The 19th International Symposium on Primatology and Wildlife Science

October 30 and 31, 2024

Science Seminar House, North Campus, Kyoto University

Program & Abstract

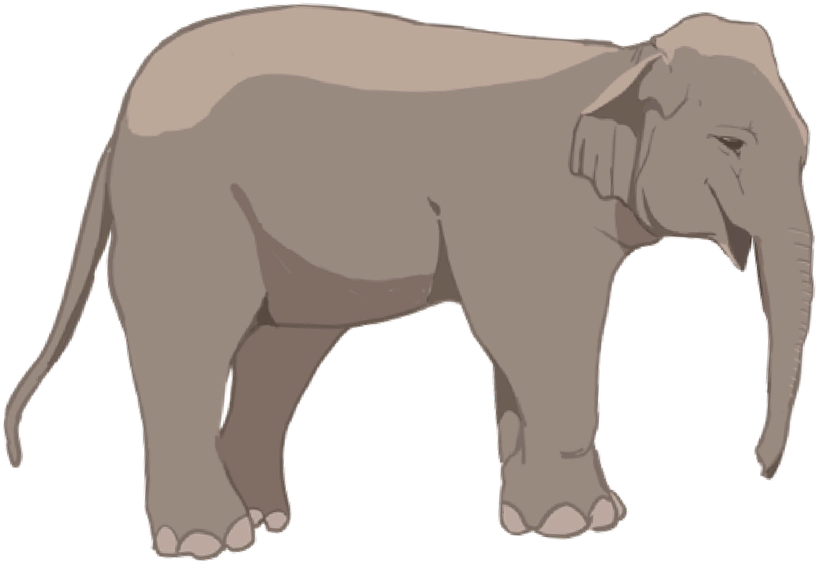


Table of Contents

Time Schedule

JST	
9:00	**Registration**
9:30	**Opening Remark** (9:30-9:45)
9:45	**Keynote Talk 1**
	Dr. Krupenye
	Talk (9:45-10:25)
	Q&A (10:25-10:35)
10:35	Break (10:35-10:50, 15min)
10:50	**Oral session 1**
	Chika Zemmoto (10:50-11:05)
	Alisa Tobe (11:05-11:20)
	Hepling Li (11:20-11:35)
	Mariam Likokeli (11:35-11:50)
11:50	Lunch break (11:50-13:00)
13:00	

13:00	**Keynote Talk 2**
	Dr. Ruppert
	Talk (13:00-13:40)
	Q&A (13:40-13:50)
13:50	**Dr. Terada**
	Talk (13:50-14:30)
	Q&A (14:30-14:40)
14:40	Break (14:40-14:50, 10min)
14:50	Panel Discussion (14:50-15:10)
15:10	Break (15:10-15:20 10 min)
15:20	**Keynote Talk 3**
	Dr. Portugal
	Talk (15:20-16:00)
	Q&A (16:00-16:10)
16:10	**Dr. Sato**
	Talk (16:10-16:50)
	Q&A (16:50-17:00)
17:00	Break (17:00-17:10, 10min)
17:10	Panel Discussion (17:10-17:30)
17:30	**Closing Remark** (17:30-17:40)
17:40	Setting, break (17:40-18:00)
18:00	**Party** (18:00-20:00)
20:00	

Day 2

JST	
8:30	**Registration**
9:00	**Oral session 2**
	Kana Arai (9:00-9:15)
9:30	Momoka Suzuki (9:15-9:30)
	Rena Numabe (9:30-9:45)
	Jie Gao (9:45-10:00)
	Fashima Tabassum (10:00-10:15)
10:15	Break (10:15-10:25, 10min)
10:30	**Lightning talk (10:25-11:10)**
	1.5 min/person
	24 people
11:10	Lunch break
	(11:10-12:10)
12:10	
12:10	**Set up** (12:10-12:20)

12:20	**Poster session**
	Group1 (even number)
	(12:20-13:10)
13:10	Group2 (odd number)
	(13:10-14:00)
14:00	Break (14:00-14:15, 15min)
14:15	**Dr. Kawazoe**
	14:15-14:55 Talk
	14:55-15:05 Q&A
15:05	**Closing Remark**(15:05-15:30)
	Prize, Group Photo, Questionnaire
15:30	

Access

- The Science Seminar House is located on North Campus.
- The nearest bus stop to the venue is either Kyodai Nougakubu-mae or Hyakumanben, depending on the bus line.
- It is also accessible on foot, approximately 15 mins from Demachiyanagi Station (KeihanLine)

Campus Map

Science Seminar House

Keynote Speakers

Johns Hopkins University

Dr. Christopher Krupenye

The social minds of humans and other apes

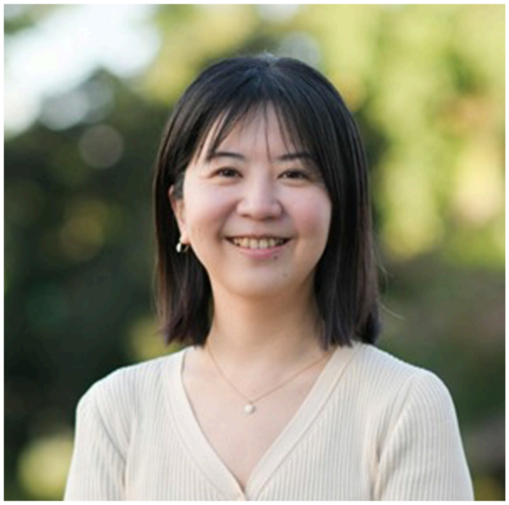
Most nonhuman primates, like humans, face a dynamic social world made up of numerous groupmates, each with their own goals, knowledge, and social ties. Navigating this social world is critical to successfully building social bonds, rank, and reproductive success. But how do they do it? What information do they extract about the social world, to enable strategic social decisions? Through a series of cognitive experiments with humans' closest relatives, chimpanzees and bonobos, my collaborators and I show that they possess rich capacities for tracking information about groupmates, their relationships, and their minds. This work suggests that these mechanisms are evolutionarily ancient features of human psychology that operate in the absence of language. Cognitive research is essential for understanding how animals interact with their environment, and for raising awareness about both the richness of their mental lives and the conservation challenges they face.

School of Biological Sciences,
Universiti Sains Malaysia

Dr. Nadine Ruppert

Impact of oil palm plantations on behaviour and fitness of southern pig-tailed macaques (*Macaca nemestrina*)

Oil palm plantations are frequently visited by wildlife, yet it is not well understood A) what impact a certain species has on plantation yield and management (pest or pest control?), and B) what impact the plantation environment has on a species (harm or benefit?). Southern pig-tailed macaques, commonly found in oil palm (*Elaeis guineensis*) plantations near intact forest, forage for food and are often regarded as nuisances due to unwanted interactions in this agricultural context. To clarify the effects of macaque presence on oil palm yield and the plantation environment on macaque health, we have conducted a long-term study on habituated macaques in a mixed forest-plantation habitat in Perak, Malaysia. For A), our study on oil palm fruit consumption by macaques found that the impact on yield is minor (<0.03%). More importantly, macaques act as biological pest control by feeding on plantation rats, which cause up to 10% yield loss. A group of 40 macaques can hunt about 3,000 rats per year, increasing net oil palm yield by USD 100 per ha annually. Conversely, rodenticides are expensive, inefficient, and harmful to non-target wildlife and the environment. Other chemicals, like herbicides and fertilizers, may also negatively impact wildlife health. Study group individuals show health issues, including infertility, facial dysplasia, and elevated infant mortality (mean annual: 57%), potentially due to poaching, intragroup aggression, and harmful chemicals. Human-induced habitat changes evoke complex behavioral responses. Our research shows significant behavioral modifications in macaques foraging in plantations, including altered mother-infant interactions, reduced positive social interactions, and increased aggression deeper in the plantation compared to near the forest edge. These findings suggest opportunities for mitigating human-wildlife conflict: protecting natural forest habitat near plantations, creating wildlife corridors, and establishing viable interfaces between forests and plantations could maintain connectivity and gene flow, increase wildlife welfare and health, and reduce conflicts while benefiting planters. By promoting sustainable palm oil production and biodiversity, macaques can become a flagship species for environmental sustainability.



Osaka Metropolitan University

Dr. Saeko Terada

Sustainable Use of Wildlife: Achievements and Challenges of International Trade Regulations under CITES

Humans use wildlife in various ways, including food, materials, medicine, pets, and objects of art and culture. To meet these demands, international trade in wildlife is glowing. The Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) is a cooperative mechanism between exporting and importing countries to conserve species threatened by over-exploitation for international trade. This presentation will introduce the CITES's mechanisms, achievements, and challenges based on trends in the deliberations of the Conference of the Parties (CoP) and the presenter's own experience of participating in the CoPs. Under CITES, commercial trade in Appendix I-listed species is prohibited, but commercial trade in Appendix II-listed species is permitted if the exporting country issues an export permit. The export permit is only granted if the scientific authority of the exporting country confirms that the trade is not detrimental to the species' survival. This mechanism allows for legalizing only trade considered to be ecologically sustainable based on scientific evidence. For example, such as vicuñas, well-regulated international commercial trade has increased population and enhanced local welfare. However, intense debate has continued about commercial trade regulations for some species, such as iconic large mammals, and some species continue to be poached and traded illegally, even though international trade is prohibited. To overcome these challenges and improve the decision-making of CTES parties, more respect is needed for scientific information, the impact of trade regulations on the behavior of local people living with the species, and the diverse values of wildlife.

University of Oxford

Dr. Steve Portugal

Living in Groups: Who is really benefiting from travelling in groups?

