

## An apparent hybrid wild bear from Cambodia

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**Abstract:** An apparent instance of hybridization in the wild between *Ursus thibetanus* and *U. malayanus* is documented via morphological and genetic comparisons.

**Key words:** bear, Cambodia, hybrid, hybridization, Ursidae, *Ursus malayanus*, *Ursus thibetanus*  
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The geographic ranges of *Ursus malayanus* (the sun bear) and the larger *U. thibetanus* (the Asiatic black bear or moon bear) overlap extensively in mainland southeastern Asia, yet no hybridization between them has been reported. Both species occur in Cambodia. In 2005 an unusual looking male bear cub (specimen TM1) was obtained in an area of dense evergreen forest along the O’Koki River in Preah Vihear Province of Cambodia. The cub was found by community rangers employed by the Forestry Administration of the Royal Government of Cambodia and supported by the Wildlife Conservation Society. The capture locality was at 14°1.7’ North, 105°20.3’ East, in the Mekong River watershed. By spring 2007, TM1 (Fig. 1, 2) was housed at the Phnom Tamao Zoological Gardens and Wildlife Rescue Center, Takeo Province, Cambodia.

There are substantial cranial and postcranial differences between *U. malayanus* and *U. thibetanus* (Pocock 1932). As in the predominant color phase of both species (Pocock 1932, Galbreath et al. 2001), the visible pelage of TM1 is largely black. TM1 differs little postcranially from *U. thibetanus*. The shape of the pale chest mark on TM1 is similar to that of *U. thibetanus*.

The mane of TM1 is relatively slight, forming a crest on each side of the neck, as in all *U. malayanus* and some *U. thibetanus*. Facial appearance of TM1 is subjectively intermediate between that of the species, though this could change during the next 2 or 3 years of growth. The small ears (Fig. 2a) and the very large, stout canines (Fig. 2b) of TM1 approximate those of *U. malayanus*. Overall, TM1 resembles a *U. thibetanus* with unusually glossy pelage and an unusual head.

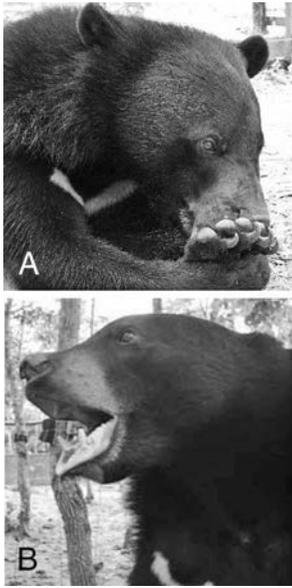
Mitochondrial DNA was extracted from hair roots of TM1, following the protocol in the Qiagen (Valencia, California, USA) tissue kit. Using appropriate primers (Kocher et al. 1989, Shields and Kocher 1991), a 185 base pair segment of nucleotides comprising sites 213 to 397 (as enumerated on the light chain) of the 1140 base pair cytochrome *b* gene, and a 135 base pair segment comprising the threonine and proline tRNA genes, were sequenced. Cycle sequencing followed the protocol of Adams et al. (2003).

The resulting sequences were identical to homologous portions of *U. malayanus* sequences L21871 (Zhang and Ryder 1993) and U18899 (Talbot and Shields 1996), and U18900 (Talbot and Shields 1996), respectively. They were notably different from homologous portions of Genbank sequences representing *U. thibetanus*, the minimum number of differing base pairs being 12 for the cytochrome *b* segment and 5 for the tRNA genes. The nucleotide sequence for light chain sites 219, 222, 273, 288, 303, 309, 318, 325, 345, 348, 351, and 369 of the cytochrome *b* gene was TCTGTCGTCTTT for specimen TM1, compared with CTCCTACTCCA for the most similar *U. thibetanus* sequence (Genbank L21880). The sequence for light chain sites 36, 54, 55, 92 and 94 of the tRNA genes was ATCGT for



**Fig. 1.** Subadult bear TM1, captured as a cub in northern Cambodia in 2005.

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**Fig. 2.** Cambodian bear TM1, displaying (a) small ears and (b) large canines.

specimen TM1, compared with GCTAC for the most similar *U. thibetanus* sequence (Genbank U23559).

At Phnom Tamao, TM1 was housed with individuals of *U. thibetanus* due to gross morphological similarity. That similarity, particularly postcranially, indicates that TM1 is not a specimen of *U. malayanus*, normal or pathological. Yet TM1 possesses *U. malayanus* mitochondrial DNA and has similar ears and canines, so is clearly not a specimen of *U. thibetanus*, either. TM1 therefore appears to be an interspecies hybrid (broadly defined, encompassing F1 and backcross generations). There are no zoos or other potential sources of escaped hybrids in the remote region from which TM1 derives. We therefore suggest that this individual constitutes evidence of hybridization in the wild between 2 tropical ursid species (*U. malayanus* and *U. thibetanus*).

Future investigation of TM1 could profitably focus on its nuclear DNA and (after growth is completed) on its morphometrics. Appropriate comparison of nuclear genes would, we suspect, provide further evidence that it is a hybrid and might elucidate its status more precisely (F1 versus backcross). For such a study, it would be desirable to obtain nuclear DNA originating in northern Cambodia from both species of bear.

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