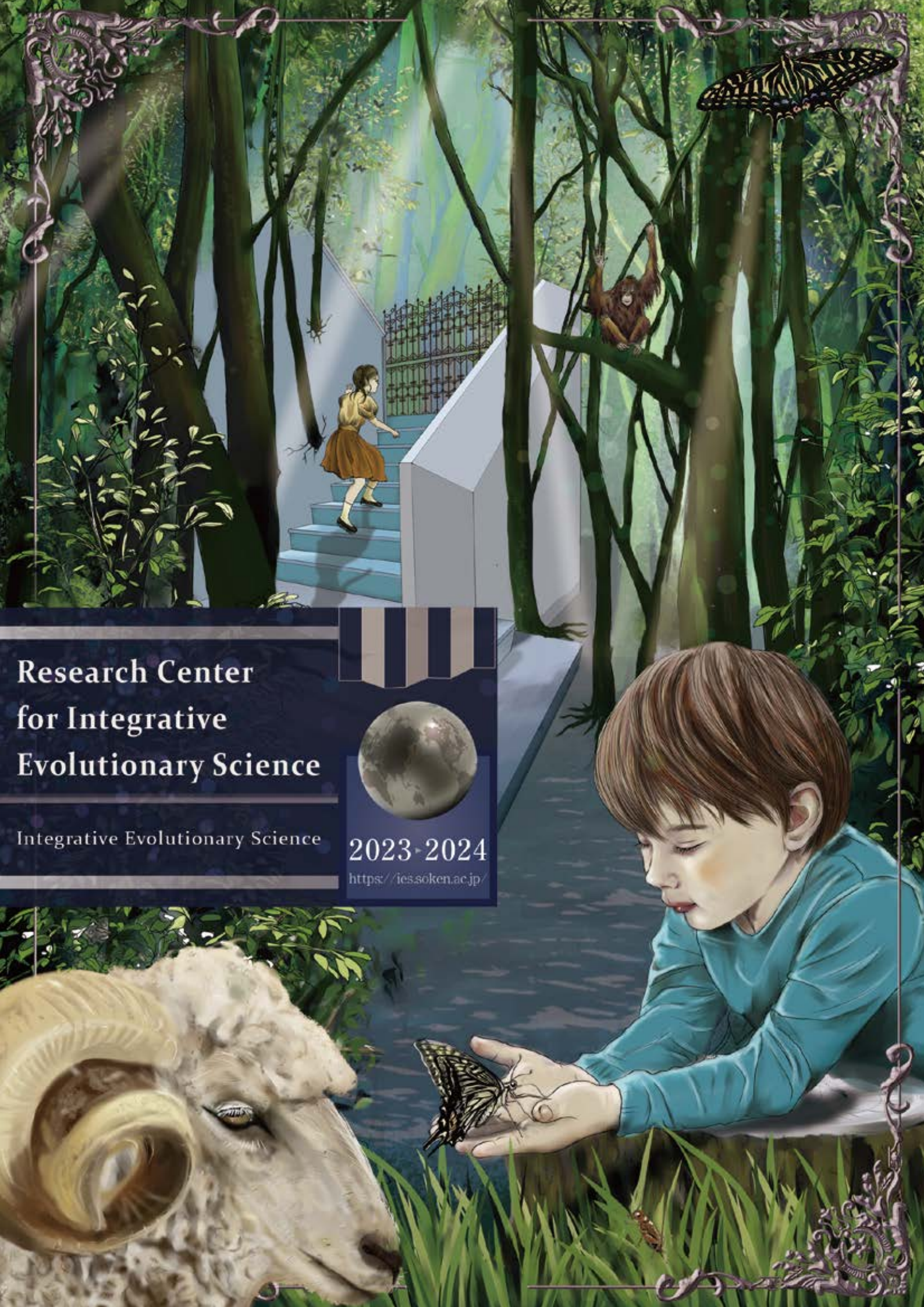

Research Center for Integrative Evolutionary Science

Integrative Evolutionary Science

2023-2024

https://ies.soken.ac.jp/

Research Center for Integrative Evolutionary Science
Integrative Evolutionary Science 2023

Contents

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https://www.soken.ac.jp/en/

SOKENDAI

Research Center for Integrative Evolutionary Science

The only research base in Japan for “evolution”

Message from Director

In April 2022, the Research Center for Integrative Evolutionary Science (RCIES) was established, serving as the sole domestic research hub centered around "evolution." In RCIES' precursor, we have specialized research on evolution of organisms. The new center seeks to expand this scope more broadly to define “integrative evolutionary science” . Beyond biological realms, it embraces the study of the evolution of all living organisms, including ourselves, and their surrounding environments, societies, technologies, and cultures.

At present, the environment surrounding us is evolving at an extraordinary pace, with the evolution of AI being particularly remarkable, surpassing our imaginations. My personal realization of this occurred in 2016 when I encountered the research paper on AlphaGo published in Nature. The proclamation that "AI had defeated the world champion of Go!" shook the community. While computer programs had already conquered games like chess and shogi, Go was considered beyond the reach of computers for this century due to its vast 19x19 board and the challenge of evaluating the game's unique "atmospheric moves." Consequently, the reception from professional Go players in Japan, China, and Korea at the time was skeptical, especially when the “world champion” defeated by AlphaGo was deemed vastly inferior to the real professional Go players in Asia. However, within a few weeks, AlphaGo dramatically evolved and began defeating top professionals. Now, it has become commonplace for professionals to learn from AI. From this close-to-home event, I, as an evolutionary scholar, learned profound lessons. Go boasts a history spanning a millennium, with its predecessors conducting relentless research to find optimal moves, culminating in established patterns called "joseki." Learning Go starts with studying these joseki, yet AI confidently plays moves deemed "bad moves" in the established literature. In essence, what we believed to be optimal was actually suboptimal, and the true optimality lay in places we once considered flawed. Even in the context of simple and straightforward rules, such as Go, under conditions without any environmental changes, optimization through evolution led to such discoveries. This insight reveals the rather arbitrary nature of evolution. The complexity of the natural world far exceeds that of the Go board, and evolution's processes are, in a sense, left to chance. It is not hard to imagine that optimization through evolution in such circumstances is much more hit-or-miss than we assume. We must approach any discourse on our understanding of evolution with utmost caution.

