

1 **New evidence for the co-occurrence of two genera of Paleoparadoxiidae (Mammalia,**  
2 **Desmostylia) from the Middle Miocene of Japan: insights into taxonomic status and**  
3 **paleodiversity in Desmostylia**

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**ABSTRACT**

Desmostylia, an extinct order of marine mammals, includes two major families: Paleoparadoxiidae and Desmostylidae. Within Paleoparadoxiidae, three genera — *Archaeoparadoxia*, *Paleoparadoxia*, and *Neoparadoxia* — have been identified, with *Paleoparadoxia* the only genus found on both coasts of North Pacific Rim. In Akan, Hokkaido, Japan, one of the largest *Paleoparadoxia* fossil assemblage in the world has been discovered from the Middle Miocene Tonokita Formation. Previous studies suggested the presence of two congeneric species of *Paleoparadoxia*, while recent taxonomical revisions raise the possibility that two genera, *Paleoparadoxia* and *Neoparadoxia*, were present in Akan. Here, we describe three paleoparadoxiids specimens from Akan, consisting of two partial crania and a mandible. Based on the morphological comparisons and phylogenetic analysis, we identified these specimens as *Paleoparadoxia* sp. and *Neoparadoxia* sp.. This represents the first record of two genera of Paleoparadoxiidae in the same locality and horizon, with the potential to provide valuable insights into cladogenesis and morphological diversification within this family. In addition, the Akan specimens exhibit mosaic characteristics of *Paleoparadoxia* and *Neoparadoxia*, suggesting that a reassessment of their morphological features for the taxonomic identification and phylogenetic analysis are required. To better understand species-level diversity patterns in Desmostylia, we conducted stage-binned analysis and richness curve analysis. Our analysis revealed three significant points in their diversification history: (1) Desmostylidae reached peak diversity at the

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1 Oligocene-Miocene boundary, coinciding with a glacial event; (2) Paleoparadoxiidae,  
2 achieved peak diversity during the Middle Miocene global warming event; (3) Both families  
3 declined their diversity and gone out during the Middle to Late Miocene global cooling  
4 event. These finding indicate that desmostylian diversity could have been closely linked to  
5 climatic events, with the differing peak diversities of Paleoparadoxiidae and Desmostylidae  
6 reflecting their respective preferences for warmer and cooler climates. Our analysis provides  
7 a valuable baseline for understanding the diversity and evolutionary history of Desmostylia.

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## 9 INTRODUCTION

10 Desmostylia is an extinct order of quadrupedal marine mammals from Oligocene and the  
11 Miocene deposits of the northern Pacific Rim (*e.g., Domning, Ray & McKenna, 1986,*  
12 *Inuzuka, Domning & Ray, 1994*). This group is divided into two major clades, Desmostylidae  
13 and Paleoparadoxiidae (*Osborn, 1905; Reinhart, 1959; Matsui & Tsuihiji, 2019*).

14 Paleoparadoxiidae forms a monophyletic group with three genera **and** four species:  
15 *Archaeoparadoxia weltoni, Paleoparadoxia tabatai, Neoparadoxia repenningi* and  
16 *Neoparadoxia ceciliaalina*. These species lived from the Late Oligocene to the Late Miocene  
17 and were primarily discovered in the United States (*Barnes, 2013*). Among them, only  
18 *Paleoparadoxia* is known from both the Japan and North American coasts, with over 30 fossil  
19 localities reported in Japan (*Inuzuka, 2005; Matsui & Kawabe, 2015*).

20 In Akan, Hokkaido, Japan, one of the largest *Paleoparadoxia* fossil assemblage in the world  
21 has been found from the Middle Miocene Tonokita Formation (*Kimura et al., 1988*). Previous

1 studies suggested the presence of both a large and a small *Paleoparadoxia* species in Akan  
2 (*Akan Vertebrate Fossil Assemblage Research Group, 2000 and 2002, Inuzuka, 2005*; Fig.  
3 1A). The Akan is the only site where two *Paleoparadoxia* are suggested to co-occurrence in  
4 the same stratigraphic horizon, potentially providing a key fossil record for understanding  
5 cladogenesis within this group. However, recent studies reidentified the large *Paleoparadoxia*  
6 species as *Neoparadoxia*, a newly established genus (*Barnes, 2013*). While this study did not  
7 mention the Akan specimens, the most recent taxonomic hypotheses raise the possibility that  
8 both *Paleoparadoxia* and *Neoparadoxia* may have been present in Akan (*Matsui & Tsuihiji,*  
9 *2019*; Fig. 1B).

10 Repeated taxonomic revisions have hindered comprehensive analyses of desmostylians  
11 diversity. Some studies suggest that the body size and morphological diversity of  
12 Paleoparadoxiidae had increased from the Middle to Late Miocene (*Inuzuka, 2005; Pyenson*  
13 *& Vermeij, 2016; Matsui, Valenzuela-Toro & Pyenson, 2022*). However, it remains debated  
14 whether these changes represent cladogenesis or intraspecific variation. Additionally,  
15 research on the diversification and evolutionary drivers of Desmostylia is limited, with *Berta*  
16 *& Lanzetti (2020)* providing the only comprehensive study to date. The Akan specimens offer  
17 significant potential to enhance our understanding of their evolutionary history because they  
18 were discovered during the Middle Miocene, when evolutionary changes in  
19 Paleoparadoxiidae began.

20 Here, we describe three paleoparadoxiids specimens from Akan (AMP AK960241, AMP  
21 AK970253 and AMP AK000247). Our study represents the first record of the co-occurrence

1 of *Neoparadoxia* and *Paleoparadoxia*, shedding new light on the taxonomic status of  
2 Paleoparadoxiidae. In addition, we conducted two types of paleodiversity analyses to clarify  
3 the diversification patterns in Desmostylia. Comparing paleodiversity patterns is widely  
4 recognized as a valuable approach for examining evolutionary drivers (e.g., *Ando & Fordyce,*  
5 *2014; Boessenecker & Churchill, 2018; Berta & Lanzetti, 2020*). In this study, we apply this  
6 approach to analyze the diversification dynamics of Desmostylia, assess their potential  
7 drivers, and discuss possible biases that should be taken into consideration in future studies.

