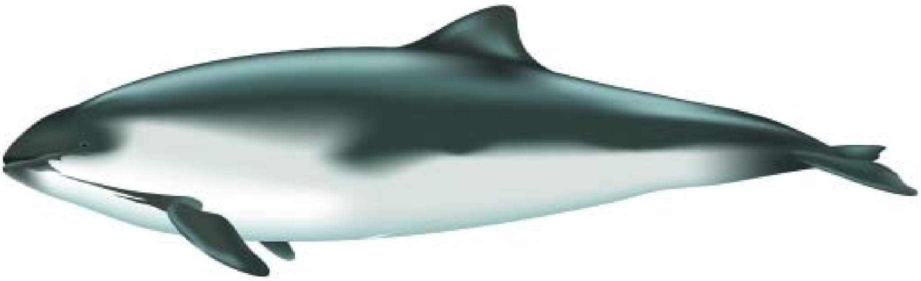
Baltic Sea Porpoise Database
Sharing across the borders



Final Report

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Summary

Early in the 20th century harbour porpoises were abundant in the central and eastern Baltic Sea (the so-called Baltic proper). During the last century whaling, ice winters, habitat loss, by-catch, and a decline of available food sources resulted in a drastic decline of these eastern harbour porpoise populations, and protective measures assumed urgency. The goal of the present database was to gather any historical and current data from the Baltic region and allow evaluations across borders. The database is based on six different categories: accidental sightings, targeted observations, strandings and animals found dead, by-catch, hunting/killings, and acoustic detection (Fig. 1). The database entries date from the early 20th century to the present. Each entry is accompanied by a data reference and an original data ID. The data reference identifies the original data source, the original data ID allows a clear identification of the original data source. The database is currently comprised of 1,237 data sets and will be accessible to scientists, governmental agencies and the general public. Access to the data occurs only in agreement with the scientists and institutions providing the data.

History of the Database on Baltic Harbour Porpoises

Early in the 20th century harbour porpoises were abundant in the central and eastern Baltic Sea (the so-called Baltic proper). Various studies have established that these animals belong to their own subpopulation, which has been shown to be distinct from harbour porpoise populations in the western Baltic. During the last century whaling, ice winters, habitat loss, by-catch, and a decline of available food sources resulted in a drastic decline of these eastern harbour porpoise populations, and protective measures assumed urgency. Because standard methods for determination of abundance and distribution – such as surveys by airplane or ship – have limited use in areas with low animal density, the need for development and application of alternative methods grew. These methods are expected to provide the foundation for possible protective measures and further research.

Goal

Knowledge of harbour porpoises in the eastern Baltic is currently sparse. However, many countries bordering the Baltic Sea possess both anecdotal and scienific proof and documentation of this population – though often unpublished and only available in the local language. Goal of this subproject of the Jastarnia Plan is the creation of a database which combines knowledge about Baltic harbour porpoises and makes it available to all littoral states.

Structure of the Database

The database is based on six different categories: accidental sightings, targeted observations, strandings and animals found dead, by-catch, hunting/killings, and acoustic detection (Fig. 1). The database entries date from the early 20th century to the present. Each entry is recorded in as much detail as possible, with older entries usually being less detailed than the more recent ones.

MAIN DATABASE POD
ID: INTEGER
PODNr: VARCHAR(255)
PODName: VARCHAR(255)
DatumDerSichtung: DATETIME
Feld4: VARCHAR(255)
Feld5: VARCHAR(255)
PrimaryKey
ID

Position POD
ID: INTEGER
Bezeichnung: VARCHAR(255)
Name: VARCHAR(255)
Abkürzg: VARCHAR(255)
Tiefe m: DOUBLE
Latitude: DOUBLE
Longitude: DOUBLE
PrimaryKey
ID