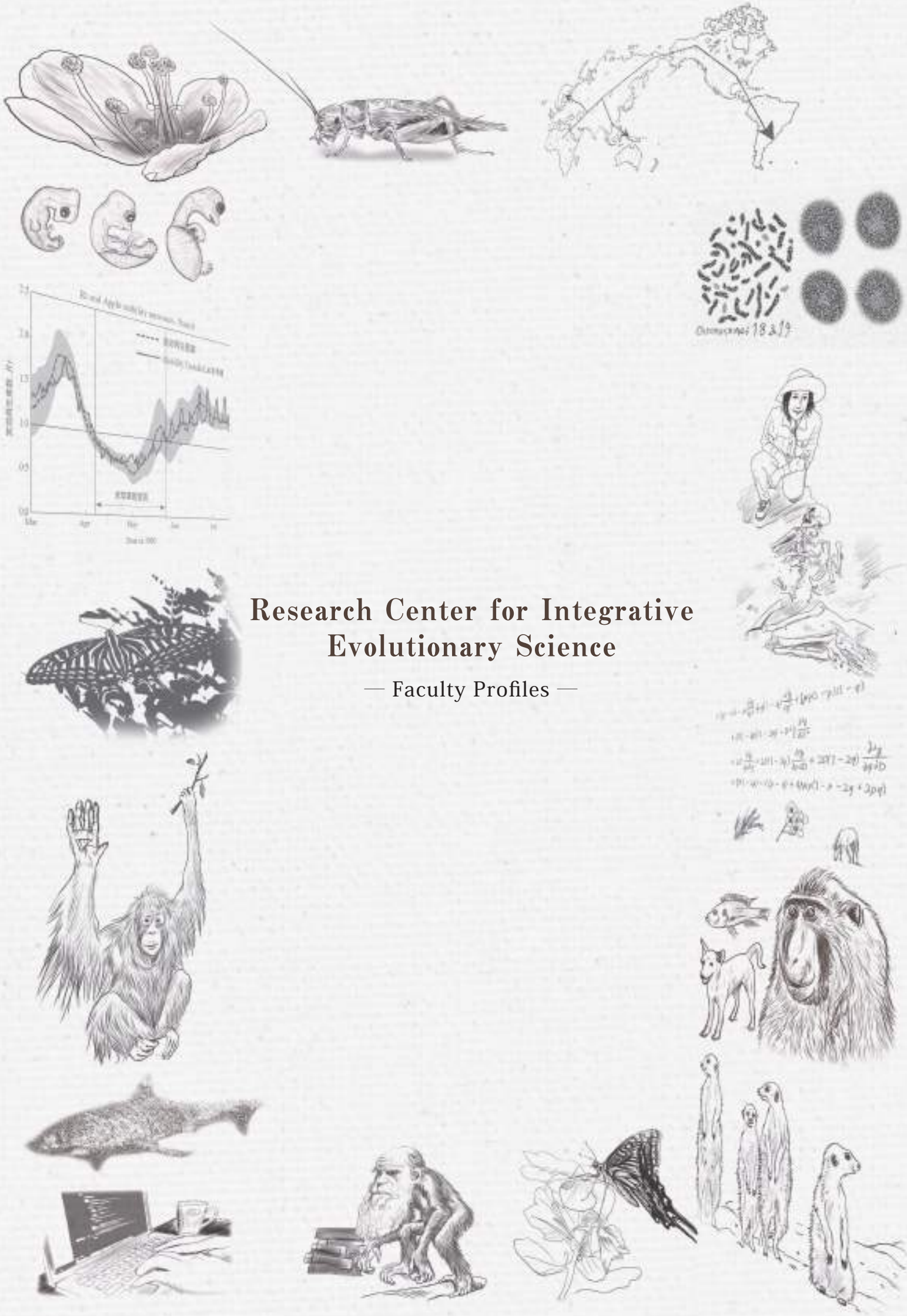
By directing our focus towards the evolution of entities beyond biology, there is much to be learned. Conversely, some of the innovations generated through biological evolution have contributed to the advancement of technology. Examples include swimsuits inspired by shark skin and injection needles based on the proboscis of mosquitoes. Furthermore, genetic algorithms find applications in AI's learning processes. In the realm of integrated evolutionary science, valuing feedback among diverse evolutionary studies, we strive to comprehend the essence of evolution holistically.

INNAN Hideki,
Director

Introduction and description of the center

The Research Center for Integrative Evolutionary Science (RCIES) aims to be the sole domestic research hub focused on "evolution," collaborating with both domestic and international research institutions to create a novel academic domain called "integrated evolutionary science." While the term "evolution" may evoke images of biological evolution, "integrated evolutionary science" encompasses research into the changes and evolutions brought about in scientific, technological, cultural, and societal realms by human activities. It seeks to encompass all these aspects under the definition of "integrated evolutionary science."

Over the course of the 3.8 billion years of the history of life, this field will explore how living systems have been constructed and transformed. Additionally, it will investigate how various human activities, such as social, psychological, linguistic, and cultural aspects, have undergone changes. Furthermore, it will take an evolutionary perspective to holistically consider the global challenges faced in the Anthropocene epoch, examining how they have progressed and exploring potential solutions. "Integrated evolutionary science" thus reevaluates the concept of "evolution," aiming not only for the advancement of the knowledge system in biology but also to incorporate the insights of evolutionary studies into the understanding of human phenomena and resolution of societal issues.