8

## 9 MATERIAL AND METHODS

### 10 Geological setting

11 The Akan specimens were found on the bank of Chichappupon river in Akan, Kushiro City,  
12 Hokkaido, Japan (Fig. 2; 43°11'42"N, 144°05'42"E). The Middle Miocene Tonokita Formation  
13 crop out in this region. The Tonokita Formation comprise conglomerate to coarse sandstone  
14 containing diatoms, pollen fossil, molluscan shells and marine vertebrates. The marine  
15 mammal fossil assemblage was found in pebbly sandstone in the Tonokita Formation, which  
16 occur in channel deposits sometimes incised into the under layer. These fossils are mostly  
17 fragmented, and the molluscan fossils are disarticulated, suggesting secondarily deposition.  
18 The marine mammals include Desmostylia (*Desmostylus* sp. and *Paleoparadoxia* sp.),  
19 Pinnipedia and Odontoceti (*Okazaki et al., 1972; Kimura et al., 1998; Akan vertebrate fossil*  
20 *assemblage research group, 2000 and 2002*). The depositional environment of the Tonokita  
21 Formation is interpreted as upper shelf or lower-shoreface (*Urabe & Hoyanagi, 2004*). The

1 paleoclimate was estimated based on marine mollusks and pollen fossil. The molluscan fauna  
2 (Atsunai Fauna; e.g. *Glycymeris idensis*, *Swiftopecten swiftii*, *Chlamys cosibensis*,  
3 *Masudapecten* sp., *Felaniella usta*, *Serripes groenlandicus*, *Mercenaria yiizukai*, *Spisula*  
4 *onnechiuria*, *Crepidula jimboana*, *Nucella tokudai*) suggests a cool temperate climate (Suzuki,  
5 Kimura & Tanaka, 1999, Suzuki, 2000). Similarly, pollen fossils indicate a temperate climate,  
6 characterized by a mixed forest of Taxodiaceae, *Alnus* and *Betula* (Igarashi, Yahata &  
7 Kimura, 2000, Yahata, 2000). Diatom fossils from the Tonokita Formation indicate an age  
8 range from 15.9 Ma to 14.9 Ma, corresponding to the *Denticulopsos lauta* zone (Urabe, Akiha  
9 & Hoyanagi, 2003).

10

## 11 **Materials**

12 The Akan specimens were discovered during five excavation surveys conducted between  
13 1996 and 2000. Although the remains are isolated, they include various parts of the body,  
14 such as cranial and limb bones, from individuals ranging from juveniles to adults (*Akan*  
15 *vertebrate fossil assemblage research group, 2000 and 2002*). In this study, we focused on  
16 three paleoparadoxiids specimens from the Akan, consists of two partial crania and a  
17 mandible (AMP AK960241, AMP AK970253, AMP AK000247). AMP AK960241 and AMP  
18 AK970253 were excavated in 1996 and 1997, respectively. These specimens were previously  
19 identified as *Paleoparadoxia* sp. In contrast, AMP AK000247, discovered in 2000, was  
20 assigned to *P. tabatai* (*Akan vertebrate fossil assemblage research group, 2000 and 2002*). All  
21 three specimens were collected from the same site and stratigraphic horizon. These

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1 specimens are currently housed at the Ashoro Museum of Paleontology (AMP).

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### 3 **Phylogenetic analysis**

4 The phylogenetic position of the Akan specimens described here was analyzed based on the  
5 data matrix of *Matsui & Tsuihiji (2019)*, adding the three Akan specimens and four new  
6 characters. These newly added characters are as follows: character 109, parietal inclined to  
7 cranial (0), slightly inclined to cranial (1), not inclined (2); character 110, paraoccipital  
8 process of ventral side: inclined medially (0), not inclined or expand laterally (1), not  
9 elongate (2); character 111, a few small foramina and sulci in supraorbital process: present  
10 (0), only foramina present (1), absent (2); character 112, mandibular fossa or mandibular  
11 condyle: long axis is oriented medio-laterally (0), oriented anterolaterally (1). All 112  
12 characters were given equal weight in the analysis. The dataset included 19 operational  
13 taxonomic units (OTUs). Outgroups were selected to reflect the three major phylogenetic  
14 hypotheses regarding the affinities of Desmostylia, following *Matsui & Tsuihiji (2019)*: the  
15 Perissodactylomorpha hypothesis (*Cooper et al., 2014; Rose et al., 2014; Rose et al., 2020*), the  
16 Afrotheria hypothesis (*Domning, Ray & McKenna, 1986*) and the Paenugulatomorpha  
17 hypothesis (*Gheerbrant, Filippo & Schmitt A, 2016*). The outgroups used were *Anthracobune*  
18 spp. (a primitive perissodactyl, coding based on *Cooper et al. (2014)*), *Pezosiren portelli* (a  
19 primitive sirenian, with coding based on *Andrews (1904 and 1906)*), and *Moeritherium* spp.  
20 (a primitive proboscidean, with coding based on *Holroyd et al. (1996)*, and *Delmer et al.*  
21 (*2006*)). The ingroup taxa include all 13 known species of Desmostylia, as well as the three

1 desmostylids specimens from Akan (AMP AK960241; AMP AK970253; AMP AK000246).

2 Phylogenetic analysis was performed using PAUP Version 4.0a10 for Windows (*Swofford,*  
3 *2002*) with a heuristic search option, optimized by the accelerated transformation criterion  
4 (ACCTRAN) using the tree-bisection-reconnection (TBR) branch swapping and a simple  
5 addition sequence. Bootstrap analysis was conducted after a full heuristic search with 10,000  
6 replications. To incorporate time constraints into the phylogenetic tree, we applied the  
7 geoscalePhylo function in the paleotree package (*Bapst, 2012*) for the R version 4.4.1 (*R Core*  
8 *Team, 2024*).