MAIN DATABASE Incidental Sightings
ID: INTEGER
Day: VARCHAR(50)
Month: VARCHAR(50)
Year: VARCHAR(50)
Time: VARCHAR(50)
Time Description: VARCHAR(50)
Country: INTEGER
Data Description: VARCHAR(50)
Data Reference: BLOB
ID of Original data: VARCHAR(50)
Species: INTEGER
Latitude: DECIMAL
Longitude: DECIMAL
Position Description: BLOB
Position Description Short: VARCHAR(50)
Distance Diviation (km): VARCHAR(50)
Position Accuracy: INTEGER
Pod size: VARCHAR(50)
Pod size Error(plus/minus): VARCHAR(50)
Calfs present: VARCHAR(50)
Number of calfs: VARCHAR(50)
Behaviour: BLOB
Sightingsplatform: INTEGER
Other Comments: BLOB
PrimaryKey
ID
Database Code
Country
ID
ID
ID of Original data
ID of Original data
MAIN DATABASE Incidental SightingsPosition Accuracy
Position Accuracy
MAIN DATABASE Incidental sightingsSpecies
Species
MAIN DATABASE Incidental sightingsTime
Time
MAIN DATABASE Incidental sightingsVesseltype
Sightingsplatform

MAIN DATABASE Effort Sightings
ID: INTEGER
Day: INTEGER
Month: INTEGER
Year: INTEGER
Time: DATETIME
Country: INTEGER
Data Description: VARCHAR(50)
Data reference: BLOB
ID of original data: INTEGER
Species: INTEGER
Latitude: DECIMAL
Longitude: DECIMAL
Position Accuracy: INTEGER
Sea State: VARCHAR(50)
Podsize: INTEGER
Calfs present: VARCHAR(50)
Number of calfs: VARCHAR(50)
Behaviour: INTEGER
Reaction to plane: VARCHAR(50)
Cue: VARCHAR(50)
PrimaryKey
ID
Database Code
Country
ID
ID
ID of original data
ID of original data
MAIN DATABASE Effort SightingsSpecies
Species
MAIN DATABASE Effort SightingsTime
Time

MAIN DATABASE Strandings
ID: INTEGER
Country: INTEGER
Data Description: VARCHAR(50)
Data Reference: VARCHAR(50)
ID of original database: VARCHAR(50)
Species: INTEGER
Sex: INTEGER
Day: VARCHAR(50)
Month: VARCHAR(50)
Year: VARCHAR(50)
Latitude: DECIMAL
Longitude: DECIMAL
Position Description: VARCHAR(200)
Distance Diviation (km): VARCHAR(50)
Position Accuracy: INTEGER
Finder: VARCHAR(50)
Calf: VARCHAR(50)
Number of calfs: INTEGER
Age of animal: INTEGER
Length of animal (cm): VARCHAR(50)
Weight of animal (kg): VARCHAR(50)
Other comments: VARCHAR(50)
PrimaryKey
ID
Database Code
Country
ID
ID
MAIN DATABASE StrandingsPosition Accuracy
Position Accuracy
MAIN DATABASE StrandingsSpecies
Species

MAIN DATABASE Bycatch
ID: INTEGER
Country: INTEGER
Data Description: VARCHAR(50)
Data Reference: VARCHAR(50)
ID of original database: VARCHAR(50)
Species: INTEGER
Sex: INTEGER
Day: VARCHAR(50)
Month: VARCHAR(50)
Year: VARCHAR(50)
Latitude: DECIMAL
Longitude: DECIMAL
Position Description: VARCHAR(200)
Distance Diviation (km): VARCHAR(50)
Position Accuracy: INTEGER
Calf: VARCHAR(50)
Number of calfs: INTEGER
Age of animal: INTEGER
Length of animal (cm): VARCHAR(50)
Weight of animal (kg): VARCHAR(50)
Finder: VARCHAR(50)
Other comments: VARCHAR(50)
PrimaryKey
ID
Database Code
Country
ID
ID
MAIN DATABASE BycatchPosition Accuracy
Position Accuracy
MAIN DATABASE BycatchSpecies
Species

