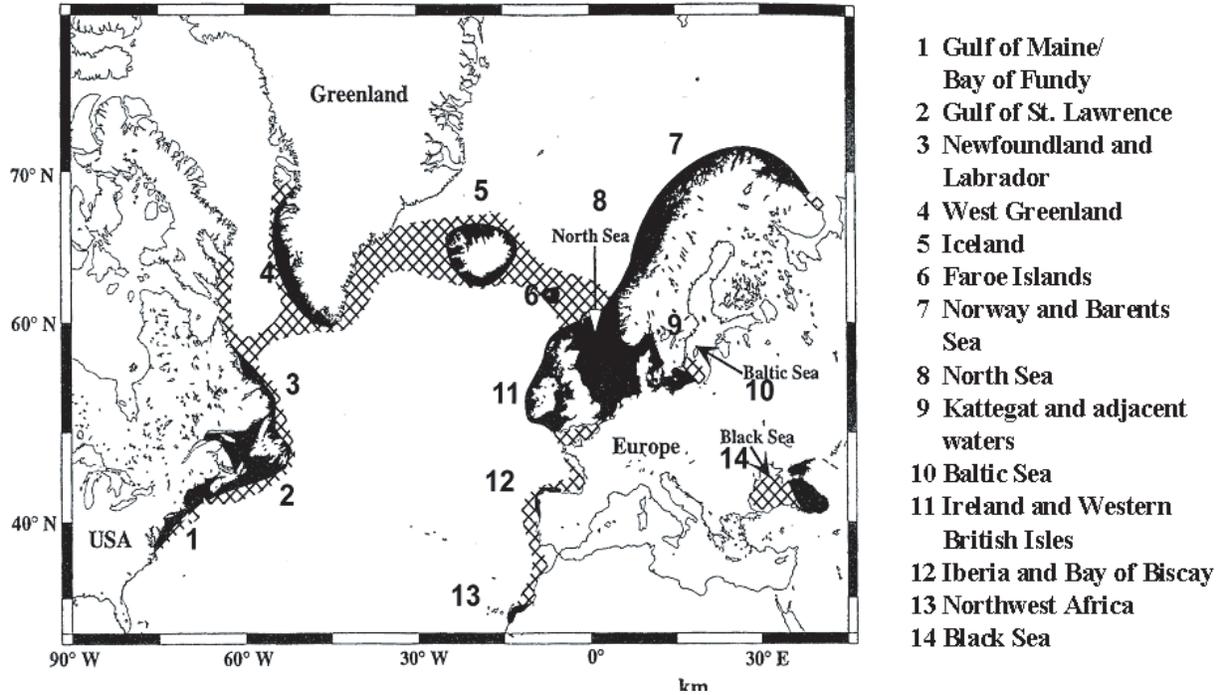


Figure 1. North Atlantic harbor porpoise subpopulations as represented in the literature based on an assumption of depth-restricted movement. From Andersen (2003). The Black Sea population is not discussed further in this document, since we are focusing on the North Atlantic and Baltic.

## Discreteness

Available information to inform our analysis of “discreteness” consists of genetic studies, skull measurements, contaminant profiles, and tooth ultrastructure. We examined the best available information in each of these categories to determine whether there is a set of individuals in the Baltic region that is discrete from the rest of the taxon (Figure 2).



Figure 2. Map depicting the Baltic region – “Baltic Sea proper” and nearby westward water bodies of the Belt Seas, Kattegat, and Skagerrak. The Limhamn and Darss underwater ridges (uw. r.) are shown in black bars with arrows which typically depict the western border of the “Baltic Sea proper”. Great Belt (Gr. Belt) and Little Belt (Ltl. Belt) are often referred to as the Belt Seas. From [Palme et al., 2008](#).

### Genetic Information

Several genetic studies on the harbor porpoise have been conducted in the Baltic region using a wide range of methods, sampling locations, sample pooling, and genetic markers, which are not consistent among research groups. The most common genetic analyses have used mitochondrial DNA, followed by microsatellites, Random Amplified Polymorphic DNA (RAPD), and isozymes to infer genetics.