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#### 10 **Estimation of Desmostylian diversity**

11 In this study, we conducted two analyses—Stage-binned analysis and Richness curve  
12 analysis—to elucidate the diversity changes within two major desmostylian families,  
13 Paleoparadoxiidae and Desmostylidae. These analyses are based on the desmostylian fossil  
14 occurrence (Supplemental information 1) and our phylogenetic analysis, which suggests that  
15 *Paleoparadoxia* sp. and *Neoparadoxia* sp. in Akan represent distinct species from those  
16 currently recognized.

17 For the stage-binned analysis, we followed the methods of *Boessenecker & Churchill*  
18 *(2018)* and *Berta & Lanzetti (2020)*. This analysis examined over 200 desmostylian fossil  
19 localities and their stratigraphic ages, determined through a comprehensive literature review  
20 of chronostratigraphic data (Supplemental information 1). The number of desmostylian  
21 species within each chronostratigraphic stage was counted under the assumption that species

1 persisted continuously throughout their confirmed temporal ranges. Diversity plots were  
2 obtained by counting the valid species for each time bin.

3 For the time-constrained richness curve analysis, we employed methods based on  
4 *Magallanes et al. (2018)* to illustrate the minimum and maximum counts of known and  
5 inferred lineages (richness) of Desmostylidae and Paleoparadoxiidae throughout their  
6 evolutionary history. This approach, accounted for chronostratigraphic uncertainty and  
7 ghost lineages. For each taxon, we estimated a minimum and maximum possible age of  
8 occurrence, building upon estimates presented in recent studies (Supplemental information  
9 1). Using these age ranges, we constructed a time-constrained 50% majority-rule consensus  
10 tree to calculate the minimum and maximum lineages counts at 0.1 Ma interval (35.0 Ma to  
11 5.0 Ma, 300 time slices). The maximum lineage count was calculated based on the assumption  
12 that each taxon existed from the earliest to the latest possible age of the rock units. For three  
13 taxa known from multiple formations (*P. tabatai*, *Cornwallius sookensis*, *Desmostylus*  
14 *hesperus*), the combined maximum age ranges of these formations were used to determine  
15 the broadest possible temporal span. The minimum lineage count was estimated by assuming  
16 originations and extinctions within the possible range that resulted in the minimized the  
17 number of lineages at any given time. In most cases, this involved counting ghost lineages, as  
18 a taxa within its estimated range could be presumed either extinct or not yet originated at  
19 any given time. Maximum and minimum age estimates for each 0.1 Ma bin among the trees  
20 was included in the curves.

21

1 **SYSTEMATIC PALEONTOLOGY**

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3 *DESMOSTYLIA Reinhart, 1953*

4 *DESMOSTYLOIDEA Osborn 1905 (sensu Matsui & Tsuihiji, 2019)*

5 *PALEOPARADIXIIDAE Reinhart, 1959 (sensu Matsui & Tsuihiji, 2019)*

6 *NEOPARADOXIA Barnes, 2013*

7

8 ***Neoparadoxia* sp.**

9 (Figs. 3-6, Table 1)

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11 **Emended diagnosis of genus:** *Neoparadoxia* can be distinguished from other desmostylians  
12 by its paraoccipital process, which is massive, elongated, thickened, and extends laterally. It  
13 differs from other paleoparadoxiids in possessing following characters: extremely large body  
14 size; a proportionally large and deeply concave temporal fossa; a large mandibular fossa.

15 **Materials:** AMP AK960241 (cranium, Figs. 3-6, Table 1).

16 **Locality:** The riverbank where the Chichappupon river in the Akan, Kushiro city, Hokkaido,  
17 Japan (Fig. 2; 43°11'42"N, 144°05'42"E).

18 **Age and horizon:** Tonokita Formation, Middle Miocene, Langhian (15.9-14.9Ma; Figs. 2B,C)

19

20 **Description**

21 **AMP AK960241 (posterior part of the cranium):** AMP AK960241 preserves supraoccipital,

1 exoccipital, basioccipital, basisphenoid, parietal and squamosal (Figs. 3-6). Although the  
2 Parietal and zygomatic arch are heavily damaged, the exoccipital is perfectly preserved. This  
3 specimen, consisting of three fragments, is extremely large—significantly larger than *P.*  
4 *tabatai* and comparable in size to *N. cecialina* (Table 1). This suggests that it is among of the  
5 largest paleoparadoxiid cranium ever discovered from Japan.

6 The occipital region is nearly complete on the right side (Figs. 3,5,6). The external  
7 occipital crest is distinct and the connection to the nuchal crest differs from the condition in  
8 *Behemotops katsui* (Inuzuka, 2000), and the external occipital protuberance is slightly  
9 developed. The occipital condyle is preserved only at its base. The paraoccipital process is  
10 massive, medially inclined, expand laterally and the tip is thickened. The ventral condylar  
11 fossa is well-developed. The hypoglossal foramen is partially damaged and can be observed at  
12 the boundary between the exoccipital and the basioccipital, at the base of the paraoccipital  
13 process. The stylomastoid foramen opens ventrally on the lateral surface of the exoccipital,  
14 posterior to the mandibular fossa. The pharyngeal and the muscular tubercles on the  
15 basioccipital are prominent.

16 The basisphenoid is nearly completed (Fig. 4). The lacerate foramen is widely open  
17 between the squamosal and basisphenoid, and the oval foramen is also situated between  
18 these two bones.

19 The parietal, preserved in its posterior portion (Figs. 3,5,6), is slightly inclined cranially.  
20 The nuchal crest is pronounced and nearly V-shaped, while sagittal crest strongly  
21 developed—unlike *Desmostylus* and *Ashoroa laticosta* (Inuzuka, 1988 and 2000). The

1 parasagittal crests are extremely narrow and positioned close to each other. The temporal  
2 fossa is notably large and the basisphenoid-occipital suture is completely closed.

3 The squamosal is partially preserved (Figs. 3-6). The squamosal foramina are present the  
4 base of zygomatic arch and near the nuchal crest, with the posterior one being the largest.  
5 There number of foramen (three to four) is consistent with *P. tabatai* and *N. cecilialina*. The  
6 foramina positions are asymmetrical as in other desmostylians. A passage connecting the  
7 anterior external auditory meatus to the skull roof is present, unlike in Desmostylidae (*Clark,*  
8 *1991*). The mandibular fossa is missing anteriorly, but the preserved portion suggests that it  
9 was extremely large. The long axis of the mandibular fossa is oriented anterolaterally, a  
10 feature shared with other paleoparadoxiids, *Behemotops* and *Seuku emlongi* (*Domning, Ray*  
11 *& McKenna, 1986; Inuzuka, 2000 and 2005; Barnes, 2013; Beatty & Cockburn, 2015*).