Many species are highly gregarious and form large groups. These groups can serve multiple functions, such as enhancing predator detection and increasing foraging efficiency. Another key feature of why animals live in groups can be the benefits brought during collective locomotion. Travelling in groups can provide aero- or hydro- dynamic benefits, while groups of animals are known to home quicker, and more efficiently, than individuals travelling alone. However, such benefits are not always distributed equally throughout group members, and some individuals within a group will be benefitting disproportionally from travelling in groups, while others may be experiencing negative consequences. What determines how costs or benefits are distributed within a group is not fully understood, with both individual physiological and personality-based traits likely to play a role. This talk will present data looking at situations where benefits of travelling in groups are equally, and non-equally distributed amongst members, and examine the underlying causes (physiological, behavioural, morphological) of this variation. Using a combination of biologging, respirometry and behavioural observations, case studies will focus on flocking in birds, the influence of dominance and social rank on movements in naked-mole rats, and how personality traits determine flock positioning in pigeons.

Atmosphere and Ocean Research Institute,
University of Tokyo

Dr. Katsufumi Sato

How can biologging contribute to society?

Biologging is a technique where small devices are attached to animals to monitor their behavior, physiology, and surrounding environment. This relatively new research method was developed to study animals in their natural habitats, where direct observation is challenging. The term “biologging” was coined when the first international symposium was held in Tokyo in 2003, and since then, biologging symposiums have been held every three years around the world. Initially, the biologging was used for seals and penguins in the Antarctic Ocean. However, study sites have since expanded to tropical and temperate regions, and the range of species studied now includes both aquatic and terrestrial animals. Recently, we have developed a database known as the “Biologging intelligent Platform (BiP) ” to store and share biologging data (https://www.bip-earth.com). This platform is designed not only for use by the original data collectors but also to promote secondary and tertiary uses of the data. Notably, environmental data collected at the boundary between the atmosphere and the ocean through biologging may prove valuable in meteorology and oceanography. In the future, biologging data might become a standard component in weather forecasting. Additionally, biologging data could be used for the assessment of offshore wind power facilities when they are constructed. We also foresee biologging data being utilized by ambitious junior and senior high school students for their independent research projects.

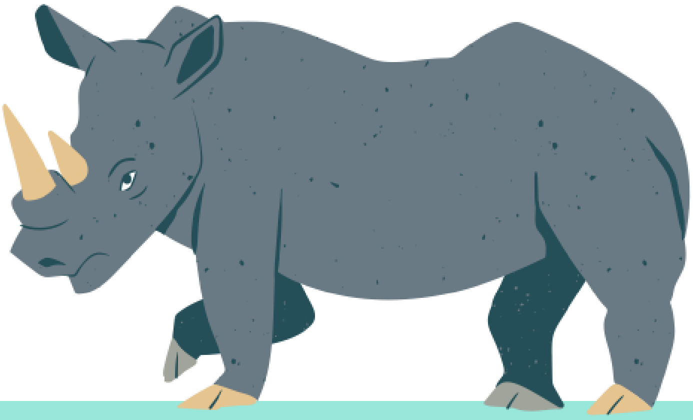
Research Institute for Satomon

Dr. Tatsuro Kawazoe

Understanding Human-Primate Interfaces: Ethnoprimatological Perspectives on Coexistence

Primatology has expanded the accumulation of long-term datasets and the diversity of species and populations studied. It acknowledges that humans and non-human primates often share habitats and resources, leading to complex dynamics that can affect both human societies and primate populations. Ethnoprimatology is an interdisciplinary field that examines the interactions and relationships between human and non-human primates. This field integrates approaches from anthropology, primatology, ecology, and conservation biology to understand how human activities, cultural practices, and beliefs influence primate behavior, ecology, and conservation, and vice versa. Human and non-human primates interact across many contexts, primarily along a gradient that extends from rural to urban areas. This gradient ranges from natural primate habitats such as forests and savannas to agricultural areas and semi-urban environments like residential buildings. Ethnoprimatology aims to study the impact of habitat destruction on primates, the roles primates play in local cultures and economies, and how human-primate interactions shape conservation efforts, striving to promote a holistic understanding of human-primate relationships and encourage coexistence and sustainable conservation practices. In this presentation, I will introduce the diverse human-macaque interfaces. Japanese macaques are widely distributed throughout Japan and have historically shared habitats with humans. Ecological and behavioral research on Japanese macaques has primarily focused on wild populations living in forests, free-ranging provisioned groups, and captive populations. However, recent changes in Japan's social landscape have brought significant attention to interactions between humans and Japanese macaques in agricultural areas. I aim to showcase the diversity of human-wildlife interactions surrounding Japanese macaques, the reality of conflicts between humans and macaques in agricultural areas, and efforts to prevent these conflicts, providing an opportunity to consider how researchers can contribute to the coexistence of humans and wildlife.

Program & Abstracts: Oral & Poster Presentations



Oral Presentation

Oral session 1 Oct 30 (10:50-11:50)

Time	Presenter	Affiliation	Title
~11:05	Chika ZEMMOTO	Wildlife Research Center, Kyoto University	The Genetic analysis of the Western Population of Domestic Yak (*Bos grunniens*)
~11:20	Alisa TOBE	Wildlife Research Center, Kyoto University	Evolutionary insights into toxin-resistance genes of the Crested serpent-eagle: A comparative analysis of ATP1A1 in raptors
~11:35	Heping LI	Wildlife Research Center, Kyoto University	Using satellite tracking to characterize the northbound movement of northern fur seals (*Callorhinus ursinus*) and their responses to oceanographic features
~11:50	Mariam LIKOKELI	Graduate School of Human Sciences, Osaka University	Cultural significance and environmental protection: a survey of public perceptions of the seasonal disappearance of barn swallow roosts in Japan and Indonesia

Oral session 2 Oct 31 (9:00-10:15)

Time	Presenter	Affiliation	Title
~9:15	Kana ARAI	Wildlife Research Center, Kyoto University	Uncovering Age-Related Genes in Asian Elephants: A Genome-Wide Epigenetic Approach
~9:30	Momoka SUZUKI	Wildlife Research Center, Kyoto University	Presence of the “Transient” and “Resident” Ecotypes in Killer Whales (*Orcinus orca*) around Hokkaido Revealed by Whole Mitochondrial Genome Analysis:
~9:45	Rena NUMABE	Wildlife Research Center, Kyoto University	Effect of the genetic polymorphism of TAS2R43 and TAS2R46 on the receptor function and bitter taste perception for caffeine
~10:00	Jie GAO	Wildlife Research Center, Kyoto University	Visual search using a touchscreen in domestic goats: a pilot study
~10:15	Fashima TABASSUM	Department of Biological Sciences, Osaka University	Description of new deep-sea species of Muusoctopus genus from Sea of Japan using integrated Taxonomic Methods

Poster Presentation

Poster session Oct 31

Lightning Talk: 1.5 min/ person

12:20-13:10 (even number), 13:10-14:00 (odd number)

	Presenter	Affiliation	Title
P-1	Mayu SHIMADA	Wildlife Research Center, Kyoto University	Audience effects of female bystanders on allopreening of affiliative male–female dyads in large-billed crows (*Corvus macrorhynchos*)
P-2	Hiroaki YANAGI	Graduate School of Science, Kyoto University	Comparison of Head Morphology in Snakes (*Ptyas*) with Different Feeding Habits
P-3	Honoka TANOHATA	Wildlife Research Center, Kyoto University	Social organization of the Bornean elephant inferred from DNA analysis and observation
P-4	Hizuki NAKAMURA	Wildlife Research Center, Kyoto University	Genomic Data Reveals the Genetic Diversity of the Red-crowned Crane – Is the Hokkaido Population Really Stable?
P-5	Chiristen LIN	Wildlife Research Center, Kyoto University	Comparing Snake Images and Videos as Emotion-Inducing Stimuli for Chimpanzees
P-6	Ashika DHIMAL	Centre for Ecological Sciences, Indian Institute of Science	The origin and evolutionary history of the endangered Golden langurs (Trachypithecus geei Khajuria, 1956)
P-7	Chinatsu NISHIMOTO	Wildlife Research Center, Kyoto University	The challenge of establishing assisted reproductive technology for wild cats' conservation -To produce mature oocytes that can be used for in vitro fertility-
P-8	Fadel AZHARI	Wildlife Research Center, Kyoto University	Population Structure, Genetic Diversity, and Past Demography of White-tailed Eagles in Hokkaido Using Whole-genome Approach and Future Plans of the Study
P-9	Hibiki NISHITANI	Graduate School of Bioresources, Mie University	Social ageing in male Indo-Pacific bottlenose dolphins: exploring the drivers of shifting sociality
P-10	Fitri SUHAIMI	Wildlife Research Center, Kyoto University	Long-term population monitoring of sympatric primates in different forest types in the Lower Kinabatangan, Sabah, Borneo, Malaysia
P-11	Tomoyuki TAJIMA	Osaka University	Genetic diversity and long-term population viability of Bornean orangutans in Malaysia
P-12	Yume OKAMOTO	Wildlife Research Center, Kyoto University	The Secret of cat sociality: comparison of *AVPR1a* genotypes among Felid species

Poster session Oct 31

Lightning Talk: 1.5 min/ person

12:20-13:10(even number), 13:10-14:00(odd number)