Research Center for Integrative Evolutionary Science

— Faculty Profiles —

Environmental Archaeology (Zooarchaeology) and Palaeoanthropology

Aiming for a comprehensive understanding of humankind and the environment in the past, present and future

HONGO, Hitomi
Associate professor

Research keywords
Zooarchaeology, Domestication,West Asia, East Asia,Neolithic Period

Career

1996 Ph.D. Department of Anthropology, Harvard University
1995-1997 Research fellow and Lecturer, International Research Center for Japanese Studies.
1997-2006 Assistant Professor, Department of Evolution, Systematics and Phylogeny, Primate Research Institute, Kyoto University. 2006-Present Associate Professor, Department of Graduate University for Advanced Studies

Membership

International Council for Archaeozoology, The Anthropological Society of Nippon, Japanese Society for Zooarchaeology, Japanese Society for West Asian Archaeology, Japan Association for Quaternary Research, Japan Society for Scientific Studies on Cultural Properties, The Japanese Archaeological Association, The Society of Biosophia Studies, The Society for Research on Native Livestock, The Society for Ecological Anthropology

To applicants

Although a small department, researchers from a wide range of fields belong to the School of Advanced Sciences and carry out interdisciplinary studies. You may be able to find an innovative research theme beyond the existing academic frameworks.

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Research details

I investigate the socioeconomic and cultural changes of past human societies through the relationship between human groups and the environment. Emergence of sedentary settlements in c. 15000 years ago and domestication of plants and animals brought significant changes in human history and facilitated the development of complex societies. On the other hand, influence of human activities on the ecosystem has increased and eventually lead to the global environmental crisis today. Aiming for an integrative understanding of relationships between humans and their environment in the past, present, and future, I carry out research in southeastern Turkey, one of the domestication centers, as well as other parts of West Asia. Since domestication is a coevolutionary process of humans and animals or plants, the process needs to be studied both from biological and sociocultural points of view. Therefore, cooperation of researchers from various fields, such as archaeology, genetics, environmental sciences, behavioral ecology, and anthropology, is essential for the investigation of domestication process.


Sheep skull


Sheep milking


View of Hasankeyf

Major Publications

❶ Hongo, H., Kikuchi, H., Nasu, H. (2021) Beginning of pig management in Neolithic China: Comparison of domestication processes between northern and southern regions. ***Animal Frontiers***, 11(3) 30-42. DOI: 10.1093/af/vfab021

❷ Hongo, H., Arai, S., Takahashi, R., Gündem, C.Y. (2019) Transition to food production suspended – a remarkable development in the Eastern Upper Tigris Valley, South Anatolia. In Peters, J., McGlynn, G., Goebel, V. (eds), ***Animals: Cultural Identifiers in Ancient Societies?, Proceedings of the 2016 international symposium, Munich, Germany. Documenta Archaeobiologiae*** 15: 155-172, Rahden/Westf.: Leidorf. 376pp

❸ Price, M. and Hongo, H. (2019) The Archaeology of Pig Domestication: Methods, Models, and Case Studies. ***Journal of Archaeological Research***. doi: 10.1007/s10814-019-09142-9

❹ Itahashi, Y., Miyake, Y., Maeda, O., Kondo, O., Hongo, H., Van Neer, W, Chikaraishi, Y.,Ohkouchi, N. & Yoneda, M. (2017) Preference for fish in a Neolithic hunter-gatherer community of the upper Tigris, elucidated by amino acid δ15N analysis. ***Journal of Archaeological Science***, 82, 40-49. doi: 10.1016/j.jas.2017.05.001

❺ Arbuckle, B.S., Price, M.D., Hongo, H. & Oksüz, B. (2016) Documenting the initial appearance of domestic cattle in the Eastern Fertile Crescent (northern Iraq and western Iran). ***Journal of Archaeological Science***, 72: 1-9. doi: 10.1016/j.jas.2016.05.008

Biological anthropology, Bioarchaeology, Primatology

The impact of differences in culture and natural environment on lived experiences and the evolution of Hominidae

TSUTAYA, Takumi
Assistant professor

Research keywords

Biological anthropology, Bioarchaeology, Primatology, Stable isotope analysis, (Palaeo)proteomics, Ancient DNA analysis, R software, Fieldwork, Orangutan

Career

Graduated at Department of Science, Tokyo Metropolitan University. Ph.D. in Lifescience at Department of Integrated Biosciences, the University of Tokyo. Works in physical anthropology. Current position since 2020, after postdocs at Kyoto University and Japan Agency of Marine-Earth Science and Technology. Likes reading novels and riding bicycles.

Membership

The Anthropological Society of Nippon, Primatological Society of Japan

To applicants

Our lab has the following features:
1. Various approaches are available, such as fieldwork at research sites and experimental works in the laboratory.
2. Human evolution and adaptation are the core research topics.
3. Our interdisciplinary style allows research activities across diverse research fields.
4. We do not want ourselves and others to give up balancing our/their research and life even under the current tough situation of academia.

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tsutaya_takumi@soken.ac.jp

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Research details

In the Laboratory of Biological Anthropology, we reconstruct the lived experiences, life histories, and evolutionary processes of Hominidae (Homo sapiens and evolutionarily related primates) using various cross-disciplinary approaches.
How were human and primate individuals born, grew up, reproduce (or not), and died? By revealing these lived experiences, we can investigate the impact of cultural and natural environmental differences on the evolutionary process over long time scales in human evolution. Specifically, data are obtained by applying stable isotope analysis, (palaeo)proteomics, and ancient DNA analysis to specimens and materials from the fields of archaeology, paleontology, and primate ecology. Such data are interpreted and discussed within the framework of ecology, history, and evolution. This allows us to reconstruct, for example, how chimpanzees and orangutans live in tropical rainforests, childrearing practices in past human populations from the Jomon to the Edo period, and how extant Hominidae had evolved.