12 The tympanic region is exposed due to damage to the zygomatic arch and lateral squamosal  
13 (Figs. 3,5). The external auditory meatus opens posteriorly on lateral surface of the zygomatic  
14 arch and is situated posterodorsally to the mandibular fossa. The epitympanic sinus lies  
15 slightly dorsally adjacent to the external auditory meatus. This positional relationship is  
16 similar to the condition in *D. hesperus* and *C. sookensis*, suggesting that it may be a shared  
17 morphological character within Desmostylia (*Clark, 1991; Uno & Kimura, 2004; Beatty,*  
18 *2009*). The tympanic bone, which connects to external auditory meatus, forms a rounded  
19 equilateral triangle and measuring approximately 2.5cm per side. The cochlea is exposed  
20 medially and features a three-tiered spiral structure measuring approximately 14.4 mm  
21 dorsoventrally, filled with sediments. The postzygomatic foramen, located adjacent to the

1 epitymapanic sinus, is wide and shallow, consistent with other desmostylians (*Ijiri & Kamei,*  
2 *1961; Inuzuka, 1988; Beatty, 2009*).

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4 PALEOPARADIXIIDAE *Reinhart, 1959 (sensu Matsui & Tsuihiji, 2019)*

5 PALEOPARADOXIA *Reinhart, 1959*

6

7 ***Paleoparadoxia* sp.**

8 (Figs. 7-12, Tables 2,3)

9

10 **Emended diagnosis of genus:** *Paleoparadoxia* differs from all other desmostylians in  
11 possessing the following characters: the zygomatic arch of squamosal inclined to caudally and  
12 not broadened dorsoventrally; the coronoid crest of the dentary curved anteriorly. It differs  
13 from *Neoparadoxia* in possessing following characters: the supraorbital process is slightly  
14 expanded laterally; the dorsal surface of cranium between supraorbital processes is not  
15 depressed; the orbit is positioned slightly dorsally; the mandibular symphysis is slightly  
16 rotated anteroventrally.

17 **Materials:** AMP AK970253 (cranium, Figs. 7-9, Table 2), and AMP AK000247 (mandible,  
18 Figs. 10-12, Table 3).

19 **Locality:** The riverbank where the Chichappupon river in the Akan, Kushiro city, Hokkaido,  
20 Japan (Fig. 2; 43°11'42"N, 144°05'42"E).

21 **Age and horizon:** Tonokita Formation, Middle Miocene, Langhian (15.9-14.9Ma; Figs. 2B,C)

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2 **Description**

3 **AMP AK970253 (posterior part of the cranium):** AMP AK970253 preserves the frontal,  
4 basisphenoid, parietal, squamosal, and vomer (Figs. 7-9). Its size is comparable to that of the  
5 corresponding part in *P. tabatai* (Table 2). The lambdoid suture is detached while the  
6 squamosal suture is fused, as seen in adult *P. tabatai*, thus we identified this specimen as a  
7 relatively mature one.

8 The frontal is heavily damaged in its middle section (Figs. 7,9). The orbits projected  
9 slightly from the frontal, and the orbital margins are thickened, porous, and rounded. The  
10 supraorbital process is weakly developed laterally and dorsally, similar to *P. tabatai*, but less  
11 prominent than in *A. weltoni* and *N. cecialina* (Clark, 1991; Barnes, 2013). Nutrient  
12 foramina and radiating sulci are supraorbital process. The space between the supraorbital  
13 processes is heavily damaged but remains flat.

14 The basisphenoid is preserved (Fig. 8). The left tympanic bulla is partially-intact anteriorly  
15 but missing posterior and medial portion. The shape of the tympanic bulla is elliptical, with  
16 its long axis is oriented posterior-laterally. The oval foramen is visible posteriorly on both  
17 sides of the sphenoid bone. The pterygoid process is preserved only at its base.

18 The vomer is heavily damaged, but its suture with the basisphenoid is fully fused.

19 The parietal (Figs. 7,9) is slightly inclined cranially, with a weakly developed sagittal crest  
20 and widely spaced parasagittal crests. The nuchal crest is pronounced and nearly V-shape—  
21 unlike *Desmostylus* and *A. laticosta* (Inuzuka, 1988 and 2000).

1 The squamosal is preserved (Figs. 7-9). The squamosal foramina are present at the base of  
2 zygomatic arch and near the nuchal crest, with the posterior foramen being the largest. The  
3 number of foramina (three to four) is consistent with *P. tabatai* and *N. ceciliolina*. The  
4 positions of these foramen are asymmetrical, a common character among desmostylians (*Ijiri*  
5 & *Kamei, 1966; Barnes, 2013; Inuzuka, 1988*). A passage connecting the anterior external  
6 auditory meatus to the skull roof is observed, unlike in Desmostylidae (*Clark, 1991*). The  
7 mandibular fossa is flat and faced outward. The long axis of the mandibular fossa is oriented  
8 anterolaterally, a character shared with other paleoparadoxiids, *Behemotops* and *S. emlongi*  
9 (*Domning, Ray & McKenna, 1986; Inuzuka, 2000 and 2005; Barnes, 2013; Beatty &*  
10 *Cockburn, 2015*). The zygomatic arch of squamosal is caudally inclined and relatively thin.  
11 The posterior end of the jugal is retracted and does not reach the mandibular fossa as seen in  
12 *P. tabatai* but not in *A. weltoni* (*Clark, 1991*). The postzygomatic foramen is wide and  
13 shallow, consistent with other desmostylians (*Ijiri and Kamei, 1961; Inuzuka, 1988; Beatty,*  
14 *2009*). A funnel-shaped external auditory meatus opens posteriorly behind the zygomatic  
15 arch and the mandibular fossa.