	Presenter	Affiliation	Title
P-13	Scott JENKIS	Graduate School of Informatics, Kyoto University	Understanding Bat Guilds: Development, Uses, and Research Implications
P-14	Shimei SHIRASAWA	Wildlife Research Center, Kyoto University	Grooming Behavior and Its Impact on Body Temperature in Japanese Macaques
P-15	Divya SHAJI	EHUB, Kyoto University	Genome sequence analysis of Plasmodium cynomolgi using malaria-infected Macaca mullata
P-16	China KOBAYASHI	Wildlife Research Center, Kyoto University	Exploring the Role of Oxytocin at the Early Stages of Social Relationship Building
P-17	Ayumi OGAWA	Wildlife Research Center, Kyoto University	A hypothesis of cognitive constraints to explain the rarity of mutual grooming
P-18	Marie SEKI	Wildlife Research Center, Kyoto University	Species distribution model for Tsushima leopard cat (*Prionailurus bengalensis euptilurus*)
P-19	Liu LIU	Wildlife Research Center, Kyoto University	Musicality in chimpanzees and bonobos
P-20	Mohamed SAIDI	Wildlife Research Center, Kyoto University	Genetic diversity and estimated geographical origin of captive critically endangered black rhinoceros in Japan: Implications for future conservation and breeding.
P-21	Abdullah LANGGENG	Wildlife Research Center, Kyoto University	Courage in the Dark: Exploring Personality Traits in Rehabilitating Javan Slow Lorises
P-22	Yeongju LEE	Wildlife Research Center, Kyoto University	Stability in Social Bonds of Mothers and the Offspring's Sociality in Free-roaming Horse Groups
P-23	Akihiro ITAHARA	Wildlife Research Center, Kyoto University	Tracking gaze-following behavior in Large-billed crows (*Corvus macrorhynchos*) using a motion capture system

Please Vote for the Best Presentation Award!

<u>Oral Presentation</u>

Day-1 **Day-2**

***Please <u>DO NOT</u> submit the same form twice**

- The standard score is 3, with higher scores for better presentations.
- Please keep in mind that the evaluation should be absolute, not relative among the presentations of the day.
- The presentation with the highest average score among the 9 presentations over the two days will receive the oral presentation award.
- Presenters are asked to refrain from voting for their own presentations.

<u>Poster Presentation</u>

***Please DO NOT select the same presenter more than once**

- Please select the posters you think were good, from first to third place.
- The best gets 3 points, the second best gets 2 points, and the third best gets 1 point.
- Up to the third highest presenter in order of total points will receive the award.
- Presenters are asked to refrain from voting for their own presentations.

The Genetic Analysis of the Western Population of Domestic Yak (*Bos grunniens*)

Chika Zemmoto*, Kadyrbai Chekirov[2], Annegret Moto Naito-Liederbach[1,3] and Miho Inoue- Murayama [1]
[1] Wildlife Research Center, Kyoto University, Kyoto, Japan
[2] Kyrgyz-Turkish Manas University, Bishkek, Kyrgyz Republic
3 Kyoto City Zoo, Kyoto, Japan
* chk.zemmoto@gmail.com

The domestic yak (*Bos grunniens*) is a popular animal in Central Asia as well as in the Qinghai-Tibet Plateau. Although they are called "domestic" yak, they frequently reside in semi-wild conditions, exhibiting characteristics, behaviors, and adaptations reminiscent of wild yak (*Bos mutus*). Domestic yak have spread not only within China, but also to other high-mountain regions of Eurasia. Despite their wide contemporary distribution, genomic analysis of yak is biased towards China. Therefore, it is unclear when and how the species expanded its distribution westward. To compare the populations of central Eurasian yaks with those in China, we sampled at two sites in Kyrgyzstan in 2022, and sequenced their whole genomes. We compared heterozygosity and historical effective population size of these samples with data from an individual in China from a previous study. Kyrgyz yak showed higher heterozygosity (0.0022~) than the domestic individual (0.0020) in Jinchuan, western China. In addition, Kyrgyz individuals seemed to show different demographic histories compared to the Chinese individual in Pairwise Sequentially Markovian Coalescent analysis. These results indicate Kyrgyz yak may have experienced different population histories, such as historically low inbreeding.

Evolutionary insights into toxin-resistance genes of the Crested serpent-eagle: A comparative analysis of ATP1A1 in raptors

Alisa Tobe[1*], Yu Sato[1], Mitsuki Kondo[2,3], Manabu Onuma[2], Miho Inoue-Murayama[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *National Institute for Environmental Studies, Tsukuba, Japan*
[3] *Joint Faculty of Veterinary Medicine, Kagoshima University, Kagoshima, Japan*
[*] `tobe.alisa.23y@st.kyoto-u.ac.jp`

The Crested serpent-eagle, inhabiting only Iriomote and Ishigaki Islands in Japan, preys on introduced cane toads with lethal cardiotonic steroid toxins. It was revealed that the resistance against this toxin is associated with specific amino acid substitutions in the α-subunit family of Na+/K+ -ATPase (ATP1A) with various species. Our previous investigations suggested that identical toxin-resistance related sequences in ATP1A of eagles from both Japanese islands and a subspecies from Simeulue Island, Indonesia. In this study, ATP1A1, an ATP1A paralog, was analyzed with other raptor species to explore the evolutionary history of these toxin-resistance related sequences. Comparative genetic analysis of ATP1A1 was performed with nine raptor species and adaptation analysis using PAML's branch-site model was also conducted. These analyses revealed that ATP1A1 sequences were more similar between the Crested serpent-eagle and Black-chested snake eagle than among other raptor species. Furthermore, although we analyzed only a limited number of raptor species and further analysis is required, the ratio of nonsynonymous to synonymous substitutions (ω) exceeded 1 in the common ancestor of these two eagle species, suggesting possible natural selection for toxin-resistance related sequences in this lineage.

Using satellite tracking to characterize the northbound movement of northern fur seals (*Callorhinus ursinus*) and their responses to oceanographic features

Heping Li[1*], Ryo Dobashi[2], Yoko Mitani[3]
[1] *Graduate School of Science, Kyoto University, Kyoto, Japan*
[2] *Department of Oceanography, University of Hawai'i at Mānoa, Honolulu, Hawaii, United States*
[3] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[*] `leeheping09@gmail.com`

Northern fur seals (*Callorhinus ursinus*, NFSs) are highly migratory otariid species that undertake seasonal migration between their breeding colonies and wintering grounds. Previous studies suggested that various oceanographic features facilitate their southward movement, and their at-sea distribution relates to prey availability. However, understanding their pelagic movement and their behavioral responses to oceanic conditions remains challenging due to the difficulties in collecting continuous spatiotemporal data from their wintering grounds. We tracked five male NFSs using satellite tags from the wintering grounds in the Sea of Japan. Tracking data demonstrated their traveling pathway, movement pattern, and their relationship with diverse oceanographic variables. Results suggested different movement patterns between the stay and northbound transition phases. Foraging-related behavior was concentrated along continental shelf and shelf break areas, likely due to the prey-rich waters created by distinctive topographic features. NFSs preferred feeding within specific water temperature ranges, possibly influenced by water masses that aggregate abundant food. Additionally, male NFSs showed reduced foraging activity at mesoscale eddy edges but transited more frequently there. High-velocity regions near eddy edges appeared to facilitate their movement rather than optimizing foraging. This strategic use of eddy edges suggests a trade-off between energy conservation and prey acquisition during NFSs' northbound migration.

O-4

Cultural significance and environmental protection: a survey of public perceptions of the seasonal disappearance of barn swallow roosts in Japan and Indonesia

Mariam Likokeli[1*], Takahiro Ota[1]
Graduate School of Human Sciences, Osaka University, Osaka City, Japan
`u172960k@ecs.osaka-u.ac.jp`

This research aims to explore the socio-cultural factors that shape public attitudes toward the conservation of barn swallow (*Hirundo rustica*) roost colonies in Japan and Indonesia. While barn swallows have a strong cultural significance in Japan, symbolizing good luck and seasonal change, they hold little cultural value in Indonesia. This difference offers a unique opportunity to investigate how cultural context influences attitudes towards the conservation of species that are more or less culturally embedded. A key focus of this study is the distinction between attitudes toward the seasonal disappearance of barn swallows, due to their migratory nature, and their potential complete extinction.

By employing a conservation psychology framework, this study aims to uncover why some species, like the barn swallow, evoke more conservation support than others and how these attitudes are shaped by socio-demographic factors, such as age, education, and social norms. The research will also explore broader questions about species popularity in conservation efforts and how cultural and psychological factors affect public engagement. The findings will contribute to the development of more effective and culturally informed conservation strategies, applicable not only to barn swallows but to other species facing similar threats across different socio-cultural landscapes.

Uncovering Age-Related Genes in Asian Elephants: A Genome-Wide Epigenetic Approach

Kana Arai[1,2*], Miho Inoue-Murayama[2]
[1] *Graduate School of Science, Kyoto University, Kyoto, Japan*
[2] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[*] `arai.kana.84p@st.kyoto-u.ac.jp`

Asian elephants (*Elephas maximus*) are classified as endangered by the International Union for Conservation of Nature (IUCN). Given their lifespan of over 70 years, obtaining accurate age information is crucial for understanding their basic ecology and supporting conservation management efforts. However, current methods to estimate age based on physical features can be subjective. In this study, we explore age-related genes in Asian elephants using genome-wide DNA methylation analysis through reduced representation bisulfite sequencing (RRBS). Investigating age at the molecular level also provides insights into ageing–a complex biological process influenced by genetic, epigenetic, and environmental factors. DNA was extracted from blood samples ($n = 96$) collected from 29 known-aged captive Asian elephants across Japan, and libraries were prepared following the RRBS protocol. From the sequenced data, we calculated methylation levels and identified 389 CpG sites with high correlation to age, which were used to construct an age estimation model with a mean absolute error of 4.82 years. Using the available annotated reference genome of Asian elephants, we identified 148 genes. Among these, 5 genes–including *KCNC4* and *FAM127A*–were associated with 8 CpG sites that exhibited very high correlations with age ($r > 0.7$). Our findings demonstrate that DNA methylation patterns could serve as reliable biomarkers for age estimation, while the identified key regions could offer valuable insights into the molecular mechanisms underlying ageing in elephants.