Three studies tested for genetic divergence of individuals inhabiting the Baltic Sea proper, as defined by the western boundary at the Limhamn and Darss underwater ridges (Stensland, 1997; Wang and Berggren, 1997; Wiemann *et al.*, 2010) (Figure 2). These studies did not find consistent support for a genetically distinct subpopulation within the Baltic Sea proper. For instance, Stensland (1997) found no significant differences between samples from the Swedish portion of the Baltic Sea proper and the Skagerrak when using a RAPD technique. Wiemann *et al.* (2010) used mitochondrial and microsatellite DNA to demonstrate a small but significant genetic separation between the Baltic Sea proper and the Belt Seas. However, migration rates between the Baltic Sea proper and adjacent Belt Seas were estimated to be high, at 7.5 migrants per generation. Due to low genetic divergence, and evidence for continued gene flow and movement, the authors admitted that “it is difficult to argue in favour [sic] of a ‘demographic independency’ of the Baltic Sea population.” Overall, existing research is consistent in supporting low or no divergence among individuals from the Baltic Sea proper as compared to others in the Baltic region, supporting continued genetic exchange and lack of reproductive isolation or demographic independence. Thus, due to the low extent of differentiation and lack of statistical confidence in these results, the weight of genetic evidence

does not support a conclusion that there is a discrete Baltic Sea proper subpopulation in accordance with our DPS Policy.

Even though available genetic information did not support the conclusion that there is a discrete Baltic Sea proper population, a thorough review of available genetic information for harbor porpoises in the entire Baltic region revealed consistent support that individuals from the region are genetically differentiated from those individuals inhabiting the North Sea. First, all of the microsatellite and mitochondrial DNA methods used by Andersen (1993; Anderson et al., 1995; Anderson et al., 1997; Anderson et al., 2001) differentiated samples from Inner Danish Waters (pooled sample set from the Kattegat, Belts, and Baltic Seas) and the North Sea. Tiedemann et al. (1996) also found a highly significant difference in mitochondrial haplotype compositions between their North Sea and Baltic Sea (pooled sample set from the Baltic Sea proper and Belt Seas) samples. These earlier studies provide consistent support that individuals in the North Sea have diverged from those inhabiting the waters of the Baltic region.

The study by Wiemann et al. (2010) provides further evidence supporting divergence of North Sea individuals from other Baltic region individuals. They suggested that this genetic transition occurs in the Kattegat Sea, based on the most comprehensive mitochondrial and microsatellite DNA study on 497 harbor porpoises in the Baltic region. They detected overall weak population structure in the region. However, the population structure that was detected showed a tendency for the North, Skagerrak, and Kattegat Seas to cluster separately from the Belt and Inner Baltic Sea samples, with strong evidence for mixture of genetic lineages throughout the region. The transition zone in the Kattegat Sea area was supported by an abrupt shift in haplotype composition; one particular haplotype that is almost absent in the North Sea was the most abundant in the Belt Sea and Inner Baltic Sea. Furthermore, mitochondrial DNA

pairwise comparisons of genetic divergence among Skagerrak and Kattegat samples showed significant divergence between them, indicating that the genetic split likely occurs somewhere within the Kattegat Sea. This study obtained generally strong agreement between independent data from microsatellite and mitochondrial haplotypes, providing robust support for this genetic transition zone in the Kattegat Sea.

Based on the best available genetic data, there is evidence that the harbor porpoise is weakly diverged between the North Sea and the Baltic region past Kattegat and south/eastward into the Baltic Sea.

#### Skull Comparison Information

Skull comparisons of harbor porpoises in the Baltic Region have also been used to explore morphological evidence for population structure. The weight of available skull information aligns with genetic information in that it differentiates North Sea harbor porpoises of both sexes from those in the Baltic region. A finer population structure is seen for females within the Baltic region, but this same skull differentiation is not seen in males.

Skull studies support the genetic information indicating a genetic break, or transition zone, between the North Sea and the Baltic region. Non-metric (not measured) skull characters of harbor porpoises from the North Sea and Baltic Sea are found to differ (both sexes; Kinze 1990, Huggenberger *et al.* 2000). In addition, harbor porpoise skull measurements are different between the North Sea and Baltic Sea (both sexes; Kinze, 1985, 1990; Borjesson and Berggren, 1997; Huggenberger *et al.*, 2000; Galatius *et al.*, 2012).

Some skull studies achieved a finer-scale geographic resolution of harbor porpoises in the Baltic region. However, the statistical results of these studies are more robust in females than in males, suggesting male migration and mixing between areas (Huggenberger *et al.*, 2002).

Borjesson and Berggren (1997) examined harbor porpoise skulls from the Baltic Sea proper and the Kattegat and Skagerrak Seas and their statistical analyses showed geographically-relevant differences in skull characters between females from the Baltic Sea proper and the Kattegat and Skagerrak Seas, but not the same for males; five of 16 skull characters were significantly different in female samples, whereas one of 16 skull characters significantly differed in male samples.