16  
17 **AMP AK000247 (mandible):** AMP AK000247 is mostly preserved, with the exception of  
18 anterior portion of the mandible (Figs. 10-12). It is slightly smaller in size compared to the *P.*  
19 *tabatai* and *A. weltoni* (Table 3). The mandibular body is straight in medial and lateral view,  
20 with the upper margin curving slightly posteriorly —unlike the sigmoid shape observed in  
21 *Desmostylus* (*Inuzuka, 2000 and 2005*). The mental foramina are present on the lateral side

1 of the mandibular body while the interalveolar margin of the mandible is nearly straight,  
2 featuring a large depression on the lingual side. The mandibular symphysis is rotated  
3 anteroventrally, becoming approximately horizontal and aligning incisors and canines  
4 anteriorly, as seen in Paleoparadoxiidae (*Barnes, 2013*). The masseteric fossa is wide and  
5 shallow, while the mylohyoid groove is distinct. The mandibular ramus and the mandibular  
6 body form a nearly right angle. The mandibular foramen is oval-shaped, measuring 11.9 mm  
7 in short diameter and 23.1 mm in long diameter. The mandibular notch is shallow and the  
8 mandibular angle is rounded, bending nearly perpendicularly. The long axis of the  
9 mandibular condyle is oriented anterolaterally, as observed in Paleoparadoxiidae,  
10 *Behemotops* and *S. emlongi* (*Domning, Ray & McKenna, 1986, Inuzuka, 2000 and 2005;*  
11 *Barnes, 2013, Beatty & Cockburn, 2015*). The coronoid crest (anterior margin of coronoid  
12 process) curves anteriorly, with a small angle between the anterior and posterior margin of  
13 the coronoid process.

14 The teeth are not preserved but the alveoli for p1, p2, p4, m1, and m2 are preserved. The  
15 alveolus of p1 is elongated sagittal direction, with a diastema present between p1 and p2. The  
16 p2 and p4 teeth are closely positioned near the distal end of the mandibular symphysis m1  
17 and m2 are slightly compressed laterally, each displaying two distinct roots. m2 is larger in  
18 the sagittal direction compared to m1. The absence of the m3 alveolus suggests that this  
19 specimen is a large juvenile.

20

## 1 **RESULT**

### 2 **Phylogenetic analysis**

3 Our phylogenetic analysis resulted in 136 most parsimonious trees with a tree length 206  
4 after 311,144 rearrangements were attempted. The consistency index (CI) is 0.623, the  
5 rescaled consistency index is 0.407, the retention index (RI) is 0.652 and the homoplasy  
6 index (HI) is 0.377. Figure 13 shows the 50% majority-rule consensus tree, which indicates  
7 the same Desmostylian topology as *Matsui & Tsuihiji (2019)*, except for Paleoparadoxiidae.  
8 The Akan specimens are placed as the derived paleoparadoxiids together with *P. tabatai*, *N.*  
9 *repenningi* and *N. cecialina*. AMP AK960241, *N. repenningi* and *N. cecialina* form a  
10 monophyletic clade. AMP AK970253, AMP AK000247 and *P. tabatai* form a monophyletic  
11 clade in which AMP AK970253 is most closely related to *P. tabatai*. This topology of derived  
12 paleoparadoxiids is not supported by the bootstrap value.

13

### 14 **Identification**

15 The Akan specimens exhibit a mosaic of characters shared with *Paleoparadoxia* and  
16 *Neoparadoxia*. AMP AK960241 exhibits a majority of characters that are diagnostic of  
17 *Neoparadoxia*: an extremely large body size; the paraoccipital process is massive, thickened  
18 and expand laterally; partially large and deeply concave temporal fossa; a large mandibular  
19 fossa. In contrast, this specimen shares the following characters with *Paleoparadoxia*: the  
20 paraoccipital process extends slightly medially, and the external occipital protuberance is  
21 moderately developed. The 50% majority-rule consensus tree shows that AMP AK960241

1 and *Neoparadoxia* form a monophyletic clade. Based on these results, we identify this  
2 specimen as *Neoparadoxia* sp. This is the first record of *Neoparadoxia* from the western  
3 Pacific coast. In addition, the morphological features of AMP AK960241 do not entirely  
4 correspond to those of the holotype specimens of *N. cecilialina* (LACM150150) and *N.*  
5 *repenningi* (UCMP81302), suggests that it may represent a previously unrecognized species  
6 of *Neoparadoxia*. However, their fragmentary condition requires careful assessment prior to  
7 species-level identification.

8 On the other hand, AMP AK970253 and AMP AK000247 exhibits the majority of  
9 characters shared with *Paleoparadoxia*: the zygomatic arch inclined cranially and lacks  
10 dorsoventral expansion; the supraorbital process is slightly developed; the dorsal surface of  
11 cranium between supraorbital processes is not depressed; the orbit is located slightly dorsally;  
12 the mandibular fossa is smaller compared to *N. cecilialina*; the coronoid crest of the dentary  
13 curved anteriorly; the mandibular symphysis is slightly rotated anteroventrally; the  
14 relatively lower position of the mandibular condyle and mandibular foramen; the  
15 mandibular body is straight unlike *N. repenningi*; the dorsal side of the mandibular  
16 symphysis lacks foramina, distinguishing it from *N. cecilialina*. In contrast, these specimens  
17 possess the following characters of *Neoparadoxia*: numerous nutrient foramina with sulci on  
18 the dorsal surface of the supraorbital process; the small angle between the anterior and  
19 posterior margins of the coronoid process. The 50% majority-rule consensus tree indicates  
20 that AMP AK970253, AMP AK000247 and *P. tabatai* form a monophyletic clade. Therefore,  
21 we identify these specimens as *Paleoparadoxia* sp. However, as their morphological

1 characters do not fully correspond to those of the holotype of *P. tabatai* (NMS PV-5601),  
2 suggesting that they may represent a different species. Given their fragmentary condition,  
3 cautious evaluation is necessary before making a species-level identification. These results  
4 reveal that two genera of Paleoparadoxiidae coexisted in Akan.