Position Accuracy_Incidental sightings
Position Accuracy: INTEGER
Distance Diviation: VARCHAR(50)
PrimaryKey
Position Accuracy

Sightingsplatform
Sightingsplatform: INTEGER
Platform Description: VARCHAR(50)
PrimaryKey
Sightingsplatform

Species
ID: INTEGER
Species: INTEGER
Scientific Name: VARCHAR(50)
Danish Name: VARCHAR(50)
English Name: VARCHAR(50)
Estonian Name: VARCHAR(50)
Finnish Name: VARCHAR(50)
German Name: VARCHAR(50)
Latvian Name: VARCHAR(50)
Lithuanian Name: VARCHAR(50)
Polish Name: VARCHAR(50)
Russian Name: VARCHAR(50)
Swedish Name: VARCHAR(50)
PrimaryKey
ID
SpeciesSpecies
Species

Sex
Sex_: INTEGER
Sex: VARCHAR(50)
PrimaryKey
Sex_
SexSex
Sex

Position Accuracy_StrandingsBycatches
Position Accuracy: INTEGER
Distance Diviation: VARCHAR(50)
PrimaryKey
Position Accuracy

Day Description
Time: VARCHAR(50)
Day Description: VARCHAR(50)

Animal Behaviour
Behaviour Code: INTEGER
Animal Behaviour: VARCHAR(200)
PrimaryKey
Behaviour Code
Behaviour Code
Behaviour Code

Age
Age Code: INTEGER
Age: VARCHAR(50)
PrimaryKey
Age Code
Age Code
Age Code
AgeAge
Age

Figure 1: Database structure. The amount of information varies from entry to entry.

Each database entry is accompanied by a data reference and an original data ID. The data reference identifies the original data source. The original data ID allows a clear identification of the original data source should additional information about certain entries be required. The country and institution providing the respective data are identified in each entry. Date, time and position of the registration (collection) for each data set are stored as well.

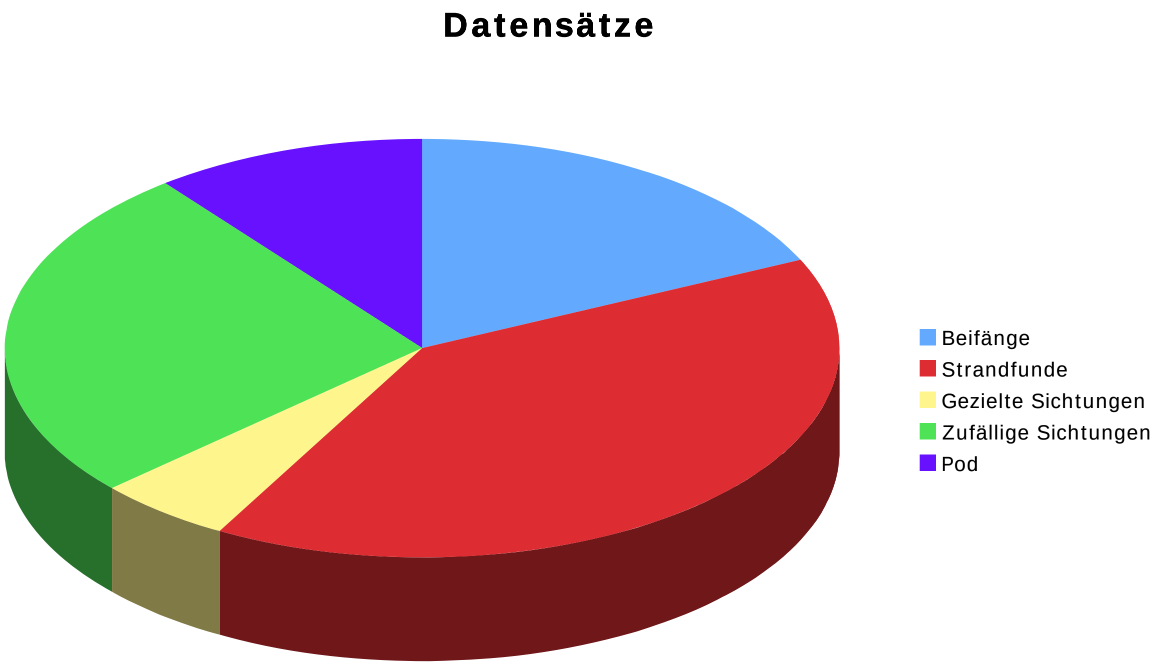
For both targeted and accidental sightings, the type of sighting platform used (e.g. airplane, ship) and the existing sighting conditions (swell, misting, cloud cover, sun reflection on the water, etc.) are registered. Observations about the group size, presence of calves and behaviour are recorded.

