LRH: MARINE MAMMAL SCIENCE, VOL. **, NO. *, ****

RRH: NOTES

Taxonomic status of a “finner whale” (*Balaenoptera swinhoei* Gray, 1865) from southern Taiwan

FREDERICK ARCHER[1] and **KELLY ROBERTSON**, Southwest Fisheries Science Center, 8901 La Jolla Shores Drive, La Jolla, California 92037, U.S.A.; **RICHARD SABIN**, Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom; **ROBERT L. BROWNELL, JR.** Southwest Fisheries Science Center, 8901 La Jolla Shores Drive, La Jolla, California 92037, U.S.A.

Balaenoptera Lacépède, 1804 is the most polytypic genus of baleen whales and the most widely distributed cetacean genus. This genus, whose species are colloquially known as “rorquals” has over 50 nominal species (Hershkovitz 1966). The most recent taxonomic revision included six species (Rice 1998) and one more, *B. omurai*, described by Wada *et al.* (2003) bring the total to seven. Six of the seven occur in the North Pacific with the exception being *B. bonaerensis*. However, taxonomy has remained uncertain for some of the nominal species, many of which were named between 1840 and 1870. John E. Gray at the British Museum

(Natural History) alone named 35 nominal species of baleen whales (Hershkovitz 1966). One species name that has been the most perplexing has been *B. swinhoei* Gray, 1866, which was given to a single specimen collected in Taiwan. The proximity of its collection has led us to assume that this specimen came from the east China Sea (ECS) population of fin whales (*B. physalus*). There is strong evidence that ECS fin whales represent a resident population genetically isolated from those off of the northeastern coast of Japan and the Kamchatka Peninsula, based on differences in blood type (Fujino 1960), body size measurements (Ichihara 1957), and limited distribution (Brownell 1981). The level of differentiation is sufficiently great that it is likely that they represent a distinct subspecies. Therefore, as part of a worldwide study on fin whale taxonomy, we wanted to genetically confirm that *B. swinhoei* was a fin whale as the name would be available for the ECS subspecies.

The type specimen for this nominal species was collected in 1864 by Robert Swinhoe from a whale that stranded 2 yr prior on a beach two miles (3.2 km) south of Takow, Formosa [Kaohsiung, Taiwan on the southwest coast around 22°38′N, 120°16′E] (Swinhoe 1870). Swinhoe sent the bones, which included “part of the head, three cervical vertebrae, the first and seven other dorsal vertebrae, and eight ribs” (Gray 1865), to the British Museum where they were examined by John E. Gray. Due to the similarity in the shape of the vertebral neural canal to other balaenopterids, as well as a similarity in overall size, Gray (1865) believed the specimen, which he designated as *Balaenoptera swinhoii*, was most closely related to fin whales. The following year Gray modified the species name to "*swinhoei*," also including illustrations of the second and third vertebrae, the sixth or seventh cervical vertebrae, and the first dorsal vertebra of the type specimen (Gray 1866). In addition, he provided more details of the parts of the skeleton recovered noting that they consisted of the "Upper maxillary bone, left side (the upper surface is 6 feet 6 inches, under edge of the same bone 7 feet 8 inches); three cervical vertebrae; eight dorsal vertebrae, seven of which are more or less imperfect; eight ribs, all with simple heads" (Gray 1866). Two years later, Gray (1868) elevated it to its own monotypic genus, *Swinhoia,* and renamed the species, *chinensis*, based only on a description of the lateral processes of the third to sixth cervical vertebrae, but not providing the measurements from the left side of the upper maxillary bone given in Gray (1866). Without explanation, Trouessart (1905) listed *B. swinhoei* questionably under *B. schlegelii* suggesting it was a synonym. This leads to periodically confused listings as *B. schlegelii* is currently recognized in the synonymy of sei whales, *B. borealis* (Hershkovitz 1966), or as the Southern Hemisphere sei whale subspecies *B. b. schegelii* (Rice 1998). However, Hershkovitz (1966) corrected this placement and returned *B. swinhoii*, *B. swinhoei*, and *Swinhoia chinensis* to the synonymy of *B. physalus* based on Gray's original examination and description.

