Phylogenetic positions of the Middle Pleistocene otariid pinnipeds (Mamalia: Carnivora) from Japan and their implications

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The Otariidae (7 extant genera and 14 extant species) belongs to the Pinnipedia in the Carnivora that suit both living on land and in water. Otariids are different from other pinnipeds (phocids and odobenids) by having distinctive sexual dimorphisms and forming large harems. Extant otariids live along the coast of the North Pacific and the coast of the Southern Hemisphere. The number of species and habitat ranges of the extant otariids in the North Pacific are smaller than those in the Southern Hemisphere. However, the number of fossil records of extinct otariids known from the North Pacific are larger than those from the Southern Hemisphere. It indicates that the North Pacific is more important to understand the initial stage of the evolutionary process of the otariids. Neverthless, the fossil record of the otariids were limited, and most of them were too incomplete to discuss their taxonomies and phylogenetic relationships.

Recently, almost complete skulls of the otariids were found from the Middle Pleistocene Mandano Formation (0.6 Ma) on the Boso Peninsula. central Japan. These specimens have been stored at the Natural History Museum and Institute, Chiba, where they now bear catalog numbers CBM-PV 7616 and 7617 respectively. CBM-PV7616 is a nearly complete skull except for the rostral tip. CBM-PV7617 preserves almost complete braincase. The cranial material of the Pleistocene otariids is the first to be reported from the Japanese Islands.

The Middle Pleistocene has been recognized as the transitional period to be established the extant fauna and flora. Also, the Middle and Late Pleistocene are transitional periods for the cyclic changes of climate and sea-level stands. Therefore, information of the otariids from the Middle Pleistocene is important to understand their "final" evolutionary process. This study aims, accordingly, to determine the taxonomic and phylogenetic positions of the above-mentioned new specimens to understand their evolutionary processes in the North Pacific. For this purpose, we prepared the data matrix for the phylogenetic analysis based mainly on the morphological characters. As a result, our analysis included 16 ingroup and 14 outgroup taxa, and we coded 150 morphological and morphometric characters including 132 cranial and 18 postcranial characters. Also, we constrained the relationships of extant pinnipeds with the results of molecular analyses of previous studies in our analysis.

Our analysis revealed that the new fossils belonged in the Family Otariidae. CBM-PV7616 was located most closely to the Middle Pleistocene extinct sea lion *Proterozetes ulysses* that was previously known only from the eastern North Pacific. Also, we did not find any autapomorphy on CBM-PV7616 and in *P. ulysses*. Therefore, CBM-PV7616 is identified as *P. ulysses*. In addition, *P. ulysses* were confirmed to be closely related to the Steller sea lion *Eumetopias jubatus*. On the other hands, CBM-PV7617 was located most closely to the species of *Zalophus* that is the sister taxon to the *Eumetopias* plus *Protherozetes* clade. However, we could not find any autapomorphy nor synapomorphy to unite CBM-PV7617 to *Z. californianus* or *Z. japonicas*. Therefore, it is plausible to identify CBM-PV7617 as *Zalophus* sp.

Our result also revealed that the number of species of otariids in the Middle Pleistocene of the western North Pacific was much more than in the Recent western North Pacific, and the distribution of the otariids during that time was extended much southerly unlike their present day northern distribution. Although *P. ulysses* is known only from the restricted age (Middle Pleistocene) and

area (mid-latitude of the North Pacific), their circum-North Pacific distribution suggests that the Middle Pleistocene pinniped fauna was once or temporarily much higher in variety during the Middle Pleistocene.

Keywords: Pleistocene, North Pacific, Kazusa Group, Mandano Formation, Otariidae, Phylogenetic analysis