5

#### 6 **Estimation of desmostylian diversity**

7 The results of the stage-binned analysis are shown in Figs. 14A and 14B. For  
8 Paleoparadoxiidae (Fig. 14A), species diversity remained low, with only one or two species  
9 (*P. tabatai* and *A. weltoni*) present from the Oligocene Chattian to the Miocene Burdigalian  
10 (28.1-16 Ma). However, during the Middle Miocene Langhian (16-13.8 Ma), species diversity  
11 increased sharply to five species, coinciding with the appearance of the Akan  
12 paleoparadoxiids and *Neoparadoxia*. Subsequently, diversity declined from the Serravallian to  
13 the Tortonian (13.8-7.2 Ma), culminating in the complete extinction of Paleoparadoxiidae by  
14 the Late Miocene Messinian. In contrast, for Desmostylidae (Fig 14B), species diversity  
15 exhibited minimal fluctuation, resulting in a more stable pattern. From the Oligocene  
16 Rupelian to the Chattian (33.9–23 Ma), two basal desmostylids species (*A. laticosta* and *C.*  
17 *sookensis*) were present. During the Early Miocene Aquitanian (23-20.4 Ma), *A. laticosta* and  
18 *C. sookensis* went extinct, and the emergence of more derived desmostylids  
19 (*Ounalashkastylus tomidai* and *D. hesperus*) increased the species count to three, marking a  
20 peak in diversity. From the Burdigalian to the Serravallian (20.4-11.6 Ma), despite the  
21 extinction of *O. tomidai*, the appearance of *D. japonicus* and *D. coalingensis* maintained the

1 number of species at two. By the Late Miocene Tortonian (11.6-7.2 Ma), only a single species  
2 of *D. hesperus* remained, and like Paleoparadoxiidae, Desmostylidae became completely  
3 extinct by the Messinian (7.2-5.3 Ma).

4 The results of the richness curve analysis are shown in Figs. 14C and 14D. For  
5 Paleoparadoxiidae (Fig. 14C), the maximum and minimum richness curve exhibited similar  
6 trends. Both curves gradually increased from the Oligocene Chattian to Aquitanian, with  
7 high richness persisting throughout this period (28.1-20.4 Ma). The peak richness was  
8 reached during the mid-Burdigalian to Langhian (approximately 18-15 Ma). Since the  
9 Langhian, both curves have shown a sharp decline, with possible extinction suggested by  
10 the Late Miocene Tortonian (11.6-7.2 Ma). For Desmostylidae (Fig. 14D), the maximum and  
11 minimum richness curves also exhibited similar patterns, particularly from the Late  
12 Oligocene to the Miocene. The maximum richness curve indicated a gradual increase in  
13 richness during the Oligocene, while the minimum curve showed a decrease in richness from  
14 the mid-Rupelian to the Early Chattian in the Late Oligocene (approximately 31-27 Ma).  
15 Both curves showed an increase in richness after the mid-Chattian, peaking around the Late  
16 Chattian and near the Oligocene-Miocene boundary (approximately 25-23 Ma). While both  
17 curves were relatively stable during the Miocene, a stepwise decline was observed at the  
18 Middle to Late Burdigalian (approximately 17 Ma) and at the Serravallian-Tortonian  
19 boundary (11.6 Ma). Both curves also indicated the extinction of Desmostylidae by the  
20 Tortonian (11.6-7.2 Ma).

21

## 1 DISCUSSION

### 2 Taxonomic status within Paleoparadoxiidae

3 Previous studies suggested that two types of Paleoparadoxiidae were present in Akan (*Akan*  
4 *Vertebrate Fossil Assemblage Research Group, 2000 and 2002; Inuzuka, 2005*). Our results  
5 are consistent with previous studies and represent the first record of *Paleoparadoxia* and  
6 *Neoparadoxia* occurring at the same locality and stratigraphic horizon. The Middle Miocene  
7 was a period of morphological diversification in Paleoparadoxiidae (*Inuzuka, 2005; Pyenson*  
8 *& Vermeij, 2016; Matsui, Valenzuela-Toro & Pyenson, 2022*), and the morphological analysis  
9 of the Akan specimens has the potential to provide valuable insights into the cladogenesis  
10 and diversification of this family.

11 As discussed in the identification section, the Akan specimens exhibit a mosaic of  
12 characters shared with both *Paleoparadoxia* and *Neoparadoxia*. In AMP AK960241  
13 (*Neoparadoxia* sp.), two characters resemble those of *P. tabatai*: (1) the paraoccipital process  
14 extends slightly medially; (2) the external occipital protuberance is moderately developed  
15 (*Barnes, 2013*). Similarly, in AMP AK970253 and AMP AK000247 (*Paleoparadoxia* sp.),  
16 exhibit two diagnostic characters of *Neoparadoxia* are present: (1) numerous nutrient  
17 foramina with sulci on the dorsal surface of the supraorbital process (*Barnes, 2013*); (2) the  
18 small angle between the anterior and posterior margins of the coronoid process (*Inuzuka,*  
19 *2005*). These findings underscore the need for a comprehensive reexamination of the  
20 diagnostic characters of both genera. In addition, Akan specimens do not fully correspond to  
21 the morphological characters of the holotype of *P. tabatai* and *Neoparadoxia*, and the

1 topology of derived Paleoparadoxiidae is not supported by the bootstrap value. These results  
2 indicate that the Akan specimens are difficult to identify at the species level within the  
3 existing taxonomic framework of Paleoparadoxiidae, requiring a reevaluation of their  
4 phylogenetic hypothesis and diagnostic characters (*Kohno, 2024*).

