

## Recent changes in the genetic structure of the Asian black bear *Ursus t. japonicus* in the Japanese Alps region

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Asian black bear *Ursus thibetanus* habitats are dotted intermittently across South and East Asia. They have been divided into seven subspecies. In Japan, the subspecies *U. t. japonicus* inhabits two of the main islands, Honshu and Shikoku. It is considered that the population of Kyushu is extinct. The Japanese Alps region is one of the most significant habitats for the Japanese black bears, since it provides a habitat, which is largely contiguous and as such their density is very high. The black bear is omnivorous, but they mainly rely upon a herbivorous diet plant-origin foods. In particular in late autumn before hibernation, it is estimated that they have to consume food amounting to ca. 5500kcal per day (per individual of 60kg bear). Their main food is a kind of beechnut, which are the also-called "acorns". As such, during years when the beech species provides a poor yield of nuts, many of the black bears come down to areas of human habitation in search of sufficient food to prepare for hibernation. In such years, damage to crops and attacks on humans by bears increase, so as a result a larger number of bears will be killed as a pest control under the "prefectural wildlife conservation and management plan". Nagano Prefecture carried out to estimation of the number of individual of black bears, it has also set an upper limit of ca. 150 on the maximum number of individuals that can be killed each year. Since then, a report the Wildlife Conservation and Management Program of Nagano Prefecture recently estimated that the number of black bear habiting Nagano Prefecture has increased significantly in this decade; 1913 individuals in 2001, 2771 in 2006 and 3624 in 2011. However, during in this decade, in 2006 and 2010, the number of bears killed has unfortunately exceeded the upper limit set, as higher population has resulted in a higher incidence of conflict with humans; 558 individuals in 2006 and 361 in 2010. In this present study, we have performed genetic analyses, in order to understand in more detail the population and genetic structures of black bears in the Japanese Alps and around the surrounding regions,. We analyzed 625-based sequences in the D-loop region of mitochondrial DNA using approximately 100 samples collected from diverse locations across Nagano Prefecture. We compared our analyzed data with the data of several previous analyses (Ohnishi et al., 2007, 2009), and also an impact assessment was carried out into the higher killing rate of recent years; i.e., we evaluated whether any effect of genetic bottleneck was resulting or not. As a result, the genetic diversity of black bears in Nagano Prefecture was found to be much higher than the previously evaluated; the haplotype diversity (Hd) found in this study was 0.679, and the nucleotide diversity (Pi) was 0.0031, whereas in Ohnishi et al. (2009), Hd=0.4734, Pi=0.0012. Of particular note, it was revealed that the genetic diversity observed amongst the northern bear populations was clearly higher, whilst the genetic diversity was comparatively low amongst the southern bear populations. Based upon the analysis of molecular variance (AMOVA), it was revealed that gene flow of black bears was significantly restricted between three identifiable regions of Nagano Prefecture; i.e., the northern, central and southern regions. This localized genetic population level data for the Japanese Alps and surrounding areas will be utilized in the formulation of future protection and management planning and policy.