A 1,000-year-old canine skull excavated from an archaeological site.

Wild orangutan baby

Clean laboratory for ancient biomolecules

Major Publications

❶ Tsutaya T, Mizushima N. in press. Evolutionary biological perspectives on current social issues of breastfeeding and weaning. ***Yearbook of Biological Anthropology***. doi: 10.1002/ajpa.24710.

❷ Tsutaya T, Wong A, Malim PT, Bernard H, Ogawa NO, Ohkouchi N, Hongo S, Tajima T, Kanamori T, Kuze N. 2022. Stable isotopic investigation of the feeding ecology of wild Bornean orangutans. ***American Journal of Biological Anthropology*** 179: 276–290.

❸ Tsutaya T, Mackie M, Sawafuji R, Miyabe-Nishiwaki T, Olsen JV, Cappellini E. 2021. Faecal proteomics as a novel method to study mammalian behaviour and physiology. Molecular Ecology Resources 21: 1808–1819.

❹ Tsutaya T, Meaghan M, Koenig C, Sato T, Weber AW, Kato H, Olsen JV, Cappellini E. (2019) Palaeoproteomic identification of breast milk protein residues from the archaeological skeletal remains of a neonatal dog. ***Scientific Reports*** 9: 12841. doi: 10.1038/s41598-019-49183-0

❺ Tsutaya T, Shimatani K, Yoneda M, Abe M, Nagaoka T. (2019) Societal perceptions and lived experience: infant feeding practices in premodern Japan. ***American Journal of Physical Anthropology*** 170: 484–495. doi: 10.1002/ajpa.23939

Animal behaviour, ethology, behavioral ecology, primatology

How do animals live and what do they think?

KUTSUKAKE, Nobuyuki

Professor

Research keywords

behaviour, sociality, ecology, cognition, evolution, vertebrates

The observation of animals leads us to a number of questions such as "How do animals live?", "Why do animals behave in a certain way?", "What do animals know and understand?", and "Why are there so many species?" A goal of my studies is to understand animal behavior and ecology from a standpoint of evolution. I have two ongoing projects. The first one is on social evolution in group-living mammals. I want to know how individuals should behave in order to maximize their (inclusive) fitness in a complex social environment.

So far, I have been working on cooperation, conflict, conflict resolution, and communication in mammals and other vertebrates (birds, amphibians, and fish; reptiles not yet, unfortunately!). The second one is on phenotypic evolution and comparative approaches with information of phylogeny. I am applying a new computational framework of phylogenetic comparative analyses to complex and heterogeneous data to infer processes of trait evolution.

Career

I have been studying primate social behaviour since my graduated period.
I am studying behaviour, ecology, cognition, and evolution in mammals and other vertebrates.

Membership

Animal Behavior Society,
Evolution Society

To applicants

We welcome proposals for research topics and research species by students.
I am looking forward to studying with enthusiastic students.

E-mail

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URL

https://sites.google.com/view/nkutsukake/

https://sites.google.com/site/sokendarwin

Research details

Japanese macaques in heavy snowfall areas

Eusocial naked mole rat

Kalahari Meerkat

Major Publications

❶ Nomano FY, Kutsukake N. 2022. Aggression induced by ornament similarity is limited to females in a mutually ornamented fish, Betta brownorum. ***Anim Behav*** 190, 233-240.

❷ Haba Y, Kutsukake N. (2019) A multivariate phylogenetic comparative method incorporating a flexible function between discrete and continuous traits. ***Evolutionary Ecology*** 33: 751-768. doi: 10.1007/s10682-1019-10011-6

❸ Hasegawa M, Kutsukake N. (2019) Kin selection and reproductive value in social mammals. ***Journal of Ethology***. 37: 139-150. doi: 10.1007/s10164-019-00586-6

❹ Takeda FK, Hiraiwa-Hasegawa M, Kutsukake N. (2019) Uncoordinated dances associated with high reproductive success in a crane. ***Behavioral Ecology*** 30: 101-106. doi: 10.1093/beheco/ary159

❺ Ito MH, Yamaguchi M, Kutsukake N. (2018) Redirected aggression as a conflict management tactic in the social cichlid fish *Julidochromis regani*. ***Proceedings of the Royal Society of London. Series B, Biological Sciences***, 285: 2017.2681. doi: 10.1098/rspb.2017.2681

❺ Mizuno K, Irie N, Hiraiwa-Hasegawa M, Kutsukake N. (2016) Asian elephants acquire inaccessible food by blowing. ***Animal Cognition***.19: 215-222. doi: 10.1007/s/1007/-015-0929-2

Ecology, Marine Biology

Measuring and understanding the behavior, ecology, and physiology of marine predators

WATANABE, Yuuki
Professor

Research keywords
Biologging, Behavioral Ecology, Shark, Seal

Career

Finished Ph.D at the University of Tokyo (2007). Research Fellow of the Japan Society for the Promotion of Science at the University of Tokyo (2007-2008). Assistant Professor at the National Institute of Polar Research (NIPR) (2008-2015). Associate Professor at NIPR (2015-2023). Professor at SOKENDAI (2023-present).

Membership

Japan Society for Bio-Logging Science

To applicants

I welcome students interested in studying the ecology of marine predators using biologging technique.
Fieldwork will be conducted in Japan or overseas with many collaborators. Please email me for more information.