O-6

Presence of the “Transient” and “Resident” Ecotypes in Killer Whales (*Orcinus orca*) around Hokkaido Revealed by Whole Mitochondrial Genome Analysis

Momoka Suzuki[1*], Mami Kawai[2], Takashi Hayakawa[3], Yuki F. Kita[4], Motoi Yoshioka[5], Hiroshi Ohizumi[6], Fumio Nakahara[7], Shigeo Saino[8], Tadasu K. Yamada[9], Yuko Tajima[9], Akira Shiozaki[9], Shimpei F. Hiruta[10], Shin Nishida[11], Masao Amano[12], Yoshikazu Uni[13], Ayaka T. Matsuda[14], Takashi F. Matsuishi[14], Miho Murayama[1], Yu Sato[1] and Yoko Mitani[1]

[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *School of Environmental Science, Hokkaido University, Hakodate, Japan*
[3] *Faculty of Environmental Earth Science, Hokkaido University, Sapporo, Japan*
[4] *School of Biological Sciences, Tokai University, Sapporo, Japan*
[5] *Graduate School of Bioresources, Mie University, Tsu, Japan*
[6] *School of Marine Science and Technology, Tokai University, Shizuoka, Japan*
[7] *Faculty of Human Sciences, Tokiwa University, Mito, Japan*
[8] *Kobe Animals-and-Plants Environmental College, Kobe, Japan*
[9] *National Museum of Nature and Science, Tsukuba, Japan*
[10] *The Mt. Fuji Institute for Nature and Biology, Showa University, Fujiyoshida, Japan*
[11] *Faculty of Education, University of Miyazaki, Miyazaki, Japan*
[12] *Graduate School of Integrated Science and Technology, Nagasaki University, Nagasaki, Japan*
[13] *Faculty of Bioindustry, Tokyo University of Agriculture, Abashiri, Hokkaido, Japan*
[14] *Faculty of Fisheries Sciences, Hokkaido University, Hakodate, Japan*
[*] `suzuki.momoka.75k@st.kyoto-u.ac.jp`

There is a previous study suggested that killer whales (*Orcinus orca*) around Hokkaido have mammal-eating (“transient” ecotype) and fish-eating (“resident” and/or “offshore” ecotypes) groups, and these were revealed with cytochrome *b* and partial D-loop region in mitochondrial genomes. However, this analysis was not enough to discriminate between the “resident” and “offshore” ecotypes due to the sequence length. Moreover, the “resident” ecotype in the eastern North Pacific was separated into different conservation units based on two haplotypes in the D-loop, called “southern resident” and “northern resident”. For future conservation management, it is necessary to clarify the phylogenetic differentiations of killer whales around Hokkaido. In this study, we analyzed whole mitochondrial genomes with a total of 25 individuals sampled around Hokkaido. The maximum-likelihood tree was constructed with previously reported mitochondrial genomes of killer whales in the North Pacific, and two clades were identified, which were also related to ecotypes: “transient” and “resident” around Hokkaido and no individual of “offshore.” Although ten individuals out of 19 “transient” whales had a previously found haplotype which was frequently detected in Okhotsk Sea group, seven haplotypes were newly identified from remaining nine individuals in this study. On the other hand, all the “resident” whales of our samples shared the same haplotype, which was frequently found in Russian Far East group and assigned to “southern resident” based on the D-loop haplotype. Our results indicated that killer whale populations might have connectivity between Hokkaido area and Far East Russian area, while further investigations of genetics and ecology are necessary for understanding phylogenetic positions of new haplotypes in “transient” whales.

O-7

Effect of the genetic polymorphism of TAS2R43 and TAS2R46 on the receptor function and bitter taste perception for caffeine

Rena Numabe[1,2*], Alon Rainish[3], Masha Niv[3] and Hiroo Imai[2]
[1] *Division of Biology, Graduate School of Science, Kyoto University, Kyoto, Japan*
[2] *Center for the Evolutionary Origins of Human Behavior, Kyoto Univ., Japan*
[3] *Biochemistry and Food Science, Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University, Israel*
[*] `numabe.rena.44c@st.kyoto-u.ac.jp`

Bitter taste receptors, TAS2Rs, have genetic polymorphism some of which are suggested to be responsible for interindividual differences of human bitter taste sense. For example, TAS2Rs cluster in chromosome 12 is reported to be associate with the bitter sense to coffee and caffeine, including 3 TAS2Rs (TAS2R14, -43 and -46) respond to caffeine. Here, we investigated the effect of missense SNPs (Single Nucleotide Polymorphisms) in TAS2R43 and -46, because TAS2R14 has few missense SNPs. TAS2R43 and -46 have 2 major haplotypes due to 2 and 1 missense SNPs, respectively. We examined the effects on their function using the expressed protein in HEK293T cells. We also carried out human tasting test with volunteer subjects to analyze their threshold of bitterness perception with their genotyping data. We found the difference in the reaction to caffeine between the protein haplotypes of TAS2R43 and -46, due to the expression levels in the membrane. In both receptors, the ancestral types which mainly distribute in Africa showed higher response than those of derived types which mainly distribute in East Asia. There was a tendency that people having the ancestral types can detect caffeine bitterness at lower concentration than those having the derived types. These SNPs may contribute to the bitter sense to some foods and drinks received by the receptors.

Visual search using a touchscreen in domestic goats: a pilot study

Jie Gao[1,2*], Yumi Yamanashi[1,3] and Masayuki Tanaka[1,3]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Hakubi Center for Advanced Research, Kyoto University, Kyoto, Japan*
[3] *Center for Research and Education of Wildlife, Kyoto City Zoo, Kyoto, Japan*
[*] `gao.jie.7u@kyoto-u.ac.jp`

Land mammals are an important part during the course of evolution. Little is known about their cognition. Studying their cognition will fill this gap and will help understand the evolution of cognition from a broader perspective. In this study, we chose domestic goats and did a pilot study to see if they could complete a visual search task on shape discrimination using a touchscreen. We trained three goats in Kyoto City Zoo to use a 23.8-inch touchscreen for cognitive tasks. They were first familiarized with touching one target, a black circle, on one of the six places on the screen. Then, they were tested in an odd-item search task with the target being the black circle and distractors being black triangles. The number of distractors were from 2 to 5 in five conditions. Their performances were better than the chance level when the distractor number was bigger than 1 (for two goats) and 2 (for one goat) respectively. This suggests that they can complete the visual discrimination, especially when the distractor number is bigger. This study shows the visual discrimination ability of goats. It also provides a promising method for future cognitive testing in goats and other animals.

Description of new deep-sea species of Muusoctopus genus from Sea of Japan using integrated Taxonomic Methods

Fahima Tabassum
Department of Biological Sciences, Osaka University, Osaka Prefecture, Japan
* `U252482j@ecs.osaka-u.ac.jp`

The onset of modern molecular techniques and advanced phylogenetic methodologies coupled with a multidisciplinary perspective, revolutionized taxonomic research in the early 21st century. This holistic approach not only streamlines the description of new species but also enhance the precision and robustness as integrated taxonomy, describes a new species within the Muusoctopus genus. Previously identified by Sasaki (1929) as Polypus fujiitai, this species remained taxonomically ambiguous for an extended period. However, it has been rediscovered in the same region where it was originally documented.

Morphological analysis showed moderate size (ML:83mm) with the light brown coloration and long slender arms. The species is distinguished by its arm formula (3<4<2<1) and large hectocotylus, which deviates from the typical pattern observed in many congeners. Bio geographically analysis explain northwest Pacific distribution, with haplotype networking revealing genetic distinctiveness. Ecological analysis confirms significant negative allometric growth($p<0.05$) suggesting a vigorous ecological pattern.

Combination of the analyses offer basic insights into deep-sea octopod diversification. For advancing the understanding of cephalopod biogeography and marine biodiversity I am planning to obtain molecular data towards the same species in future.

Audience effects of female bystanders on allopreening of affiliative male−female dyads in large-billed crows (*Corvus macrorhynchos*)

Mayu Shimada[1*], Shinya Yamamoto[1,2], Ei-Ichi Izawa[3]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Institute for Advanced Study, Kyoto University, Kyoto, Japan*
[3] *Department of Psychology, Keio University, Tokyo, Japan*
[*] `s.mayu315@gmail.com`

A biological theory predicts that socially monogamous animals, such as *Corvus* spp, would show mate guarding in both sexes. In *Corvus* spp, subadults aggregate mixed-sex flocks where male−female affiliative relationships are formed as a potential partnership of pair-bonds after maturation. Thus, it is predicted that a subadult male−female dyad with affiliative relationship would show mate guarding such as increasing allopreening to strengthen their partnership and to signal to same-sex bystander rivals, although such audience effects remain untested in *Corvus* birds. We further hypothesized that their mate guarding would vary depending on the bystanders' competence as rivals. In this study, we investigated whether the presence of a bystander female with different competence affects allopreening of affiliative male−female dyad of subadult large-billed crows (*C. macrorhynchos*). Based on daily social interactions in a group-living environment, we determined affiliative male−female dyads as subject dyads, a rival female that exchanged allopreening second-frequently with the subject male, and a non-rival female that had no allopreening with the subject male. Each subject dyad was exposed to a rival female or a non-rival female as a bystander stimulus. The subject females, but not the males, demonstrated more frequent and longer allopreening to their affiliated partner in the rival condition than in the non-rival condition. These results confirm audience effects concerning mate guard in crows, and this effect varies according to the competitors' competence.