Acoustic data collected by the German Oceanic Musem during part 1 of the Jastarnia project with acoustic harbour porpoise detectors (TPODs) are also integrated in the database. For each POD station the exact geographic position is included. In addition, date and time of the registration are noted. POD data from other countries have not been made available to the project as of yet.

Regarding the by-catches, strandings and hunted harbour porpoises (historical data) the finder and/or hunter were registered, in addition to general information such as sex, age, length and weight. Data regarding reproductive biology (pregnancy, weight and measurements of the gonads) and health status (pathological, microbiological and virological findings) collected and/or evaluated at the FTZ during part 4 are also included in the database. For by-catches, the net type in which the animal was caught is also recorded.

Information obtained from the genetic investigations of the University of Potsdam during part 3 is included. The genetic population structure of the Baltic harbour porpoises was investigated using sequencing of the polymorphous mitochondrial control region and fragment length analysis of 15 highly polymorphous nuclear microsatellite loci. In the MtDNA 45 different genotypes (= haplotypes) were found. The frequency of these haplotypes and the microsatellite distribution differ significantly from one ICES region to another, which indicates a limited gene exchange.

Currently, the database contains 1,237 data sets subdivided as follows (Fig. 2):



Figues 2: Breakdown of the data sets in the database

The database will be accessible to scientists, governmental agencies and the general public. Access to the data occurs only in agreement with the scientists and institutions providing the data. Last but not least, the database will serve as a teaching tool to increase knowledge about the Baltic harbour porpoise.

To ease access the database will be available as an interactive map at a special website (www.balticseaporpoise.org) on the internet. Here, general information about the harbour porpoise and this project may be found as well as information on other harbour porpoise projects in the Baltic Sea and links to websites featuring related topics (Fig. 3). The contributing institutions are named and their logos presented. Contact information for the database, contact addresses in the different countries as well as links to their websites will be listed. Research projects to be presented by these countries will be introduced.

Baltic Sea Porpoise Project

Welcome

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The harbour porpoise

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Webmaster: Ida Carlén

The Baltic Sea Porpoise Project is a part of the Jastarnia project, and funded by the Federal Agency for Nature Conservation in Germany. The project is based on a database for sightings, strandings and bycatches of harbour porpoises in the Baltic Sea, and the idea is that all organisations/agencies around the Baltic Sea can provide data. The goal of the project is to work as a forum for researchers as well as an educational tool for the general public.

We thank the following parties for their contributions
Valdis Pilats, Latvia; Carl Kinze, Denmark; Ivar Jussi, Estonia and Heini Kujala, Finland

Figure 3: Internet page for the database: www.balticseaporpoise.org

Development

Since the beginning of the project in 2004 almost all littoral states have contributed data to the database. On the German side, the Research and Technology Centre Westcoast, the German Oceanic Museum Stralsund and the Gesellschaft zum Schutz der Meeressäugetiere e.V. [Society for the Protection of Marine Mammals e.V.] have provided information about by-catches, targeted and accidental sighting data and animals found dead. The Swedish Museum of Natural History and Valdis Pilates (Gauja National Park Administration, Latvia) transmitted information regarding by-catches and animals found dead in their waters. For Danish waters, Carl Kinze compiled a listing of by-catches, animals found dead and accidental sightings from data of the Natural Forest and Nature Agency and the Fishery and Maritime Museum. In Finland, Heini Kujala and Penina Blankett (Finish Ministry of the Environment) collected information regarding accidental sightings, and Estonia provided data about animals found dead and killed animals through Ivar Jüssi (Governmental Centre for Nature Protection, Estonia). From Poland, Iwona Kuklik (Hel Marine Station, University of

Gdansk) contributed data on accidental sightings and animals found dead. The ESAS database made it possible to add further targeted sightings to this database.