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URL
https://rcies.soken.ac.jp/labs/ywatanabe/

Research details

I study the ecology of marine predators (large fishes, marine mammals, and seabirds) using the technique called biologging, where miniaturized sensors are attached to animals. With modern biologging devices, it is now possible to record the behavior, surrounding environment, and internal state (e.g., body temperature, heart rate) of marine predators. It is also possible to observe what they do in the water by attaching video cameras to the back of the animals. My main approach is to obtain such data in the field and then analyze data from ecological perspectives, often with the information collected using other research methods or from the literature. By doing so, I aim at understanding the ecological significance (or ultimate causes) of the behavioral or physiological traits shown by the species in question. My main research target is currently sharks, although I also conduced many field studies on marine mammals and seabirds in the past. My study areas include Kochi and Okinawa Prefectures in Japan as well as various areas off Taiwan, Australia, and Canada. In addition, I recently began fieldwork in Sagami Bay near the Hayama Campus of SOKENDAI. A key component of biologging studies is the development of new devices. Thus, I am collaborating with several manufacturers in Japan, aiming to record truly innovative data from free-moving marine predators.

A white shark with biologging package attached.

Working on a great hammerhead shark (Photo Credit: R. Snow)

Major Publications

❶ Watanabe YY and Payne NL (2023) Thermal sensitivity of metabolic rate mirrors biogeographic differences between teleosts and elasmobranchs. ***Nature Communications*** 14:2054. doi:10.1038/s41467-023-37637-z

❷ Watanabe YY, Papastamatiou YP (2023) Biologging and biotelemetry: tools for understanding the lives and environments of marine animals. ***Annual Review of Animal Biosciences*** 11:247-267. doi: 10.1146/annurev-animal-050322-073657

❸ Watanabe YY, Baranov EA, and Miyazaki N (2020) Ultrahigh foraging rates of Baikal seals make tiny endemic amphipods profitable in Lake Baikal. ***Proc Natl Acad Sci USA*** 117:31242-31248. doi:10.1073/pnas.2014021117

❹ Watanabe YY, Ito K, Kokubun N, and Takahashi A. (2020) Foraging behavior links sea ice to breeding success in Antarctic penguins. ***Science Advances*** 6:eaba4828. doi:10.1126/sciadv.aba4828

❺ Watanabe YY, Goldman KJ, Caselle JE, Chapman DD, and Papastamatiou YP (2015) Comparative analyses of animal-tracking data reveal ecological significance of endothermy in fishes. ***Proc Natl Acad Sci USA*** 112:6104–6109. doi:10.1073/pnas.1500316112

Biological anthropology, Bioarchaeology, Primatology

The impact of differences in culture and natural environment on lived experience of "us" (Homo sapiens and other evolutionarily related species)

TERAI, Yohey
Associate professor

Research keywords
Adaptation, speciation, and symbiosis

Career

Ph.D. (Science), Graduate School of Life Science and Technology, Tokyo Institute of Technology
Assistant Professor of GCOE, Tokyo Institute of Technology
Assistant Professor, Graduate School of Advanced Studies, Graduate School of Integrated Studies

Membership

Society of Evolutionary Studies, Japan
Primate Society of Japan
Society for Molecular Biology and Evolution

To applicants

"Better be the head of a dog than the tail of a lion"
If you are interested in evolutionary biology and want to research your own theme, studying in IES is the best choice for you.

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https://researchmap.jp/speciation

Research details

Today, many species inhabit the earth, and their interactions generate biodiversity. Biodiversity has been acquired through "speciation" (one species divides into two species) and through "adaptation" (organisms survive in their habitat). We focus on four primary research areas to elucidate the mechanisms of adaptation and speciation in organisms.

○Speciation: a genomic approach
Based on genomic analysis, we are studying the speciation of seven species of macaques endemic to Sulawesi Island and corals.

○Adaptation by symbiosis
We are studying the mechanism of adaptation to a new environment by symbiosis, using a volcano lichen that grows only in the areas where volcanic gases are venting.

○Adaptation to the Human environment
The ancient genomes of the Japanese wolf and the ancient dog are used to study the origins of the dog and how dogs have adapted to their living environment with humans.

○Adaptation of vision to light environments
We use fish and reptiles to study how organisms have adapted their vision to different light environments underwater.


Japanese wolf/Japanese dog genome


Speciation in Sulawesi macaques


Environmental adaptation of vision and speciation


Environmental adaptation of lichens through symbiosis

Major Publications

❶ Gojobori J, Arakawa N, Xiayire X, Matsumoto Y, Matsumura S, Hongo H, Ishiguro N, Terai Y. The Japanese wolf is most closely related to modern dogs and its ancestral genome has been widely inherited by dogs throughout East Eurasia. doi: bioRxiv, (2021), doi.org/10.1101/2021.10.10.463851

❷ Kono M, Kon Y, Ohmura Y, Satta Y, Terai Y(2020) In vitro resynthesis of lichenization reveals the genetic background of symbiosis-specific fungal-algal interaction in Usnea hakonensis. ***BMC Genomics***, 21:671 doi: 10.1186/s12864-020-07086-9

❸ Arakawa N, Utsumi D, Takahashi K, Matsumoto-Oda A, Nyachieo A, Chai D, Jillani N, Imai H, Satta Y,Terai Y(2019) Expression changes of structural protein genes may be related to adaptive skin characteristics specific to humans. ***Genome Biology and Evolution*** 11:613-628. doi:10.1093/gbe/evz007

❹ Shiho Takahashi-Kariyazono, Kazuhiko Sakai, Yohey Terai(2018) Presence–absence polymorphisms of highly expressed FP sequences contribute to fluorescent polymorphisms in Acropora digitifera. ***Genome Biology and Evolution***, 10:1715-1729. doi:10.1093/gbe/evy122