Comparison of Head Morphology in Snakes (*Ptyas*) with Different Feeding Habits

Hiroaki Yanagi[1*] and Akira Mori[1]
[1]*Graduate School of Science, Kyoto University, Kyoto, Japan*
[*]`yanagi.hiroaki.82k@st.kyoto-u.ac.jp`

Head morphology is a critical trait of animals, influencing food utilization and foraging strategy. Snakes have significant adaption in heads because they have no limbs and swallow their prey whole without chewing. Therefore, snakes are suitable for the study of the relationship between head morphology and feeding habits. In the genus *Ptyas*, species exhibit a wide range of diets, from earthworms to various vertebrates. Recent molecular phylogenetic studies have revealed that earthworm-feeding species are polyphyletic, having evolved independently across different lineages. In this study, we compared the external head morphology of three vertebrate-feeding and two earthworm-feeding *Ptyas* species using principal components analysis. The results showed that the head morphology of earthworm-feeding species is similar across different lineages and is significantly distinct from that of vertebrate feeders. Earthworm feeders exhibited narrower head width, lower head height, and longer snout. In contrast, vertebrate feeders exhibited wider and thicker head with shorter snout. In our field observations, one of the earthworm feeders, *Ptyas semicarinatus* frequently poked the head under leaf litter in search for food. The morphological traits of earthworm feeders would be advantageous for foraging in the habitat, whereas those of vertebrate feeders would increase gape size for larger prey ingestion.

Sex identification and efficient microsatellite genotyping using fecal DNA samples in endangered Bornean elephants

Honoka Tanohata[1*], Shintaro Hagiwara[2], Ikki Matsuda[3] and Miho Murayama[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto city, Kyoto, Japan*
[2] *Fukuyama Zoo, Fukuyama city,Hiroshima, Japan*
`tanohata.honoka.78w@st.kyoto-u.ac.jp`

In endangered mammals, genetic sex identification and microsatellite genotyping from fecal samples are crucial for assessing genetic diversity and improving conservation management. Feces also provide key ecological data, such as information on diet and gut microbiota, allowing for the analysis of sex- or individual-based differences when combined with genetic identification. The Bornean elephant (*Elephas maximus borneensis*), endemic to the island of Borneo, faces severe extinction threats due to habitat loss, decreasing genetic diversity, and conflicts with local communities. On the other hand, studies on genetic relationships within individuals and among wild populations remain limited. Therefore, the aim of this study is to develop methods for sex identification and efficient microsatellite genotyping from fecal DNA in Bornean elephants, applying these tourniquets to both wild and captive populations to better understand their ecology, social structure, and conservation needs. As a first step, an efficient DNA extraction and sex identification protocol was developed using fecal samples collected from a Bornean elephant housed at Fukuyama Zoo in August 2024. In this presentation, I will introduce these methods and discuss the future prospects for broader genotyping efforts.

Genomic Data Reveals the Genetic Diversity of the Red-crowned Crane – Is the Hokkaido Population Really Stable?

Hizuki Nakamura[1*],Yu Sato[1], Manabu Onuma[2] and Miho Inoue-Murayama[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Biodiversity Division, National Institute for Environmental Studies, Tsukuba, Japan*
[*] `nakamura.hizuki.73r@st.kyoto-u.ac.jp`

The Red-crowned Crane (*Grus japonensis*) is an endangered crane species that inhabits Hokkaido and eastern Eurasia, and has been classified as vulnerable (VU) by Japanese Ministry of the Environment. In Hokkaido, this bird was nearly extinct once due to a rapid population decrease in the 1800s, but it has been recovered now and the current population size is estimated to be approximately 1,800. On the other hand, serious bottleneck in the past might led severe inbreeding and loss of genetic diversity. In addition, there is also concern that the recent avian influenza pandemic could devastate the Hokkaido population of the Red-crowned Cranes, as they gather in clusters during winter, especially if disease resistance has disappeared due to the loss of genetic diversity. Hence, there is an urgent requirement to reveal the genetic diversity of the Red-crowned Cranes and to establish effective conservation strategies.

This study evaluated the genetic diversity mainly with whole genome data. To compare genetic diversity between Hokkaido and Continental populations, the origin of samples (Hokkaido or Continental) was inferred based on haplotypes of the mtDNA control region. Then genetic diversities with genome-wide heterozygosity and nucleotide diversity of samples originated from the two populations were calculated. We also evaluated inbreeding between the two populations using information from contiguous homozygous alleles in the genome (Runs of Homozygosity: ROH). For assessing genetic diversity of the endangered species, it is effective not only to compare within species, but also between closely related species. Thus, as the next step, we intend to compare the diversity using other species with different historical backgrounds: Hooded Crane (*Grus monachal*), White-naped Crane (*Antigone vipio*) and Common Crane (*Grus grus*).

Comparing Snake Images and Videos as Emotion-Inducing Stimuli for Chimpanzees

Christen Lin[1*], Sakumi Iki[2], Sanjana Kadam[2], Sarv Dashti[2], Ikuma Adachi[2], and Shinya Yamamoto[1,3]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Center for the Evolutionary Origins of Human Behavior, Kyoto University, Inuyama, Japan*
[3] *Kyoto University Institute for Advanced Study, Kyoto University, Kyoto, Japan*
[*] `linchristen@gmail.com`

Judgment bias tasks have potential to be used to determine the emotional state of chimpanzees and other primates, but the type of stimuli used to induce an affective state during such experiments must also be considered. Previously, we investigated whether the presentation of snake images could induce a negative judgment bias in chimpanzees in a touch screen discrimination task, in which chimpanzees were trained to associate different colored buttons with positive and negative outcomes. The chimpanzees were then presented snake images followed by buttons of intermediate color to measure potential changes in pessimism or optimism based on their response to these ambiguous stimuli. However, the snake images appeared to vary in effectiveness between the two chimpanzee participants, and so the study was replicated with snake videos to investigate whether a relatively stronger negative stimulus would induce a stronger negative judgment bias for the chimpanzees under the same touch screen task. While it is possible that snake videos caused a shift in bias that was more consistent between the two chimpanzees this time, the possibility of a potential learning effect or a reduced effectiveness due to repeated exposure to the snake stimuli must also be considered. Regardless, comparing various types of stimuli for usage in chimpanzee judgment bias tasks helps pave the way for developing the methodologies of future experiments using this paradigm for investigating emotional contagion and other related phenomena.

The origin and evolutionary history of the endangered Golden langurs (*Trachypithecus geei* Khajuria, 1956)

Ashika Dhimal[1*], and Praveen Karanth[1,2]
[1] *Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India*
[*] `ashikadhimal@iisc.ac.in`

The Golden langur is one of the most range restricted colobine monkeys, confined to the region between Sunkosh and Manas rivers in Bhutan and adjoining Assam in India. It is closely related to the widely distributed Capped langurs found in Eastern Bhutan, Northeast India, Northern Bangladesh, and Northwestern Myanmar. Golden langur has been divided into two subspecies whereas Capped langurs into four. However, the subspecies status of Golden langur is still being debated. Previous studies have hypothesized that an isolated population of Capped langurs might have speciated into Golden langurs due to geographical barriers like rivers and mountains (Wangchuk, 2005; Ram et al., 2016). This would represent a plausible case of peripatric speciation; wherein peripheral isolates of widely distributed species evolve into a distinct lineage. Here, we aim to investigate the subspecies status of Golden langur by testing their genetic integrity and examine the phylogenetic position of Golden langur vis-à-vis Capped langur. We sequenced and analysed around 518 bp of mitochondrial DNA, hypervariable region-I (HVRI) from 35 faecal samples of the wild langurs collected across Bhutan and combined with the sequences generated by Ram et al. (2016). In the maximum likelihood tree, the golden langurs from the southern fragments in Assam formed a separate cluster with high bootstrap support, consisting of few Golden langur individuals from Bhutan, however, Golden langurs from Manas Biosphere clustered together with Golden langurs from Bhutan, which cannot rule out some gene flow between these regions. The same trend was observed in median-joining network. Further, the maximum likelihood tree which includes both Golden and Capped langurs shows they are not reciprocally monophyletic. In the median joining network, the Capped langurs are interspersed with Golden langurs from Bhutan. However, more works are being carried out to include samples from both Bhutan and India to cover wider distribution range and genotype microsatellite towards understanding the convoluted evolutionary history of Golden langurs.

The challenge of establishing assisted reproductive technology for wild cats' conservation
-To produce mature oocytes that can be used for in vitro fertility-

Chinatsu Nishimoto[1*], Mayako Fujihara[1], Miho Murayama[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
nishimoto.chinatsu.56x@st.kyoto-u.ac.jp

Many wild felids are threatened as endangered and their captive breeding needs the help of assisted reproductive technology (ART), including oocytes in vitro maturation (IVM). IVM has the advantage of utilizing oocytes from ovaries obtained after ovariohysterectomy or death for future reproduction as genetic resources. Our laboratory has also been gathering and preserving oocytes from endangered feline species (Panthera tigris, Puma concolor, etc.) that have died in zoos or the wild for future conservation usage since 2016. However, IVM in feline animals has many difficulties. Using domestic cats (Felis catus) as a model of wild feline species, we aimed to develop the optimal culture condition for oocytes IVM. Oocytes were collected from domestic cat ovaries one day after ovariectomy to imitate the ovarian condition of individuals who had died in the wild. We investigated the effects of the activators of the sirtuin gene, which helps maintain cell function, including oxidative stress—nicotinamide mononucleotide (NMN) and niacin (NA) on oocyte maturation. Oocytes were cultured with different concentrations of NMN and NA. Their effects on oocyte maturation were evaluated by tubulin staining. Also, oxidative stress was measured by the fluorescence intensity of reactive oxygen species (ROS) and glutathione (GSH). Across all experiments, a combination of NA and NMN showed the highest maturation rate. The ROS level was suppressed strongest in a medium containing a combination of NA and NMN. The GSH level was the highest in a medium containing 400µM NA. This study improved oocyte IVM medium by supplementation NA and NMN in felines as a potentially applicable condition for wild felids.