Galatius et al. (2012) used geometric morphometric skull comparisons (70 cranial landmarks registered with a 3-D digitizer) from six geographic areas - the North Sea, Skagerrak Sea, Kattegat Sea, Belt Seas, western Baltic, and Inner Baltic Sea and found highly significant shape differences in skulls among these six geographic areas. There were no significant differences between males and females or sampling seasons within any of the samples. Their results indicate a morphometric segregation of harbor porpoises within the Belt Seas/Inner Baltic Sea. However, this study stands alone in differentiating this fine population structuring within the Baltic region, as the weight of genetic and other skull information does not support the same conclusion.

The weight of available skull information aligns with genetic information in that it differentiates North Sea harbor porpoises of both sexes from those in the Baltic region. Available skull information provides evidence of a finer population structure within the Baltic region for females, but not for males. This difference provides evidence of exchange of male, but not female, individuals between and among the Baltic region and the North Sea. One skull study was able to detail a fine population structure for both sexes within the Baltic region, but the weight of other available evidence does not support such a conclusion.

#### Contaminant Profile Information

A few studies have distinguished North Sea or Skagerrak harbor porpoises from the rest of the Baltic region based on contaminant levels and patterns. Bruhn et al. (1997; 1999) analyzed blubber samples in harbor porpoises from the German North Sea, Baltic Sea proper, and off the west coast of Greenland. Clear differences existed between the Baltic Sea proper and North Sea animals for certain contaminants. Berggren et al. (1999) found that mature males in the Swedish part of the Baltic Sea had significantly different contamination patterns of polychlorinated biphenyls (PCBs) than animals from the Swedish Kattegat and Skagerrak coasts and from western Norway. This information is consistent with genetic information to show population differences between the North Sea and Baltic region.

#### Tooth Ultrastructure Information

Tooth ultrastructure in the harbor porpoise has been examined to differentiate between porpoises from different regions. Lockyer (1999) found different characteristics in tooth layers, which may be genetic in origin or influenced by life history events or other factors. The author found significant differences in several tooth characteristics between the North Sea, Skagerrak Sea, Kattegat Sea, Inner Danish waters, and the Baltic Sea proper. Lockyer (1999) stated the use of tooth ultrastructure alone “is not sufficient to allow an individual animal to be assigned to a particular management unit.” Thus, her results are not informative alone and should be combined with other studies when helping to delineate a population structure. The tooth ultrastructure study does not align with genetic and other information, since it differentiates a finer scale than is supported by the weight of available information. Therefore, we do not find this information persuasive.

#### Conclusion Regarding Discreteness

After combining the weight of evidence from genetic, skull, contaminant, and tooth studies we conclude that there is a discrete subpopulation of harbor porpoises in the Baltic region (from the Kattegat Sea, at the genetic break found by Wiemann et al. (2010), eastward into and including the Baltic Sea proper). Although there are shared haplotypes among harbor porpoises in the Baltic region and evidence of some male movement to suggest that a certain level of gene flow exists within the Baltic region, the repeated evidence of statistically significant genetic divergence from North Sea/Skagerrak samples guides our conclusion that this can be considered a discrete subpopulation. Available information on skull measurements and contaminant studies supports our conclusion based on genetic information, since these studies also differentiate North Sea/Skagerrak harbor porpoises from those in the Baltic region. Lockyer's (1999) study differentiated tooth structure among harbor porpoises from the North Sea, Skagerrak, Kattegat, Inner Danish waters, and the Baltic Sea; however, she caveats that this must be combined with other supporting information, and we did not find that the weight of other available information supports her proposed population structure. The weight of all evidence favors our conclusion of a population split at the Kattegat Sea.

Since we determined that there is a discrete Baltic region subpopulation, we next determine whether the discrete population is significant to the taxon. From this point forward in the document, we define the Baltic harbor porpoise subpopulation as beginning at the Kattegat inward (south/east) to and including the Baltic Sea proper.

### Significance

The identified discrete Baltic subpopulation does not persist in an ecological setting unusual or unique for the taxon. Differences seen in harbor porpoise morphological characteristics (skull and tooth analyses) may be related to differences in environment, but

available information is not informative enough at this point to link these characteristics to distinct habitats or specific adaptations at present. The habitat utilization reported for the Baltic harbor porpoise does not differ from general descriptions of the species' habitat preference. They are found in the shallow coastal areas of the Baltic region and their preference for shallow water calving and nursing does not differ from the general preference of the species. The opportunistic feeding nature of the Baltic harbor porpoise also does not show it to persist in a unique ecological setting. They target high lipid content fish to fulfill large energetic requirements, similar to the general preference of the species.