❺ Terai Y, Miyagi R, Aibara M, Mizoiri S, Imai H, Okitsu T, Wada A, Takahashi-Kariyazono S, Sato A, Tichy H, Mrosso HDJ, Mzighani SI, Okada N (2017) Visual adaptation in Lake Victoria cichlid fishes: depth-related variation of color and scotopic opsins in species from sand/mud bottoms ***BMC Evolutionary Biology*** 17: 200. doi: 10.1186/s/2862-020-01725-1

Behavioral neuroscience,(Neuroethology)Visual ecology

Experience the sensory world of butterflies

KINOSHITA, Michiyo
Associate Professor

Research keywords

Foraging behavior, Olfaction, Lepidopteran insect, Vision, Neural processing, Cognition, Brain

Career

I graduated from Yokohama City University. After going through two postdoctoral positions, JSPS Postdoctoral fellow and Canon fellow (University of Marburg, Germany), I was offered a faculty position in SOKENDAI.
My research motto is to "play" with animals to learn from them.

Membership

Zoological Society, Japanese Society of Comparative Physiologyand Biochemistry, International Society of Neuroethology

To applicants

Behavioral neuroscience is a field of experimental biology where we study the cognitive world by analyzing animal behavior and the neural systems underlying the behavior. I hope that you would accumulate great experience in this field directly facing living animals.

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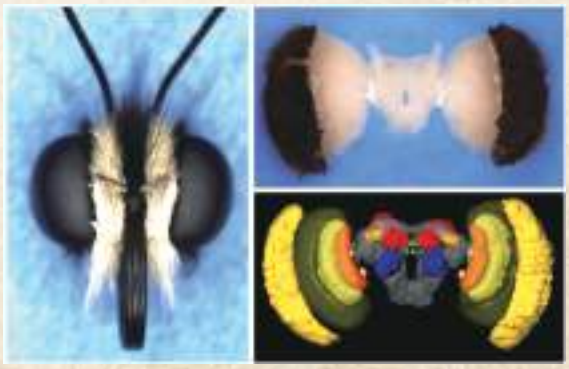
Research details

The sensory world of animals can be very different from ours. One of the fields to reveal their sensory world is behavioral neuroscience.
My research interest is "Biology of flower foraging butterflies." I have studied visual abilities and spectral organization of the compound eye in the Japanese swallowtail butterfly, Papilio xuthus. Papilio butterflies have sophisticated color vision, which rivals our own. The compound eye, providing the most peripheral light processing, contains at least six classes of spectral receptors in a complicated manner. Based on the previous studies, we further explore visual processing in higher brain regions and the integration processes of visual and olfactory signals for flower foraging.
I recently started two new projects. One is a comparative study on the brain structure in Lepidopteran insects. The other is visual ecology to investigate which flower species butterflies visit in their habitat. These studies would reveal the evolution of flower foraging behavior.

Behavioral experiment –Test of color constancy – Experimental setup (left). A yellow-trained butterfly seeking nectar on a yellow patch under white (right-top) and reddish illumination (right-bottom).



The whole view of a head of Papilio butterfly (left), Appearance of the brain (right-top), 3D map of neuropils in the brain (right-bottom)

Major Publications

❶ Kinoshita M, Arikawa K. (2023) 'Color' processing in the butterfly visual system. ***Trends in Neuroscience***. 46: 338-340

❷ Céchetto C, Arikawa K, Kinoshita M. (2022) Motion-sensitive neurons activated by chromatic contrast in a butterfly visual system. ***Philosophical Transactions of the Royal Society B***. 377: 10.1098/rstb.2021.0277

❸ Kinoshita M. Stewart J. F. (2022) Cortical-like colour-encoding neurons in the mushroom body of a butterfly. **Current Biology**. 32: 114-15

❹ Kinoshita M, Stewart FJ (2020) Retinal organization and visual abilities for flower foraging butterflies. ***Current Opinion of Insect Science***. 42:76-83. doi: 10.1016/j.cois.2020.09.009

❺ Kinoshita M, Stewart FJ, Ômura H. (2017) Multisensory integration in Lepidoptera: insight into flower-visitor interactions. ***Bioessays***. 39 (4): 1600086 doi: 10.1002/bies.201600086

Evolutionary developmental neurobiology

Uncovering the developmental mechanism of the nervous system in the direct-developing insects to elucidate the evolution of the insect nervous system

WATANABE, Takayuki
Assistant professor

Research keywords

Postembryonic development of the nervous system,Sexually dimorphic circuits,Social behavior,Crickets, Direct-developing insects

Career

Education PhD in Science: The University of Tokyo, Bunkyō-ku, Japan (March 2010) MA in Science: Hokkaido University, Sapporo, Japan (March 2007) BA in Science: Hokkaido University, Sapporo, Japan (March 2005) Research Experience JSPS research fellow (DC1) JSPS postdoctoral fellow Postdoctoral research fellow in Hokkaido University Research area Neuroethology Neurogenetics Molecular evolution

Membership

The Zoological Society of Japan The Society of Evolutionary Studies, Japan Japanese Association of Neuroethology

To applicants

Since October 2020, we study the Evo-Devo of the insect nervous system in SOKENDAI, using the two-spotted cricket Gryllus bimaculatus as an experimental model. We are establishing Neurogenetics in cricket to understand the molecular/neural/developmental bases of social behaviors such as aggression and courtship behaviors

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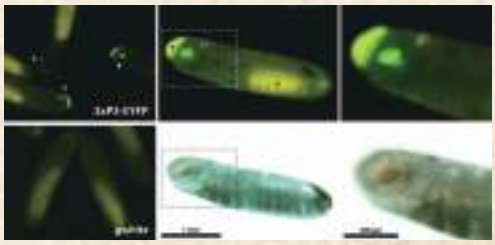
http://researchmap.jp/TakayukiWatanabe/