Population Structure, Genetic Diversity, and Past Demography of White-tailed Eagles in Hokkaido Using Whole-genome Approach and Future Plans of the Study

Fadel Abdurrahman Azhari*[1,2], Yu Sato[2], Keisuke Saito[3], Yukiko Watanabe[3], Manabu Onuma[4], Miho Murayama[2]
[1] *Graduate School of Science, Kyoto University, Kyoto, Japan*
[2] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[3] *Institute for Raptor Biomedicine Japan, Kushiro, Japan*
[4] *National Institute for Environmental Studies, Tsukuba, Japan*
* `fadelf2@gmail.com`

The large sea eagle, White-tailed eagle (*Haliaeetus albicilla*), has a broad distribution range extending from Greenland to Hokkaido in Japan. Despite being listed as endangered species (VU) by the Japanese Ministry of the Environment, little is known about the genome information of White-tailed eagles (WTE) in Hokkaido to ensure their long-term sustainability. To reveal genetic diversity, population structure and past population demography of WTE in Hokkaido, whole-genome analyses was conducted, and results were compared with those in Europe. Past population demography was inferred using a pairwise sequential Markovian coalescent (PSMC) model, suggesting different patterns of demography of effective population size (*Ne*) during the last glacial period. Our results showed significant genetic differentiation between Japanese and European WTE. Importantly, Hokkaido population was also suggested to be divided into three possible clusters of genetic differentiation. Our analyses also indicated that WTE in Hokkaido has higher genetic diversity and lower inbreeding levels than the European counterparts. Based on these outcomes, we are planning to analyze more WTE sampled in Hokkaido to clarify the population structure within this locality, and to conduct inference of more recent population demography. These information of the series of genomic analysis might be applied to effective conservation managements of WTE in Hokkaido and to understand the global genetic diversities which is essential to conduct worldwide conservation program of the species. The specimen was provided by the MoE and this research was performed by the Environment Research and Technology Development Fund (JPMEERF20244M01) of the Environmental Restoration and Conservation Agency provided by MoE.

Social ageing in male Indo-Pacific bottlenose dolphins: exploring the drivers of shifting sociality

Hibiki Nishitani[1*], Koki Tsujii[2] and Tadamichi Morisaka[1]
[1] *Graduate School of Bioresources, Mie University, Tsu, Mie, Japan*
[2] *Ogasawara Whale Watching Association, Ogasawara-mura, Tokyo, Japan*
[*] `hbki352w@gmail.com`

Most primates exhibit age-related shifts in sociality (social ageing). Some species have smaller social networks in older age, which has been explained by that they become more selective about their partners as they age (selectivity hypothesis). Declining sociality with age has also been explained by changing core habitat (spatial segregation hypothesis) and imposing physical disadvantage (physical restriction hypothesis) along with ageing. In this study, we described patterns of social ageing and explored its drivers among male Indo-Pacific bottlenose dolphins, which differ from primates in ecology and phylogeny. We recorded the number of partners among males in four age classes (adolescence, subadult, adult and senior) during 2020-2023 in Chichijima Islands, Ogasawara, Japan. We found that only adults had negative effects on the number of partners. Contrary to the expectation from the selectivity hypothesis, any age class had no effect on the strength of the dyadic relationship with partners. Furthermore, any age class had no effect on the home-range size, and home- ranges overlapped among all age classes than expected by chance. This is the first report of social ageing in males of this species, with only adults having smaller social networks. Our results suggest that these patterns are explained by neither the selectivity, spatial segregation, nor physical restriction hypothesis.

Long-term population monitoring of sympatric primates in different forest types in the Lower Kinabatangan, Sabah, Borneo, Malaysia

Muhammad Nur Fitri-Suhaimi[1*], Augustine Tuuga[2], Joseph Tangah[3] and Ikki Matsuda[1]
[1] *Wildlife Research Center, Kyoto University, Japan*
[2] *Sabah Wildlife Department, Kota Kinabalu, Sabah, Malaysia*
[3] *Sabah Forestry Department, Forest Research Center, Sandakan, Sabah, Malaysia*
[*]`fitrisuhaimi2@gmail.com`

Monitoring the long-term population dynamics of animals threatened with extinction, particularly long-lived mammals with slow life cycles such as primates, is crucial for their conservation. The ongoing habitat loss threatens sympatric primates, including proboscis monkeys (*Nasalis larvatus*), long-tailed macaques (*Macaca fascicularis*), and pig-tailed macaques (*Macaca nemestrina*), in the Lower Kinabatangan region, in Sabah, Malaysian Borneo. In this study, therefore, the long-term population dynamics of these primate species were monitored over 20 years in different forest types in this region. We carried out boat-based primate population count surveys in the late afternoon in the different forest types, i.e., riverine (1,160 surveys in total) and mangrove (295 surveys) forests. Although in-depth statistical analysis is required, the population of the primate species over the last 20 years appeared to show a trend of consistency for proboscis monkeys in both riverine and mangrove forests. Long-tailed macaques also showed consistency in riverine forests, but their populations increased in mangrove forests. Pig-tailed macaques were not found in mangrove forests, but their populations remained consistent in riverine forests. We discuss these results on the basis of differences in plant diversity and abundance in different forest types, as well as the degree of deforestation. The results would provide valuable insights into the long-term viability of these primate populations and contribute to the development of more effective conservation strategies for these habitats.

Assessing the genetic diversity and viability of semi-wild populations of orangutans

Tomoyuki Tajima[1*], Eiji Inoue[2], Vijay Kumar[3], Yu Sato[4] and Miho Inoue-Murayama[4]
*[1] Center for the Study of CO*Design, Osaka University, Toyonaka, Japan*
[2] Faculty of Science, Toho University, Chiba, Japan
[3] Biotechnology Research Institute, Universiti Malaysia Sabah, Sabah, Malaysia
[4] Wildlife Research Center, Kyoto University, Kyoto, Japan
[*] `tajima@cscd.osaka-u.ac.jp`

Orangutans (*Pongo* spp.) are endangered species, and rehabilitation programs have been conducted in many areas of Borneo and Sumatra. However, there is a general concern about the decline in genetic diversity in semi-wild populations that repeatedly breed in small numbers and with limited genetic exchange with external populations. In this study of Bornean orangutans in Sabah, Malaysia, non-invasive samples were collected from 28 individuals from a semi-wild population (Sepilok Orangutan Rehabilitation Centre) and 31 from a wild population (Danum Valley Forest Reserve). Eleven microsatellite loci were used to evaluate the genetic characteristics of the two populations. Contrary to expectations, the number of alleles and heterozygosity were higher in the semi-wild population than in the wild population, indicating no trend toward lower genetic diversity in the semi-wild population. One possible reason is that the semi-wild population includes individuals rescued from multiple remote areas. We then simulated sustainability with PVA (population viability analysis) to predict population size fluctuations over 1,000 years after accounting for differences in demographic factors, carrying capacity, and reproductive parameters of the two populations. The results indicated that the wild population had a relatively low risk of extinction. In contrast, the semi-wild population was predicted to be likely to become extinct after 200 years, depending on conditions, suggesting that systematic management is necessary to maintain the population over the long term.

The Secret of Cat Sociality: Comparison of *AVPR1a* Genotypes Among Felid Species

Yume Okamoto[1*], Minori Arahori[1,2], Madoka Hattori[3], Miho Inoue-Murayama[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto City, Kyoto prefecture, Japan*
[2] *Anicom Specialty Medical Institute Inc.,Yokohama City, Kanagawa prefecture, Japan*
[3]*Kyoto City University of Arts, Kyoto City, Kyoto prefecture, Japan*
[*] `okamoto.yume.88h@st.kyoto-u.ac.jp`

Cats (*Felis catus*) are domesticated from the ancestor African wild cat (*Felis lybica*). While most members of the family Felidae including African wild cats are solitary, cats are capable of living in groups and displaying social behaviors. However, the background of cat sociability is still not known although behaviors are reported to be associated with genetic backgrounds in addition to environmental effects. The objective of this study is to investigate cat sociability from genetics by comparing the candidate gene arginine vasopressin receptor 1A (*AVPR1A*) genotype within cats and among Felid species. A total of 156 neutered/spayed mixed breeds (91 males, 65 females) were used for the analysis. Behavioral traits were assessed using the Feline Behavioral Assessment and Research Questionnaire (Fe-BARQ) (Duffy et al., 2017). Genomic DNA was extracted from buccal swabs, and the *AVPR1A* exon 1 region was genotyped. The association was analyzed using a generalized linear model (GLM), with each of the 23 behavioral sections used treated as response variables. The explanatory variables were genotype, sex, and age. Homologous regions of Felidae were identified using a Web BLAST search. A total of 10 single nucleotide polymorphisms (SNPs) were found in cats, and several showed relations to behavioral traits. Also, all SNPs were cat-specific.