The database had originally been compiled with Microsoft Access. However, this software application provided only an insufficient interface for the publication of georeferenced data through the internet. The database was therefore exported to PostgreSQL. This application, especially with the expansion of PostGIS, is well suited to use the database for web-based GIS. Also, the software application used to compile the interactive map was replaced last year. While the previous application, ArcGIS, was ideal for creating the map, another application, ArcIMS would have been required to publish the map on the internet. Unfortunately, the project funding was insufficient to obtain a license for ArcIMS. Instead, the map and its representation on the internet are now accomplished using MapServer, an open source GIS. To increase awareness about the database, the project was introduced as a poster at last year's conference of the European Cetacean Society in Gdynia, Poland, in April 2006. The conference attendees were given opportunities during several poster sessions to ask specific questions regarding the poster and the project. They provided invaluable feedback and it was possible to intensify the cooperation.

Comparison of the Project Status with Original Planning

The project was implemented as planned. A database was developed. Data provided by the littoral states of the Baltic Sea were included in the database. Data collected during other parts of the projects, such as the POD data from the German Oceanic Musem, genetic data from the University of Potsdam as well as the pathological and biological data on animals found dead (FTZ) were integrated in the database. Once again, it should be noted that the limited available funding had a very restrictive effect on the inclusion of IT experts. The current state of the database would not have been achieved without extensive use of FTZ's own funds.

In addition to the importance of the project at the national level, it is also significant for its international cooperation, which is one reason why it is important to advertise the database in the future, to present it at international meetings and describe it in publications. The FTZ will continue to provide upkeep of the database. Contact with the scientists will be maintained. At the same time, financing is sought to expand the database and particularly its internet presentation.

1.1 Glossary

ESAS	European Seabirds at Sea
Gene locus	Location of a gene sequence
Haplotyp	Haplotype, a combination of the words haploid and genotype, designates the genetic makeup of a chromosome. Only individual sequences of a special combination of coupled genes is described. The haplotype thus is a nucleotide sequence at a specific location of the genotype unique to each individual.
Microsatellites	(syn. simple sequence repeats (SSR) or simple sequence length polymorphisms (SSLP)) are short, non-coded sequences repeating multiple times in the genome of an organism.
MtDNA	Mitochondria possess their own genome which is located in the mitochondrial matrix and frequently copied multiple times. The genome has the shape of a circular double-helix MtDNA and uses its independent duplication cycle. Mitochondria are described as semiautonomous since their genome itself codes only a small share of the proteins needed by the mitochondrion. In humans, 37 mitochondrial genes control the synthesis of 13 of the approx. 80 protein subunits of the respiratory chain, the remaining 800-1,000 different mitochondrial proteins are coded in the nuclear genome.
Nuclear microsatellites	Microsatellites located in the genome of the nucleus. Microsatellites may be used for gene analysis because the number of repetitions differs from individual to individual and therefore produces DNA fragments of varying lengths during division with a restriction enzyme. This allows determination of polymorphisms in the DNA.
POD porpoise detector	Harbour porpoise click detector
Polymorphism	In the field of genetics, the appearance of a gene variant (i.e. an allele in a population) is described as a polymorphism. According to the definition, the frequency of the appearance of the gene variant (the allele frequency) must be over one percent – otherwise it would be called a mutation.

Acknowledgment

We would like to thank all people and institutions who contributed to the database. The funding was kindly provided by the German Federal Agency for Environment.