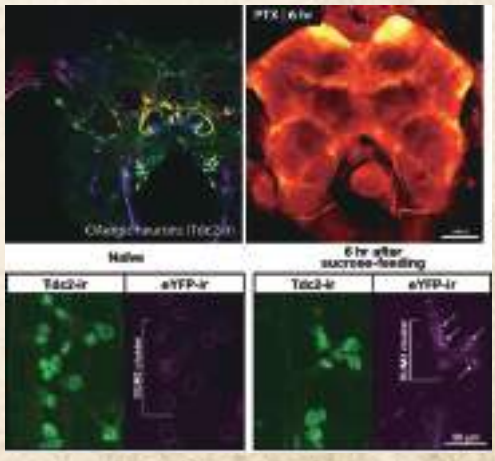
Research details

Most insects undergo metamorphosis to develop into adults. The brains of holometabolous insects (e.g., flies, butterflies, bees) drastically change their morphology during metamorphosis, which is required to prepare neural circuits for adult-specific behaviors. On the contrary, the brains of direct-developing insects (insects develop without pupal stage; e.g., cockroaches, crickets) show moderate structural changes throughout post-embryonic stages. However, similar to holometabolous insects, adults of direct-developing insects exhibit adult-specific behaviors such as courtship and mating behaviors, which are not observed in juveniles. This raises a question from the viewpoint of evolutionary developmental biology: when and how the brain of direct-developing insects becomes adult without the pupal stage? To address this question, Takayuki Watanabe is investigating the development of the neural circuits for adult-specific behaviors in a model hemimetabolous insect Gryllus bimaculatus (two-spotted cricket).

Photographs of Gryllus bimaculatus, the main research material



Fluorescence micrograph of a transgenic cricket (egg)



Fluorescence micrograph of cricket brain

Major Publications

❶ T. Watanabe. (2019) Evolution of the neural sex-determination system in insects: does *fruitless* homolog regulate neural sexual dimorphism in basal insects? ***Insect Molecular Biology***. 28:807-827. doi: 10.1111/imb.12590

❷ T. Watanabe, A. Ugajin, H. Aonuma. (2018) Immediate-early promoter-driven transgenic reporter system for neuroethological researches in a hemimetabolous insect. ***eNeuro***. 5:e0061-18.2018. doi: 10.1523/ENEURO.0061-18.2018

❸ T. Watanabe, H. Aonuma. (2013) Tissue-specific promoter usage and diverse splicing variants of the *found in neurons*; an ancestral Hu/ELAV-like RNA binding protein gene of insects, in a direct developing-insect *Gryllus bimaculatus*. ***Insect Molecular Biology***. 23:26-41. doi: 10.1111/imb.12057.

❹ T. Watanabe, H. Takeuchi, T. Kubo. (2010) Structural diversity and evolution of the N-terminal isoform-specific region of ecdysone receptor-A and -B1 isoforms in insects. ***BMC Evol Biol***. 10:40. doi: 10.1186/1471-2148-10-40

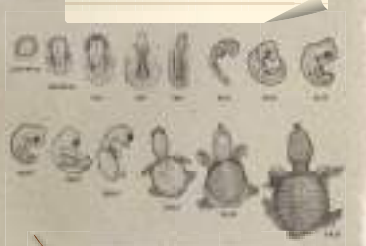
Evolutionary Developmental Biology

Elucidating the Laws of Developmental Evolution
- Exploring the Evolutionary Potential Inherent in Animal Phenotypic Systems –

Naoki, Irie
Professor

Research keywords

Evolutionary Developmental Biology, Animal Evolution, Evolvability, Developmental Constraints, Bioinformatics, Molecular Biology



Career

Graduated from Kyoto University, Graduate School of Medicine (Ph.D.) in 2008. Postdoc in Congenital Anomaly Research Center (Kyoto University), RIKEN Center for Developmental Biology, and became an associate professor at the University of Tokyo, Graduate School of Science. Professor in Research Center for Integrative Evolutionary Science (SOKENDAI) from 2023.

Membership

AsiaEvo, The European Society of Evolutionary Developmental Biology, The International Society of Developmental Biology, Society for Evolutionary Studies, Japan, The Japanese Society of Developmental Biologists, The Molecular Biology Society of Japan, The Zoological Society of Japan, The Genetics Society of Japan

To applicants

Depending on the interests of each lab member, we enjoy science with a free spirit and without being bound by methodology. If you are interested, please do not hesitate to contact us.

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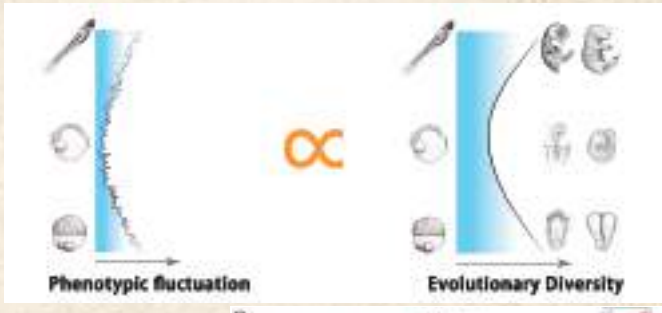
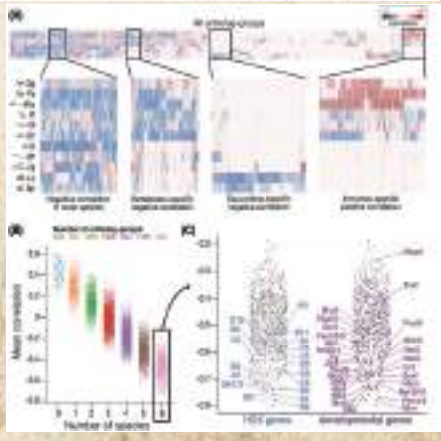
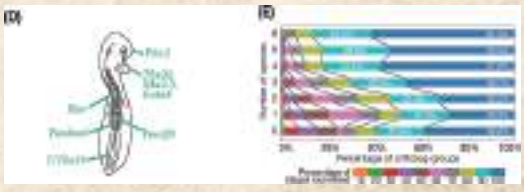
Research details