5

### 6 **Paleodiversity insights of Desmostylia**

7 The stage-binned analysis and the richness curve analysis revealed new insights into the  
8 evolutionary history of desmostylian diversification. For Paleoparadoxiidae (Figs. 14A, C),  
9 during the Langhian of the Middle Miocene (16-13.8 Ma), the stage-binned analysis shows  
10 an increase in the number of species, attributed to the appearance of Akan paleoparadoxiids  
11 and *Neoparadoxia*. The richness curve analysis suggests that high richness **revel ware level**  
12 was sustained from the Oligocene Chattian through the Miocene Aquitanian (approximately  
13 28.1-20.4 Ma), and peaked from the Mid-Burdigalian to Langhian (approximately 18-15 Ma).  
14 This diversity peak is roughly coinciding with the Middle Miocene Climatic Optimum  
15 (MMCO; 16.9-14.7 Ma), a global warming event (e.g., *Zachos, Dickens & Zeebe, 2008*,  
16 *Tripathi, Roberts & Eagle, 2009*). Several marine mammal lineages diversified during the  
17 MMCO, including Cetaceans and Pinnipediamorpha (*Marx & Fordyce, 2015; Boessenecker &*  
18 *Churchill, 2018; Guo & Kohno, 2023*). Previous studies suggested that *Paleoparadoxia*  
19 preferred subtropical to warm-temperate zone (*Chinzei, 1984; Itoigawa, 1984; Ogasawara,*  
20 *2000; Inuzuka, 2005*), and the rise in sea level associated with global warming may have  
21 expanded the shallow water habitats suitable for Paleoparadoxiidae. Therefore, the MMCO

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1 may have promoted the diversification of Paleoparadoxiidae. Following the MMCO, both  
2 analyses indicate a significant decline in species diversity during the mid-Langhian to  
3 Serravallian (approximately 14.5-11.6 Ma). This decline coincides with the Middle Miocene  
4 Climate Transition (MMCT; -14 Ma), a global cooling event associated with the expansion of  
5 the East Antarctic Ice Sheet (EAIS) and accelerated cooling (e.g., *Flower et al., 1994; Hamon*  
6 *et al., 2013; Frigola, Prange & Schulz, 2018*). This climate shift is considered a contributing  
7 factor to extinctions across various taxa (*Lewis et al., 2008; Guo & Kohno, 2023*), and may  
8 have played a role in the reduced diversity of Paleoparadoxiidae. After the MMCT, the  
9 cooling event of the Late Miocene became more severe (e.g., *Herbert et al., 2016; Rousselle et*  
10 *al., 2013; Wen et al., 2023*), and both analyses suggest that Paleoparadoxiidae may have gone  
11 extinct during the Late Miocene Tortonian to Messinian (11.6-5.3 Ma).

12 For Desmostylidae (Figs. 14B, D), the stage-binned analysis indicates that two basal  
13 species, *A. laticosta* and *C. sookensis*, appeared during the Oligocene. Near the Oligocene-  
14 Miocene boundary, the emergence of *O. tomidai* and *D. hesperus* led to a peak in species  
15 diversity during the Early Miocene Aquitanian (23-20.4 Ma). The richness curve analysis  
16 shows a gradual increase in both maximum and minimum richness curves toward the late-  
17 Chattian (approximately 26-23 Ma). These results suggest that the diversity of Desmostylidae  
18 may have peaked from the Late Oligocene to the Early Miocene. Around the Oligocene-  
19 Miocene boundary (approximately 23 Ma), a brief glacial event known as the Oligocene-  
20 Miocene Transition (OMT; e.g., *Miller, Wright & Fairbanks, 1991; Zachos, Flower & Paul,*  
21 *1997; Greenop et al., 2019*) occurred, coinciding with ocean current changes, including

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1 gradual development of the modern Antarctic Circumpolar Current. The OMT had been  
2 associated with faunal turnovers (*Marx and Fordyce, 2015; Marx, Fitzgerald & Fordyce, 2019;*  
3 *Deng et al., 2021*). Previous studies suggest that Desmostylidae preferred cooler  
4 environments (*Chinzei, 1984; Itoigawa, 1984; Ogasawara, 2000*), with some species  
5 discovered in cold polar regions (*Ijiri & Kamei, 1961; Beatty, 2006; Chiba et al., 2016*). Thus,  
6 the OMT may have driven an increase in diversity of Desmostylidae. From the Early to  
7 Middle Miocene (Burdigalian to Serravallian; 20.4-11.6 Ma), species diversity remained  
8 relatively stable in both analyses, showing little impact from the MMCO or MMCT.  
9 However, as with Paleoparadoxiidae, their species diversity declined during the Serravallian  
10 to the Tortonian (13.8-7.2 Ma) and is suggested to have gone completely extinct by the  
11 Messinian.

12 These results indicate that desmostylian diversity may have been closely linked to climate  
13 change. This study identified three major shifts in species diversity: (1) Desmostylidae  
14 reached peak diversification at the OMT, coinciding with a glacial event; (2) Paleoparadoxiidae  
15 experienced its highest diversity during the MMCO, a global warming event; (3) Both families  
16 experienced declining diversity and eventual extinction during the Middle to Late Miocene  
17 global cooling period. The interaction of desmostylian diversity and these climatic events has not  
18 yet been proven to be the direct cause of their rise and fall. Nevertheless, the vicissitudes of  
19 desmostylian diversity were obviously influenced by these climatic changes. Interestingly,  
20 Desmostylidae and Paleoparadoxiidae exhibited distinct responses to climate change.  
21 Desmostylidae diversified during the Oligocene-Miocene boundary event, while

1 Paleoparadoxiidae diversified during the MMCO. This differences likely reflects ecological  
2 distinctions, with Paleoparadoxiidae favoring warmer climates and Desmostylidae colder  
3 ones (*Chinzei, 1984; Itoigawa, 1984; Ogasawara, 2000; Inuzuka, 2005*).

4 However, the reason why Desmostylia exhibited a decline in diversity only during the  
5 Middle to Late Miocene cooling event remains uncertain. Previous studies suggested that  
6 Desmostylia had successfully adapted to cold environments in other periods (*Chinzei, 1984;*  
7 *Matsui & Kawabe, 2015*). One possible explanation is that the Middle to Late Miocene  
8 cooling was more severe than previous cooling events (*Herbert et al., 2016; Rousselle et al.,*  
9 *2013; Wen et al., 2023*), their survival more difficult. Another potential factor is ecological  
10 competition with Sirenia for food resources (*Vélez-Juarbe, Domning & Pyenson, 2012;*  
11 *Pyenson et al., 2014; Matsui, Valenzuela-Toro & Pyenson, 2022*). *Berta & Lanzetti (2020)*  
12 noted that the appearance of the genus *Hydrodamalis* and other dugongids in the Tortonian  
13 (11.6 Ma-) coincides with the decline of desmostylians. While Desmostylia and Sirenia are  
14 known to have coexisted in the United States (*Parham, Barron & Vélez-Juarbe, 2022*), the  
15 extent of competitive replacement between these groups in the western Pacific remains  
16 poorly understood and requires further investigation.