Understanding Bat Guilds: Development, Uses, and Research Implications

Scott H. Jenkins[1,2*], Hideyuki Doi[1], Danilo Russo[3] and Christian E. Vincenot[2,4]
[1] *Bioresource Laboratory, Graduate School of Informatics, Kyoto University, Kyoto, Kyoto, Japan*
[2] *Island Bat Research Group (IBRG), Kyoto, Kyoto, Japan*
[3] *Laboratory of Animal Ecology and Evolution (AnEcoEvo), Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Napoli, Italy*
[4] *Faculty of Science, Technology and Medicine, University of Luxembourg, Esch-sur-Alzette, Luxembourg*
[*] `shjenkins94@gmail.com`

Guilds are groups of species that exploit the same resources in a similar manner. They provide a useful alternative to systems based on taxonomic relationships. Bat ecologists often use guilds to study resource partitioning among coexisting bat species, identify distantly related species that have undergone adaptive convergence, recognize species that have diverged from their closest relatives to exploit novel resources and understand variations in species' responses to ecological disturbances or conservation efforts. Most importantly, guilds can be used to infer what resources a species might exploit, even if data on that species is limited.

To better understand how guilds are used in bat research, we conducted a semi-systematic literature review using PRISMA protocols. The result was a collection of 528 bat studies using guilds, including several key seminal papers. We also analyzed the studies' citations to identify seminal bat guild papers.

Our analysis identified five major guilds used in bat research. Most studies used guilds based on what bats eat (trophic guilds,) where they forage (microhabitat guilds,) and how they forage (foraging mode or echolocation guilds). This review summarizes the underlying principles and methodologies for each guild, identifies gaps in geographical and taxonomic coverage, discusses current applications for bat guild research, and makes recommendations for future bat guild studies.

Grooming Behavior and Its Impact on Body Temperature in Japanese Macaques

Shimei Shirasawa[1*], Shinya Yamamoto[1]
[1] *WRC, Kyoto University, Kyoto, Japan*
[*] `Shirasawa.shimei.75x@st.kyoto-u.ac.jp`

This study examines the relationship between grooming behavior and body temperature changes in monkeys, focusing on individual relationships and social dynamics. Grooming is a crucial social behavior in primates, often linked to social bonds and emotional states. Using infrared thermal cameras, we recorded body temperatures before, during, and after grooming sessions. Results indicate that grooming leads to an increase in body temperature, particularly in recipients (groomy) compared to providers (groomer). A chi-square test showed that certain individual pairs engaged in grooming more frequently than expected by chance, suggesting a preference in partner selection. This preference may be indicative of closer social bonds or kinship. Generalized Linear Mixed Models (GLMM) revealed that both kinship and grooming frequency significantly influenced the magnitude of temperature change, with more frequent grooming pairs showing a greater increase in body temperature. These findings imply that grooming not only has a social bonding function but also affects physiological states, potentially reflecting positive emotional arousal. This research enhances our understanding of the physiological underpinnings of social behavior in primates and highlights the complex interplay between social interactions and physiological responses.

Genome sequence analysis of *Plasmodium cynomolgi* using malaria-infected *Macaca mullata*

Divya Shaji[1*], Yukako Katsura[1], Takeshi Annoura[2], Tamasa Araki[2,] Kentaro Itokawa[3],
Satoru Kawai[4], Okamoto Munehiro[1]

[1]*Genome Evolution section, EHUB, Kyoto University, Inuyama, Aichi, Japan*
[2] *Department of Parasitology, National Institute of Infectious Diseases, Toyama, Tokyo, Japan*
[3]*Department of Medical Entomology, National Institute of Infectious Diseases, Toyama, Tokyo, Japan*
[4]*Department of Tropical Medicine and Parasitology, Dokkyo Medical University, Mibu, Tochigi, Japan*
`*shaji.divya.4m@kyoto-u.ac.jp`

To investigate the infection mechanism of the malaria parasite in *M. mullata*, we performed the nanopore sequencing of *P. cynomolgi* by PromethION. To remove the white blood cells from the host, the blood of malaria-infected *M. mullata* was filtered by PLASMODIPUR, and for nanopore sequencing, DNA was extracted from the filtered blood by the Monarch HMW DNA Extraction Kit. After sequencing, 36.38% of the nanopore reads were mapped to the reference genome of *M. mullata* using the minimap2 program. To remove the genome of *M. mullata* from the nanopore reads, the unmapped reads that indicate the genome of *P. cynomolgi* were mapped to the reference genome of *P. cynomolgi.* The mapping rate was 85.87%. To identify the content of the unmapped reads in both genomes, we searched for the similarities with bacteria, plasmodium, and primate species in the NCBI database using BLAST analysis. The percentage of similarity in the databases of bacteria, plasmodium, and primate was 97.9%, 0.6%, and 1.5%, respectively. The results of this analysis showed that most of the unmapped reads in both genomes had similarities with 81 distinct bacterial species due to sample contamination or infection. To analyze the *P. cynomolgi* genome, we constructed a denovo assembled genome using Flye assembler and compared it to the published genomes of malaria.

Exploring the Role of Oxytocin at the Early Stages of Social Relationship Building

China Kobayashi[1], Plotine Jardat[2], Fabrice Reigner[3], Monamie Ringhofer[4], Léa Lansade[2] & Shinya Yamamoto[1,5]

1. Wildlife Research Center, Kyoto University, Kyoto, Japan
2. CNRS, IFCE, INRAE, Université de Tours, PRC, Nouzilly 37380, France
3. UEPAO, INRAE, Nouzilly 37380, France
4. Department of Animal Sciences, Teikyo University of Science, Japan
5. Institute for Advanced Study, Kyoto University, Kyoto, Japan
* `2011.1b16@gmail.com`

Oxytocin is a neuropeptide hormone conserved across mammals, implicated in social behaviors. Recent studies have suggested that it may promote not only prosociality but also promote hostile attitudes towards the outgroup. Although this context-dependent effect can be crucial for social group formation, it has mostly been studied in a limited range of species. This study investigated the effects of exogenous oxytocin on dyadic interactions in horses, a highly social species known to form long-term bonds. We randomly paired individuals from different groups and intranasally administered oxytocin or saline (control). Social interactions were observed in a stable setting, with food competition introduced at the early stage of observations to stimulate social interactions. Prior to these experiments, we conducted pre-experimental observations to measure proximity as a baseline for initial social relationships. Testing 20 pairs, we found that the effects of oxytocin varied according to proximity in pre-experimental observations. Oxytocin more effectively reduced aggression in pairs with greater initial proximity while promoting exploratory behavior in pairs with lower proximity. The results suggest that oxytocin plays a role in modulating social interactions, even between newly paired individuals, which could be key to elucidating the hormonal basis of the early stages of social relationship building.

P-17

A hypothesis of cognitive constraints to explain the rarity of mutual grooming

Ayumi Ogawa[1*], Tamao Maeda[2], Shinya Yamamoto[1,3]
[1]*Wildlife Research Center, Kyoto University*
[2]*Research Center for Integrative Evolutionary Science, The Graduate University for Advanced Studies(SOKENDAI)*
[3]*Institute for Advanced Study, Kyoto University*
[*] `ogawa.ayumi.35x@st.kyoto-u.ac.jp`

Many social animals groom each other (i.e., allogrooming). Allogrooming is known not only as a hygienic role but also as a social interaction to maintain social relationships within a group. Unidirectional grooming, in which the roles of groomer and groomee rotate within a single session, is a common form among many species. In contrast, mutual grooming is very rare in which participants groom each other simultaneously. Mutual grooming, as observed in chimpanzees and ring-tailed lemurs, has been shown to have specific functional significance, such as enhancing social bonds. Moreover, mutual grooming is an efficient form of grooming in which both parties can benefit simultaneously. Nevertheless, the question remains as to why mutual grooming is so rare throughout animal species. To address this question, we hypothesize that the complexity of the cognitive mechanisms involved in mutual grooming may affect the rarity of mutual grooming. In this study, we focused on mutual grooming in horses. We examined the presence of communicative signals for sharing intentions and coordinating behaviors among participants at the onset of grooming and the influence of social relationships between partners on communication.

Species distribution model for Tsushima leopard cat (*Prionailurus bengalensis euptilurus*)

Marie Seki[1*], Takashi Shibahara[2], Kodzue Kinoshita[3] and Satoshi Hirata[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Tsushima Ranger Office, Ministry of the Environment, Nagasaki, Japan*
[3] *Graduate School of Asian and African Area Studies, Kyoto University, Kyoto, Japan*
`* seki.marie.74s@st.kyoto-u.ac.jp`

The Tsushima leopard cat is an endangered species that inhabits only Tsushima Island. Due to environmental degradation and an increase in road-kill incidents, the current population is estimated to be fewer than 100 individuals. To support proper planning processes for conservation, we used species habitat suitability models, such as the MaxEnt model, to estimate the current habitat suitability on Tsushima Island.

We collected 365 occurrence data points, including locations of road-kill, scat, and incidental captures, and utilized 26 environmental variables in the analysis. Our results showed that the accuracy of the MaxEnt model was good (AUC = 0.800). According to the results of the jackknife test, the most important variables affecting the habitat suitability of the Tsushima leopard cat were the mean diurnal range, distance from rice fields, precipitation of the driest month, and annual precipitation, with contribution rates of 30.3%, 15.1%, 8.6%, and 8.5%, respectively.

Building on this understanding, future research will aim to investigate the underlying factors contributing to the variation in the quantity of Tsushima leopard cat scats collected across different sampling routes. This study will provide valuable insights into the ecological and environmental determinants influencing scat availability, which may be critical for improving conservation strategies and understanding the habitat use patterns of this endangered subspecies.