All of the bones from *B. swinhoei* listed in Gray (1865) remain in the collection of the Natural History Museum, London under the catalog number NHMUKGERM 1464a (see Supplemental Materials for descriptions, measurements, and photos). Bone powder from the partial basicranium (Fig. 1) was collected at the museum by RS by low-speed drilling and then sent to the Southwest Fisheries Science Center (SWFSC) Ancient DNA (aDNA) Lab (SWFSC LabID 173864, Tissue ID 210751). Protocols for sterile technique including sterilization of equipment and surfaces with 10% bleach and single use of drill bits followed those presented in Morin *et al.* (2006). DNA extractions were performed using the method of Höss and Pääbo (1993), modified as described in Hofreiter *et al.* (2004), yielding 100 µL of DNA. PCR reactions were performed as describe by Morin *et al.* (2006), except that 5–10 µL of DNA was used per reaction, and 45 PCR cycles were performed. Negative controls were also extracted and PCR amplified to monitor the process for contamination.

Because of degradation in the aDNA, PCR was performed by amplifying three overlapping sections of the mitochondrial DNA (mtDNA) control region using several primer pairs, each approximately 200–270 base pairs (bp), in an attempt to obtain a final sequence of 400 bp. The PCR products were generated using the primers pairs TRO-A3, AD1-DL1, and D-A3r from Robertson *et al.* (2007). The amplified product was sequenced in both directions using the above primers on the Applied Biosystems Inc. (ABI) 3130 Genetic Analyzer using standard protocols and BigDye Terminator v3.1 (Applied Biosystems, Inc.) chemistry. Sequences were aligned and edited by eye using Sequencher (v4.8, Gene Codes Corp., Ann Arbor, MI) to create a consensus sequence.

A 460 bp sequence of the mtDNA control region was obtained (GenBank Accession# MF979886) and compared to sequences stored in GenBank using BLAST (NCBI Resource Coordinators 2017). The sequence was a 100% match to three humpback whale (*Megaptera novaeangliae*) sequences in GenBank: AP006467 (Sasaki *et al.* 2005) over its entire 460 bp length, and GQ352999 (Jackson *et al.* 2009) and KF477249 (Baker *et al.* 2013) over the entire 452 bp length of those sequences. These sequences all correspond to North Pacific humpback haplotype E1, a common haplotype centrally located in the humpback mtDNA parsimony network (Baker *et al.* 2013). The next 97 most similar GenBank matches were all humpback whales matching at 98%-99% identity over 460 bp.

Contamination by another humpback sample was considered very unlikely as neither the extraction or PCR negative controls showed presence of DNA on gels, and there has not been any humpback whale work conducted in the SWFSC aDNA Lab. We sought to confirm the species identification by obtaining additional samples (SWFSC LabID 173864, Tissue IDs 215614, 215615, 215616) of bone powder from the left maxillary, a transverse process, and a rib (Fig. 2). Extraction, PCR, and sequencing were completed on each sample independently as described above. We used the same primer pairs as before, but were only able to amplify and sequence the last 220 bp (primers D-A3r) of the 460 bp sequence from the maxillary and transverse process. The rib sample did not amplify after multiple attempts. However, the 220 bp sequence from the maxillary and transverse process perfectly matched the first 220 bp of the 460 bp humpback whale sequence from the original partial basicranium sample. When compared to sequences on GenBank, this shorter fragment had 100% identity over its entire length to 40 other entries, all of which were North Pacific humpback haplotypes (Baker *et al.* 2013, Jackson *et al.* 2014).

Obtaining the same mitochondrial sequences from the bones sampled is consistent with them coming from the same individual.

Because the age, markings, general shape, and size (Fig. 3) match those described and illustrated by Gray (1866), the bones sampled from NHMUKGERM 1464a are most certainly the same ones sent by Swinhoe in 1864 that became the holotype for *B. swinhoei*. Thus, the most likely explanation of the discrepancy is that Gray simply misidentified these bones as coming from a fin whale, which is understandable given the limited amount of skeletal material available to work with.

Gray may also not have been aware that a diagnostic feature of *Megaptera* is the lack of a distinct fold in the squamosal as it transitions from the temporal wall to the zygomatic process at the rear of the temporal fossa (a “squamosal crease”; Kellog 1924, Deméré *et al.* 2005). In *Megaptera*, unlike other *Balaenoptera* species, the anterior margin of the squamosal is marked by a smooth and continuous surface as can be seen in Figure 1 and SM2b. Additionally, the configuration of the lateral palatal foramina as seen in Figure SM2b is also characteristic of *Megaptera*.[2] Thus, the genetic identification is consistent with morphological characteristics of the specimen.