There are insufficient data to conclude that loss of the identified discrete Baltic subpopulation would result in a significant gap in the range of the taxon. The Baltic subpopulation comprises only a small geographic area in the total range of the species and even the subspecies. There are purported to be around ten other subpopulations in the North Atlantic (Tolley *et al.*, 1999) and other harbor porpoise populations in the North Pacific and Black Sea. Additionally, available information reveals movement and some level of gene flow throughout the Baltic region through evidence of shared haplotypes, which is discussed further below. Although there are caveats to determining the exact level of mixing between the North Sea and Baltic region (and vice versa), there is evidence to show at least some level of mixing, such that a loss of the Baltic subpopulation would not lead to a significant gap in the range of the taxon. There is evidence of continued admixture and gene flow between these regions. This gene flow may be sustained by the high dispersal capacity and movement of these animals, and the lack of obvious physical barriers between the regions.

While multiple studies confirm divergence between individuals from the North Sea and those inhabiting the Baltic region past the Kattegat Sea, the absolute extent of divergence is

consistently weak. For instance, all analyses of mitochondrial haplotype distribution have revealed shared haplotypes throughout the region, even across the Kattegat ‘transition zone’ (Tiedemann *et al.*, 1996; Wang and Berggren, 1997; Wiemann *et al.*, 2010). In Wiemann *et al.* (2010), an abrupt shift in microsatellite haplotype distribution was observed between the North Sea and Baltic region past the Kattegat Sea, but the two most abundant haplotypes only differ by a single point mutation. No physical barrier exists between the Kattegat and the North Sea, porpoises are known to move long distances (Teilmann *et al.*, 2009), and evidence suggests that genetic connectivity can occur among harbor porpoises separated thousands of kilometers in the North Atlantic (Tolley *et al.*, 1999; Fontaine *et al.*, 2007). So, while the weak divergence (separating the North Sea from the Baltic region) is well supported, continued genetic exchange, connectivity, and ongoing reproduction among animals throughout the region is likely.

There is no evidence that the identified discrete Baltic subpopulation represents the only surviving natural occurrence of a taxon that may be more abundant elsewhere as an introduced population outside its historical range. Harbor porpoises are historically widespread in the northern hemisphere. As stated previously, within the North Atlantic subspecies, genetic studies differentiate harbor porpoises between the Eastern and Western Atlantic, with some level of mixing. The Baltic subpopulation does not represent the only surviving natural occurrence of a taxon that may be more abundant elsewhere as an introduced population outside its historical range, as there are clearly many other existing natural populations.

There is no evidence that the identified discrete Baltic population differs markedly from other populations of the species in its genetic characteristics. The attachment of skull characters to unique environments or conditions would show evidence of adaptive genetic characteristics; however, the available harbor porpoise skull information from the Baltic region does not

definitively attach characters to environmental connections to show that any skull differences are adaptive. One harbor porpoise skull study suggests that skull morphology could be attached to particular environments or conditions (Galatius et al., 2012). However, this is not supported by the weight of genetic evidence and is not even supported by other skull analyses, as they did not test adaptive skull characteristics and attach them to local or unique environmental conditions in the Baltic region. In addition, we did not find much discussion in the available literature about how differences in skull character for harbor porpoises may relate to adaptation to a particular prey item. Most of these skull studies attempt to delineate a population structure without testing the attachment of particular skull distinctions or characteristics.

#### Conclusion Regarding Significance

In conclusion, we find that the Baltic harbor porpoise subpopulation, while it may be discrete, does not meet any factors under the significance criterion. As such, we conclude that the Baltic harbor porpoise subpopulation is not a DPS as defined by our joint DPS Policy.

#### Finding

We find that the Baltic harbor porpoise subpopulation does not meet the DPS Policy criteria for qualifying as a DPS. Therefore, listing the petitioned entity under the ESA is not warranted.

#### References Cited

A complete list of all references cited in this notice can be found on our Web site and is available upon request (see ADDRESSES).

Authority

The authority for this action is the Endangered Species Act of 1973, as amended (16 U.S.C. 1531 et seq.).

Dated: March 18, 2015.

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Samuel D. Rauch, III.

Deputy Assistant Administrator for Regulatory Programs,

National Marine Fisheries Service.

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