Exceptional Occurrence of a Leatherback Sea Turtle (*Dermochelys coriacea*) in the Baltic Sea

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Leatherback sea turtles (*Dermochelys coriacea*) are the most widely distributed of all extant sea turtle species, inhabiting tropical and temperate oceans globally (Davenport 1998). Their circumglobal distribution encompasses the Atlantic, Pacific, and Indian Oceans, although precise range delineation remains challenging due to their highly pelagic nature and the difficulties in tracking these elusive animals (Witt *et al.* 2008). Known nesting sites are primarily located in tropical and subtropical regions, with significant nesting aggregations observed in certain areas of the Americas, the Pacific Islands, and the Indian Ocean (Wallace *et al*. 2023). The occurrence of leatherbacks outside their typical range, especially in colder brackish waters like the Baltic Sea, is exceedingly rare.

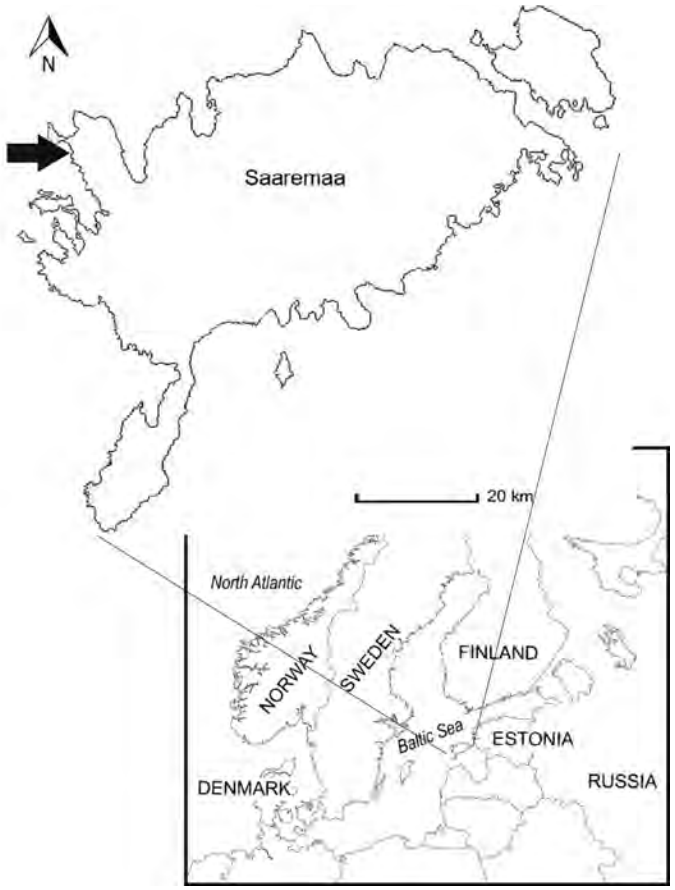

Figure 1. Location of leatherback turtle (*Dermochelys coriacea*) discovery, on 13 July 2024

On 22 July 2024, a deceased leatherback turtle (*Dermochelys coriacea*), assessed as probably subadult based on size, was discovered in shallow coastal waters off Saaremaa Island (58.459361N, 21.910643E) (Fig. 1). The specimen, measuring 108 cm in straight carapace length (Fig. 2), was deposited at the Natural History Museum of the University of Tartu (TUZ660119). Multiple muscle tissue samples (TUE007991-TUE007696) were collected for DNA analysis, preserved at -86°C, and cataloged in the PlutoF database (plutof.ut.ee; Abarenkov *et al.* 2010). Due to the absence of expertise in leatherback turtle genetics within Estonia, sample TUE007695 was sent to the Kwata NGO, Cayenne, French Guiana for genotyping and storage in the collection JAGUARS, at the Institut Paster de la Guyane (ID collection = R5281_JAG) for DNA extraction and subsequent amplification of the tRNA-Pro gene. The mitochondrial tRNA-Pro gene was chosen for its established utility in phylogenetic and population genetic studies of leatherback turtles (Dutton *et al*. 2013).DNA was extracted with NUCLISENS® easyMAG® (Biomérieux). The mtDNA control region (CR) was amplified using the primers LCM 15382 (5` GCTTAACCCTAAAGCATTGG 3´) and H950 (5´ GTCTCGGATTTAGGGGTTTG 3´) (Abreu-Grobois *et al.* 2006) and Sanger sequenced. Extraction, amplification and sequencing were done on two independant samples from the tissue. The haplotype nomenclature follows Dutton *et al.* (2013).

Control Region mtDNA genotyping of the Saaremaa specimen showed 100% identity with the haplotype 3.1 classification (Dutton *et al.* 2013). This haplotype exhibits a notable prevalence among leatherback turtles nesting in the Caribbean region (Dutton *et al.*

Figure 2. Leatherback sea turtle found dead on the coast of Saaremaa. Anchor was used to pull the specimen out of the water. Photo: Wilhelm Tell.

2013). To our knowledge, only one prior documented instance of a leatherback turtle in the southern Baltic Sea exists. This involved a 450 kg individual, 215 cm in total length, incidentally caught in a fisherman's net near Stralsund, Germany in October 1965 (https://artsandculture.google.com/asset/extrication-of-the-turtle-from-the-baltic-sea/BwEe0OzFkHYqSw?hl=en). We hypothesize that both occurrences represent random events, reflecting the species' wide distribution and extensive migratory capabilities. Given the geographical constraints of the Danish straits and the documented occurrences of other non-indigenous species within the Baltic Sea (Rolbiecki et al. 2015; https://news.err.ee/1608648100/walrus-spotted-on-latvian-beach), the observed number of leatherbacks may not fully represent the extent of their incursions into the region. Some individuals likely perish in the Baltic Sea, while others may successfully remigrate to the Atlantic Ocean. This highlights the importance of ongoing research to better understand leatherback turtle movement ecology and distribution.

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