Our work provides resolution for the taxonomic status of *B. swinhoei* using genetics and skull morphology. We established that this nominal species belongs in the genus *Megaptera* not *Balaenoptera*. This reidentification has three taxonomic implications. First, *B. swinhoei* should be placed in the synonymy of the humpback whale, *M. novaeangliae*, and the North Pacific subspecies *M. n. kuzira* Gray, 1850, of which no type specimen was collected. Coincidentally, *M. n. kuzira*, based on *Balaena antarctica* of Temminck, 1842, was originally described from waters around the coast of Japan, which abuts the northern edge of the ECS.

Second, the misallocation to *Balaenoptera* raises a question with other nominal balaenopterid species based on fragmentary specimens or described from dubious osteological material like isolated parts of skulls or vertebrae. For example, the species *B. blythi* Anderson, 1879 was described the species from only four vertebrae and one rib collected from the Bay of Bengal. This nominal species is usually placed in the synonymy of *B. physalus*. However, fin whales are unconfirmed from the Bay of Bengal and *B. blythi* is more likely to be a junior synonym of *B. edeni* Anderson, 1879, or even a senior synonym of *B. omurai* Wada, Oishi, and Yamada 2003.

Third, given that ECS fin whales are likely to represent a separate subspecies (Ichihara 1957, Fujino 1960) our finding means that *B. swinhoei* cannot be the subspecific name for this population of whales. Therefore, there is currently no nominal name available for this taxon. If, after a global review of the taxonomy of the fin whales, their subspecific status is established, a new name would have to be proposed. Further work should be done to identify both genetic and osteological samples from fin whales in this region (China, Japan, and the Korean Peninsula) to help clarify their status.

ACKNOWLEDGMENTS

Samples were obtained under CITES permit 16US690343/9 and NMFS permit #19091. The authors wish to thank Donney Nicholson for assistance with shipping bone samples, Gabriela Serra-Valente for help with archiving, William F. Perrin, C. Scott Baker, Debbie Dietrich, and Jennifer Jackson for background research assistance, and Philip Morin for helpful comments on the manuscript. Thomas Deméré kindly provided expertise identifying diagnostic morphological characters.

LITERATURE CITED

Baker, C. S., D. Steel, J. Calambokidis, *et al.* 2013. Strong maternal fidelity and natal philopatry shape genetic structure in North Pacific humpback whales. Marine Ecology Progress Series 494:291–306.

Brownell, R. L., Jr. 1981. Review of coastal whaling by the Republic of Korea. Report of the International Whaling Commission 31:395–402.

Deméré, T. A., A. Berta and M. R. McGowen. 2005. The taxonomic and evolutionary history of fossil and modern balaenopterid mysticetes. Journal of Mammalian Evolution 12:99–143.

Fujino, K. 1960. Immunogenetic and marking approaches to identifying subpopulations of the North Pacific whales. Scientific Reports of the Whales Research Institute, Tokyo 15:85–142.

Gray, J. E. 1865. Notice of a new finner whale from Formosa. The Annals and Magazine of Natural History 16:148.

Gray, J. E. 1866. Catalogue of seals and whales in the British Museum. Second edition. Taylor and Francis, London, U.K.

Gray, J. E. 1868. Synopsis of the species of whales and dolphins in the collection of the British Museum. Taylor and Francis, London, U.K.

Hershkovitz, P. 1966. Catalog of living whales. Bulletin of the United States National Museum 246. 259 pp.

Hofreiter, M., G. Rabeder, V. Jaenicke-Despres, *et al*. 2004. Evidence for reproductive isolation between cave bear populations. Current Biology 14:40–43.

Höss, M., and S. Pääbo. 1993. DNA extraction from Pleistocene bones by a silica based purification method. Nucleic Acids Research 21:3913–3914.

Ichihara, T. 1957. An application of linear discriminant function to external measurements of fin whale. Scientific

Reports of the Whales Research Institute, Tokyo 12:127–189.

Jackson, J. A., C. S. Baker, M. Vant, D. J. Steel, L. Medrano-Gonzalez and S. R. Palumbi. 2009. Big and slow: Phylogenetic estimates of molecular evolution in baleen whales (Suborder Mysticeti). Molecular Biology and Evolution 26:2427–2440.

Jackson, J. A., D. J. Steel, P. Beerli, *et al.* 2014. Global diversity and oceanic divergence of humpback whale (*Megaptera novaeangliae*). Proceedings of the Royal Society B 281:20133222.