17 These paleodiversity estimates from the fossil record may also be influenced by three  
18 factors: (1) The volume of fossiliferous rock (*Crampton et al., 2003; Smith & McGowan,*  
19 *2007*). Rock volume is strongly correlated with the richness of higher taxa in the  
20 Phanerozoic (*Hannisdal & Peters, 2011*). Addressing and correcting this bias is essential for  
21 obtaining more accurate estimates of paleodiversity (*Smith & McGowan, 2007; Uhen &*

**Commented [GPI]:** You may want to read <https://doi.org/10.1016/j.palaeo.2013.07.013> to further discuss possible reasons for the disappearance pattern of desmostylia. Not saying it is essential for the paper presented here, but could enrich your analysis

1 *Pyenson, 2007; McGowan & Smith, 2008*). However, previous studies have suggested that  
2 rock volume containing fossils has a limited impact on marine mammal diversity (*Uhen &*  
3 *Pyenson, 2007; Marx, 2009*). Since desmostylians are confined to over 200 localities around  
4 the North Pacific within a relatively short temporal range, geological biases are likely  
5 minimal in these analyses. (2) Taphonomic bias within Desmostylia. Differences in bone  
6 microstructure may affect fossil preservation (*Ando & Fordyce, 2014*). *Hayashi et al. (2013)*  
7 revealed that *Paleoparadoxia*, *Ashoroa*, and *Behemotops* show increased bone mass, while  
8 *Desmostylus* has a spongy inner structure, reflecting secondary aquatic adaptation. Spongy  
9 bones may be less likely to be preserved in deposits, which is consistent with the fact that  
10 paleoparadoxiids are abundant in Akan while *Desmostylus* are relatively rare. However, in  
11 Utanobori, Hokkaido, Japan, *Desmostylus* is the only desmostylian taxon found (*Inuzuka,*  
12 *1988; Uno, Kaneko & Takabatake, 2016*), and *Desmostylus* and paleoparadoxiids rarely co-  
13 occur in the same formation (*Matsui, Valenzuela-Toro & Pyenson, 2022*). This suggests that  
14 differences in bone microstructure may have less influence on fossil preservation than  
15 habitat or ecological factors. While, *Hayashi et al. (2013)* suggest *Paleoparadoxia* inhabited  
16 shallow while *Desmostylus* could swim offshore based on bone microanatomical differences,  
17 *Matsui et al. (2017)* argued the opposite based on stratigraphic evidence. These conflicting  
18 hypotheses make it difficult to assess the ecological impact on paleodiversity estimates. (3)  
19 Taxonomic uncertainty of Desmostylia (*Matsui & Pyenson, 2023; Kohno, 2024*).  
20 Desmostylians have lower species diversity than other marine mammals (*Berta & Lanzetti,*  
21 *2020*), and in these analyses, the origination or extinction of a single species had a

1 remarkably large impact on the overall results. As previously mentioned, reassessment of the  
2 Desmostylian phylogenetic hypothesis is required, and the results derived from phylogenetic  
3 topology analyses should be carefully examined and discussed.

4 However, these analyses using the existing taxonomic framework provides valuable  
5 baseline for understanding Desmostylian diversity history. In the future, a taxonomic  
6 reassessment of Desmostylian and more comprehensive phylogenetic analysis will be  
7 necessary to better elucidate the drivers of their evolutionary patterns.

8

## 9 **CONCLUSIONS**

10 We described three paleoparadoxiids specimens from the Middle Miocene Tonokita  
11 Formation in Akan, Hokkaido, Japan. Based on the morphological comparisons and  
12 phylogenetic analysis, we identified these specimens as *Paleoparadoxia* sp. and *Neoparadoxia*  
13 sp. This represents the first record of the co-occurrence of two genera of Paleoparadoxiidae,  
14 with the potential to provide valuable insights into cladogenesis and morphological  
15 diversification within this family. The Akan specimens exhibit mosaic characteristics of  
16 *Paleoparadoxia* and *Neoparadoxia*. This finding indicates that species-level identification is  
17 difficult within the current taxonomic framework of Paleoparadoxiidae, highlighting the  
18 need for a reassessment of their phylogenetic hypothesis and diagnostic characters.  
19 Additionally, our stage-binned analysis and richness curve analysis shed light on the species-  
20 level diversity patterns in Desmostylian. These analyses revealed three significant points in  
21 their diversification history: (1) Desmostylidae reached peak diversification at the Oligocene-

1 Miocene boundary, coinciding with a glacial event; (2) Paleoparadoxiidae, achieved peak  
2 diversity during the Middle Miocene global warming event; (3) Both families declined their  
3 diversity and gone out during the Middle to Late Miocene global cooling event. These  
4 finding indicate that desmostylian diversity could have been closely linked to climatic  
5 events, with the differing peak diversities of Paleoparadoxiidae and Desmostylidae reflecting  
6 their respective preferences for warmer and cooler climates. However, the uncertain  
7 taxonomic status of Desmostylia may have influenced diversity estimates. While our analyses  
8 provide a valuable baseline for understanding the diversity history of Desmostylia, future  
9 efforts should focus on taxonomic reassessment and comprehensive phylogenetic analysis to  
10 refine diversity patterns and clarify their evolutionary drivers.

11

## 12 **INSTITUTIONAL ABBREVIATIONS**

13 **AMP**, Ashoro Museum of Paleontology, Hokkaido, Japan; **FMI**, The Folk Museum of  
14 Itsukaichi, Tokyo, Japan; **NSM-PV**, Fossil vertebrate collections at the National Museum of  
15 Nature and Science, Tsukuba, Japan. **LACM**, Los Angeles County Museum, California, USA;  
16 **UCMP**, University of California Museum of Paleontology, California, USA.

17

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4

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