Musicality in chimpanzees and bonobos

Liu Liu[1*], Yamamoto Shinya[1,2] and James Brooks[3]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Institute for Advanced Study, Kyoto University, Kyoto, Japan*
[3] *Department of Cognitive Ethology, German Primate Center, Göttingen, Germany.*
[*] `fibbin4fibbin@gmail.com`

The evolution of human musicality has garnered significant interdisciplinary interest, yet research on its potential roots in our closest relatives—chimpanzees (*Pan troglodytes*) and bonobos (*P. paniscus*)—remains limited. Both species exhibit collective acoustic behaviors, or joint sound production, across a variety of social contexts, but there has been limited empirical research exploring the relevance of these behaviors to the evolution of human musicality. To address this gap, our study employs a multi-layered experimental design that introduces structured acoustic stimuli (e.g., tempo, pitch, rhythm, and harmony) to assess group vocalization and percussive behaviour dynamics in both species. By leveraging previous pilot experiments conducted with tempo as stage one, we propose comparative studies on bonobos to systematically explore differences and similarities in collective acoustic behaviors between the two species. These experiments will address key gaps in understanding the evolutionary origins of musicality, with the potential to refine existing theories and provide new insights into the conserved precursors of human musicality in great apes. Our findings may ultimately illuminate the evolutionary pathways that have shaped the unique musical capacities of humans.

Genetic diversity and estimated geographical origin of captive critically endangered black rhinoceros in Japan: Implications for future conservation and breeding

Mohamed M.S Rijja[1,2,3*], Yu Sato[3], Sherif I. Ramadan[4] & Miho Inoue-Murayama[3]
[1] *Graduate School of Science, Kyoto University, Japan*
[2] *Wildlife DNA Forensic Laboratory, Government Chemist Laboratory Authority, Tanzania*
[3] *Wildlife Research Center, Kyoto University, Japan*
[4] *Faculty of Veterinary Medicine, Benha University, Egypt*
[*] `mohamedrijja@gmail.com`

Black rhinoceros are critically endangered in the wild due to illegal horn poaching and habitat loss. Captive breeding programs have become crucial as insurance for endangered wild populations. Japanese captive population contains 21 black rhinoceros, all expected to contribute to global conservation efforts. This study included nearly all available individuals in Japan to evaluate their genetic diversity and geographical origin. DNA samples of 21 individuals were extracted from blood, feces, and tissue provided from 10 Japanese zoos. We analyzed haplotypes of the mtDNA D-loop (477bp) and the diversity of 11 microsatellite (STR) loci and compared with African wild populations. Japanese captive population slightly lost genetic diversity in mtDNA D-loop while STR markers kept similar diversity as the African wild population. Among four haplotypes found, three of these matched sequences from the Eastern Africa haplogroup, while one haplotype corresponded to the Southern Africa haplogroup. Based on mtDNA and STR analysis, it was suggested that the Japanese population likely originates from Kenya, Tanzania, and Democratic Republic of Congo. In conclusion, the genetic diversity of black rhinoceros in Japan is considered satisfactory, with the potential to further enhance genetic variation by breeding combination without needing external supplementation. These results highlight the potential of the Japanese population as a source for translocation or reintroduction candidates to other breeding programs with critically low genetic diversity.

Courage in the Dark: Exploring Personality Traits in Rehabilitating Javan Slow Lorises

Langgeng A[1], Prameswari W[2], Priambada NP[2], Rianti P[3,4], Sigaud M[5], MacIntosh AJJ[1,6].
1Wildlife Research Center, Kyoto University, Inuyama-Kyoto, Japan
2Yayasan Inisiasi Alam Rehabilitasi Indonesia, Bogor, Indonesia
3Department of Biology, Faculty of Mathematics and Science, IPB University, Bogor, Indonesia
4Primate Research Center, IPB University, Bogor, Indonesia
5Muséum national d'Histoire naturelle, Paris, France
6The Wilder Institute, Calgary Zoo, Calgary, Canada *
`abdullahlanggeng@gmail.com`

Boldness, a personality trait linked to exploration and risk-taking, plays a crucial role in individual fitness and has been increasingly associated with the success of animal translocation programs. However, studies on boldness in strepsirrhines, particularly Javan slow lorises, remain limited. This study examines boldness in rehabilitating Javan slow lorises to later correlate it with translocation success. We assessed ten Javan slow lorises (six females, four males) at the YIARI rehabilitation center in Bogor, Indonesia, under varying housing conditions (enclosure size and conspecific presence). Each individual was exposed to novel objects (e.g., snake models, enrichments) for 15 minutes, and behavior was recorded to compute a boldness index. Closest approach distance was also measured. Data were collected from May to September 2024, and generalized linear mixed models were used to analyze the effects of sex, object type, and housing conditions on boldness. Across 61 experiments, males were significantly less bold than females ($p = 0.036$). Object type influenced boldness, with greater avoidance of predator-related cues. Enclosure size negatively impacted boldness ($p = 0.012$), while conspecific presence and rehabilitation duration had no effect. Bolder individuals approached objects more closely ($\tau = -0.58$, $p = 5.59e-10$). This study marks a first step toward incorporating personality traits into slow loris translocation research.

Keywords: Javan slow loris, strepsirrhine, ex-situ rehabilitation center, novel object test, personality trait

Stability in Social Bonds of Mothers and the Offspring's Sociality in Free-roaming Horse Groups

Yeongju Lee[1*], Satoshi Hirata[1]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[*] `yjroah@gmail.com`

Having an extended maternal care period due to lactation, mothers of group-living mammals have influences on their offspring's various social traits as the first social partner and social role model for their offspring.

Female horses in a polygynous group are known to have long-term social bonds with other females, which can provide their foals abundant opportunities to interact with others and form social relationships. Previous studies have reported that foals preferentially associate with another foal whose mother is the most preferred social partner of their mothers. However, there has been little study on how mothers affect the way foals build social relationships in natural social settings with less human intervention such as forced weaning and anthropogenic membership selection. Given that establishing and maintaining social bonds is known to lead to fitness benefits for horses, the stability in mothers' social relationships could be one of the important aspects of the social environment for their foals to develop sociality.

In the free-roaming Misaki horse groups with foals and yearlings in two distinct areas, the spatial locations of individuals were recorded over two breeding seasons using a drone. By assessing the stability of social associations and social tendencies along with social network analysis, the links between the mother's social life and the offspring's sociability were examined.

Tracking gaze-following behavior in Large-billed crows (*Corvus macrorhynchos*) using a motion capture system

Akihiro Itahara[1*], Fumihiro Kano[2,3]
[1] *Wildlife Research Center, Kyoto University, Kyoto, Japan*
[2] *Center for the Advanced Study of Collective Behavior, University of Konstanz, Konstanz, Germany*
[3] *Max-Planck Institute of Animal Behavior, Radolfzell, Germany*
* `itahara.akihiro.34n@st.kyoto-u.ac.jp`

Gaze-following is a behavior in which one looks at the same location as another. This behavior has been extensively studied across various species and is known to reflect basic socio-cognitive skills. In corvids, it has been reported that they follow the gaze movements of both human experimenters and conspecifics, even when the target is behind a barrier. However, it remains unclear exactly how they orient and follow the gaze of others. This is because, unlike primates, the visual orientation of birds is not straightforward due to their use of different regions of the visual fields, and tracking the visual fields has been technically challenging. Leveraging our motion-capture system, this study examined the head movements of large-billed crows in a dyadic gaze-following experiment. Two crows were released into a motion-capture room, with only one crow presented with a visual target while the other observed the demonstrator. The observer crows did follow conspecific gaze. We further examined how accurately and under what circumstances the observer crow reacted to the demonstrator crow's gaze.

The 19th International Symposium on Primatology and Wildlife Science was organized by:

Team Leader

Alisa Tobe

Sub-Leader

Akihiro Itahara Momoka Suzuki

Treasurer

Chinatsu Nishimoto Marie Seki

Symposium Program

Ayumi Ogawa China Kobayashi
Kana Arai Yume Okamoto

Panel Discussion Program

Heping Li Honoka Tanohata Kana Arai

Poster & Website Design

Fitri Suhaimi Marie Seki
Mayu Shimada Kanako Hirata

Onsite Logistics

Chika Zemmoto Christen Lin
Fadel Azhari Liu Liu Mohamed Saidi

PWS Administrative Officer

Yoko Maekawa

PWS Coordinator

Ikki Matsuda

The 19th INTERNATIONAL SYMPOSIUM on Primatology and Wildlife Science

"Genetics" "Ecology" "Behavior" "Conservation" "Cognition" "Physiology"

2024

OCTOBER 30TH – 31ST

9.00 AM – 5.00 PM

LOCATION: SCIENCE SEMINAR HOUSE, NORTH CAMPUS, KYOTO UNIVERSITY

For More Information, Visit Our Homepage

REGISTRATION

ACCESS

KEYNOTE SPEAKERS:

DR. NADINE RUPPERT
ON ECOLOGY
UNIVERSIITI SAINS MALAYSIA

DR. STEVE PORTUGAL
ON ECOLOGY/PHYSIOLOGY
UNIVERSITY OF OXFORD

DR. CHRISTOPHER KRUPENYE
ON COGNITION
JOHNS HOPKINS UNIVERSITY

DR. SAEKO TERADA
ON ECOLOGY
OSAKA METROPOLITAN UNIVERSITY

DR. KATSUFUMI SATO
ON ECOLOGY/PHYSIOLOGY
UNIVERSITY OF TOKYO

DR. TATSURO KAWAZOE
ON HUMAN-WILDLIFE CONFLICT MANAGEMENT
RESEARCH INSTITUTE FOR SATOMON