

The logo for SaSSOH, featuring the text "SaSSOH" in a bold, sans-serif font. The "O" is replaced by a circular emblem containing a stylized globe with a green and blue color scheme.

SaSSOH 2018

The 6th Sapporo Summer Symposium for
One Health (SaSSOH 2018) will be held as below;

Beyond One Health: Visualizing Our Heterogeneity

September 20th (Thu) – 21st (Fri), 2018

Lecture Building, Faculty of Veterinary Medicine,
Hokkaido University

Hokkaido University
Program for Leading Graduate Schools
Fostering Global Leaders in Veterinary Science for
Contributing to One Health

A vertical arrangement of stylized Japanese characters in white. The top character is "立" (tatsu), the middle is "風" (kaze), and the bottom is "爽" (su). Together, they read "立風爽" (Tatekaze Su), which translates to "Standing Wind is Refreshing".

Program Day 1

September 20 (Thu), 2018

8:10-8:50	Registration
8:50-9:00	Opening Remarks (Dr. Motohiro Horiuchi, Dean) From the committee (Dr. Keita Matsuno, SaSSOH 2018 organizing committee)
Session A Pathogen-host interaction	
9:00-10:20	Chairs: Dr. Okagawa & Ms. Tanaka
L-1	Dr. Logan Banadyga
O-1	Shiho Torii
O-2	Takashi Nishida
O-3	Yamato Sajiki
Break	
Session B Dynamics on population	
10:30-11:35	Chairs: Dr. Yamagishi & Mr. Kondoh
L-2	Dr. Shingo Iwami
O-4	Yukiko Nakamura
O-5	Yuri Fujimoto
Poster session I	
11:35-12:15	PI Flash Talk (Chair: Dr. Yamasaki)
Lunch break (Light meal will be provided)	
13:00-14:00	PI Poster Core Time (Lecture Room 2 & 3)
Session C Chasing diversity	
14:00-15:05	Chairs: Dr. M. Sasaki & Ms. Torii
L-3	Dr. Yasutsugu Suzuki
O-6	Kadariya Rabin
O-7	Tussapon Boonyarattanasoonthorn
Break	
Keynote Lecture I	
15:15-16:15	Chair: Dr. Orba Dr. Naoki Mochizuki
Break	
Session D Molecular diagnosis	
16:25-17:30	Chairs: Dr. Kajihara & Mr. Okuya
L-4	Dr. Cameron Myhrvold
O-8	Kentarou Koide
O-9	Jussiaea Valente Bariuian
Break	
Leading Program Symposium	
17:40-18:40	Chair: Dr. Horiuchi Dr. Hirofumi Sawa Michael Henshaw Dr. Tomohiro Okagawa Kazuyoshi Sasaoka

High genetic diversity and distinct ancient lineages of Himalayan black bear revealed by noninvasive surveys in the Annapurna Conservation Area, Nepal



Rabin Kadariya, Mohamed Abdallah Mohamed Moustafa, Mariko Sashika, Michito Shimozuru, Toshio Tsubota
 Lab. of Wildlife Biology and Medicine
 Hokkaido University, Japan
 September 20, 2018
 Email: rkadariya@yahoo.com



Acknowledgements



(Day 1: 14:35-14:50 on September 20)

O-6 High genetic diversity and distinct ancient lineages of Himalayan black bear revealed by noninvasive surveys in the Annapurna Conservation Area, Nepal

Rabin Kadariya¹, Jesús E. Maldonado², Mohamed Abdallah Mohamed Moustafa¹, Mariko Sashika¹, Michito Shimozuru¹, Toshio Tsubota¹

¹Lab. of Wildlife Biology and Medicine, Department of Environmental Veterinary Science, Graduate School of Veterinary Medicine, Hokkaido University, Sapporo, Japan
²Center for Conservation Genomics, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, DC, USA
 (rabin@vetmed.hokudai.ac.jp)

The Himalayan black bear (*Ursus thibetanus laniger*) is one of the least conservation priority species with a widespread distribution in the mountain landscape of Nepal. Globally, habitat fragmentation, illegal killing and human-bear conflict are the major threats for bear conservation. Adequate level of genetic variation is an important consideration for a wildlife population to better adapt to a rapid changing environment.

We conducted noninvasive surveys throughout the ACA and sequenced mitochondrial DNA to understand the phylogenetic relationship of Himalayan black bear from this region of Nepal compared to other subspecies. In order to assess levels of genetic diversity and population genetic structure, we genotyped 8 microsatellite loci using 147 noninvasive samples collected from ACA. We identified 60 individuals in an area of about 525 km², of which 25% frequently visited nearby cropland in rainy season to fulfill the available high quality crop food. We found high levels of genetic diversity ($H_E = 0.76$) and no population sub-structure among sampling localities in the ACA. Genetic diversity was progressively maintained in ACA as compare to other bear habitats whereas bear related conflict should address for its long-lasting survival of future viable population. Bear specific primers were designed for the amplification of a 675 bp fragment of mitochondrial control region (CR) and three haplotypes were observed from the entire conservation area. We also sequenced the complete mitochondrial genome (16,771 bp) in order to have the power to resolve the phylogenetic relationships of closely related subspecies of Asiatic black bears. This is the first complete mitochondrial genome to be sequenced from the wild population of Himalayan black bear. The mitochondrial phylogeny indicated that Himalayan black bear populations from Nepal form a distinct evolutionary unit from other reported subspecies.