Kellogg, R. 1924. Description of a new genus and species of whalebone whale from the Calvert Cliffs, Maryland. Proceedings of the U.S. National Museum 63:1–14.

Morin, P. A., R. G. LeDuc, K. M. Robertson, *et al.* 2006. Genetic analysis of killer whale (*Orcinus orca*) historical bone and tooth samples to identify western U.S. ecotypes. Marine Mammal Science 22:897–909.

NCBI Resource Coordinators. 2017. Database resources of the National Center for Biotechnology Information. Nucleic Acids Research 45:D12–D17.

Rice, D. W. 1998. Marine mammals of the world: Systematics and distribution. Special Publication Number 4, Society for Marine Mammalogy.

Robertson, K. M., C. A. LeDuc, R. G. LeDuc and P. A. Morin. 2007. Extraction of DNA from formalin-fixed cetacean tissues. National Marine Fisheries Service Technical Memorandum NOAA-TM-NMFS-SWFSC-400 (unpublished). 26 pp. Available from SWFSC, 8901 La Jolla Shores Drive, La Jolla, CA 92037.

Sasaki, T., M. Nikaido, H. Hamilton, *et al.* 2005. Mitochondrial phylogenetics and evolution of mysticete whales. Systematic Biology 54:77–90.

Swinhoe, R. 1870. Catalogue of the mammals of China (south of the River Yangtsze) and of the Island of Formosa. Proceedings of the Zoological Society of London 615–652.

Temminck, C. J. 1842. Fauna Japonica sive Descriptio animalium, quae in itinere per Japoniam, jussu et auspiciis superiorum, qui summum in India Batava imperium tenent, suscepto, annis 1825–1830 collegit, notis, observationibus et adumbrationibus illustravit Ph. Fr. de Siebold. Conjunctis studiis C. J. Temminck et H. Schlegel pro vertebratis atque W. de Haan pro invertebratis elaborata. Lugduni Batavorum.

Trouessart, E.-L. 1905. Catalogus mammalium tam viventium quam fossilium. R. Friedländer & Sohn, Berolini.

Wada, S., M. Oishi and T. K. Yamada. 2003. A newly discovered species of living baleen whale. Nature 426:278–281.

Received: 21 September 2017

Accepted: 25 January 2018

SUPPORTING INFORMATION

The following supporting information is available for this article online at http://

Appendix S1. Description of specimen NHMUKGERM 1464a.

Figure S1. Dorsal (a) and ventral (b) view of left maxillary bone of NHMUKGERM 1464a. Red lines indicated measurement landmarks.

Figure S2. Dorsal (a) and posterior (b) views of partial basicranium of NHMUKGERM 1464a.

Figure S3. Anterior view of fused second and third cervical vertebrae of NHMUKGERM 1464a.

Figure 1. Ventral view of left side of basicranium of NHMUKGERM 1464a. White arrow indicates location of bone powder sample.

Figure 2. Thoracic transverse process (a) and rib (b) from NHMUKGERM 1464a. Red circles indicate location of bone powder samples.

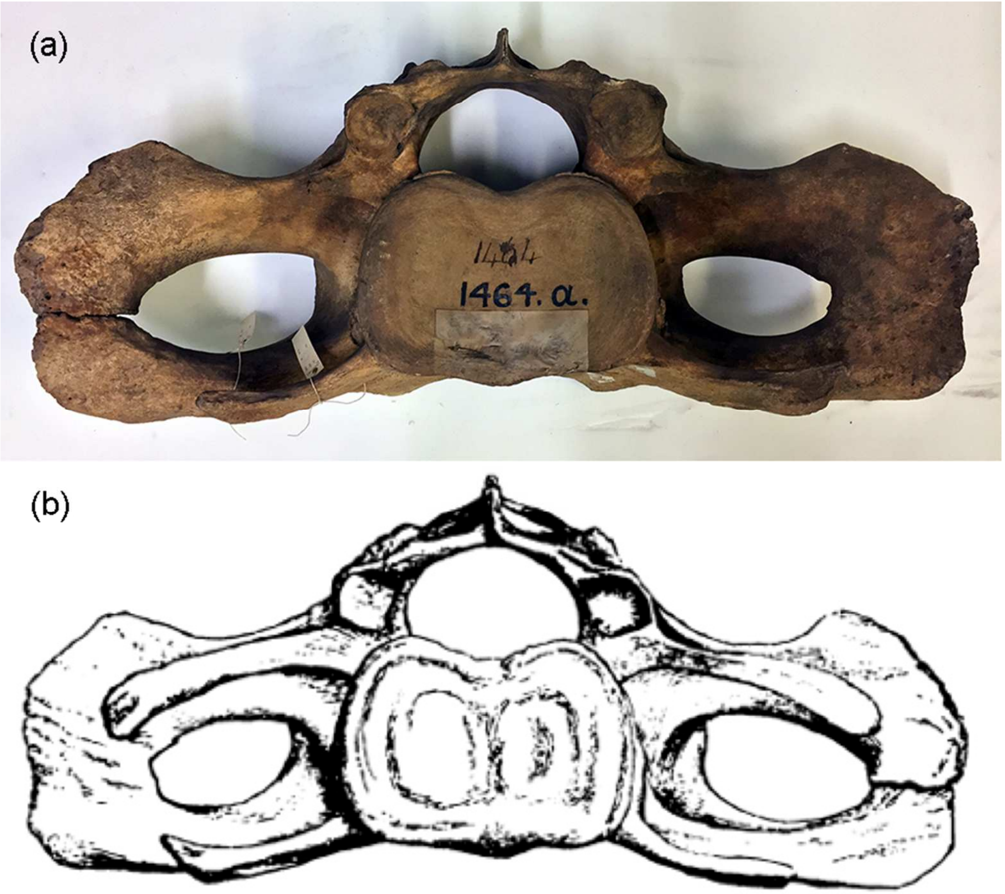
Figure 3. Posterior view of fused second and third cervical vertebrae from (a) NHMUKGERM 1464a and (b) figure 88 from Gray (1866).

[1] Corresponding author (e-mail: eric.archer@noaa.gov).

[2] Personal communication from T. Deméré, San Diego Natural History Museum, 1788 El Prado, San Diego, CA 92101, January 2018.

152x114mm (300 x 300 DPI)

407x395mm (154 x 154 DPI)



165x151mm (150 x 150 DPI)

Appendix S1. Description of specimen NHMUKGERM 1464a.

The partial basicranium and partial postcranial skeleton of specimen number NHMUKGERM 1464a are composed of the left maxillary bone, partial basicranium, 13 complete ribs, 3 cervical vertebrae, 7 thoracic vertebrae, and multiple fragments of transverse and spinous processes (vertebral positions unallocated). All bones are marked with "1464a" in the same script. The partial basicranium is full of fine, dark gray sand. The thoracic vertebrae have all been extensively modified, with chop-marks clearly visible where transverse processes/neural arches have been detached from vertebral bodies. These signs of butchery and processing may be contemporary with the original stranding of the whale. Descriptions and measurements of individual bones follow.

Left Maxillary Bone (Fig. S1)

- Greatest width = 57 cm.
- Greatest length (ventrally) = 216 cm.
- Greatest length (dorsally) from lateral point of posterior maxillary crest to anterior tip (see photograph) = 203 cm.

Partial Basicranium (Fig. S2)

- Greatest width = 1.83 m.

Vertebrae

- C2 & C3: fused together; complete; epiphyses fused (Fig. S3).
- C5: complete; epiphyses fused.
- T1: complete; epiphyses fused.
- ?T2: centrum entirely absent; transverse and spinous processes, laminae and articular processes/facets present (intact neural arch). Morphology compares favourably with second thoracic vertebra.
- T3: complete; epiphyses missing.
- ?T4: centrum entirely absent; transverse and spinous processes, laminae and articular processes/facets present (intact neural arch). Morphology compares favorably with fourth thoracic vertebra.
- ?T5: centrum only; epiphyses fused. Morphology compares favorably with fifth thoracic vertebra.
- ?T9: centrum only; epiphyses fused. Morphology compares favorably with ninth thoracic vertebra.
- ?T12: centrum only; epiphyses fused. Morphology compares favorably with twelfth thoracic vertebra.

Figure S1. Dorsal (a) and ventral (b) view of left maxillary bone of NHMUKGERM 1464a. Red lines indicated measurement landmarks.

Figure S2. Dorsal (a) and posterior (b) views of partial basicranium of NHMUKGERM 1464a.

Figure S3. Anterior view of fused second and third cervical vertebrae of NHMUKGERM 1464a.