The evolution of organismal characteristics (phenotypes) is not completely free in any direction, and some characteristics are more likely to change throughout evolution than others. How do such differences arise? It may simply be due to the difference between the pressures of positive selection toward different phenotypes. On the other hand, it is also possible that some phenotypes have less potential to produce phenotypic variations due to their intrinsic characteristics, which leads to less chance to diversify. In fact, a growing number of recent theoretical and experimental studies support this possibility. Then, what is the mechanism behind this difference in phenotypic evolvability? We aim to answer this question using a variety of methods, including experiments on animals and large-scale bioinformatic analyses. Ultimately, we hope to contribute to changing the field of evolutionary studies from a study that focus mainly on events that happened in the past, but to a field of study with predictive theories for phenotypic evolution.







Major Publications

❶ Hu H., et al. (2017) Constrained vertebrate evolution by pleiotropic genes. ***Nature Ecology and Evolution*** 1:1722–1730. doi:10.1038/s41559-017-0318-0

❷ Seki R., et al. (2017) Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. ***Nature Communications*** 8:14229. 10.1038/ncomms14229

❸ Green R., et al. (2014) Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. ***Science*** 346:1254449. doi:10.1126/science.1254449

❹ Wang Z., et al. (2013) The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. ***Nature Genetics*** 45:701-706. doi:10.1038/ng.2615

❺ Naoki N. and Kuratani S. (2011) Comparative transcriptome analysis reveals vertebrate phylotypic period during organogenesis. ***Nature Communications*** 2:248. doi:10.1038/ncomms1248

Population Genomics, Evolutionary Physiology

Evolution of the human genome has been driven culturally and socially, as found in food-mediated changes of digestion enzyme genes, toxin-mediated alternations of detoxification enzyme genes, and sociocultural modifications of mental disorder genes.

SATTA, Yoko
Professor

Research keywords

1000 genome database,Out of Africa, Human evolution,Lactase persistence, Cytochrome P 450,mental disease

Interaction of time, space and genome

Career

After obtaining a Ph degree, I carried out molecular evolutionary studies of immune related genes. Throughout this initial career, I also became interested in causal effects of external environments on genome evolution, especially sociocultural effects in the case of humans. Currently, I pursue this theme by conducting researches on the evolving human genome with special reference to genes that have been subjected to positive Darwinian selection mediated through foods, toxins and acculturation.

Membership

The Genetics Society of Japan, Society of Evolutionary Studies, Japan, The Anthropological Society of Nippon, Primate Society of Japan, The Molecular Biology Society of Japan, Japanese Society of Immunology, Society of Molecular Biology and Evolution

To applicants

Whole genome sequences from many ethnic groups and ancient genome sequences are now freely available. At the same time, a number of sophisticated methods for analyzing these bigdata have been developed. Since we have both materials and methods in our hands, it is time to raise biologically and evolutionarily significant questions. Let's seek for such questions and find answers together!

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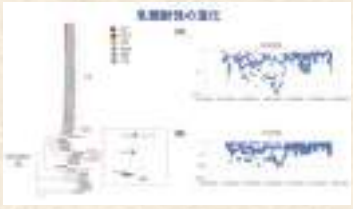
Research details

Modern humans, *Homo sapiens sapiens*, migrated from Africa approximately 60,000 years ago and rapidly spread to every corner of the Earth. In this migration process, our ancestors encountered new environments and developed various cultures to survive. Culture is a strong evolutionary agency that drives evolution of human and other organisms' genomes. Gene-culture coevolution is exemplified by lactase persistence alleles in milk-drinking pastoralist populations and Schizophrenia resistant SNP variants in almost all countries. It is possible to learn the process of culture-driven evolution by looking at positive Darwinian selection that operates on particular genomic regions. To this end, we conduct our evolutionary researches on 1) metabolizing enzyme genes, 2) detoxification enzyme genes, 3) mental disorder-related genes. In particular, detoxification enzyme variants are intimately related to metabolisms of luxury grocery items (e.g. spices, coffee, alcohol) as well as drugs, both essential to modern life. Learning the history of variants in these systems will provide some answers about how we got here.



The left phylogenetic tree shows that when a mutant (TA) of lactase persistence has been emerged. The right one shows T (a red point) and A (an orange point) mutations are targets of selection.

The map shows frequencies of four types of promoter in a gene related to schizophrenia. CGC type is major in East Asia. The right figure shows the phylogenetical relationship between CGC and non-CGC type sequences, indicating that positive selection has been operating on CGC type.

The figure shows a phylogenetical relationship among genes of Cytochorme P450 Detoxyfiation types, which are classified to CYP1 to CYP4 families.

Major Publications

1. Satta Y, RL Iwasaki (2023) Spatial and temporal diversity of positive selection on shared haplotypesat the PSCA locus among worldwide human populations. Heredity (in press)
2. Lau Q, T Igawa, H Ogino, Y Katsura, T Ikemura, Y Satta, (2020) Heterogeneity of synonymous substitution rates in the Xenopus frog genome. ***PLoS ONE*** 15(8): e0236515. doi: 10.1371/journal.pone.0236515.
3. Iwasaki RL, K Ishiya, H Kanzawa-Kiriyama, Y Kawai, J, Gojobori, Y Satta, (2020) Evolutionary History of the Risk of SNPs for Diffuse-Type Gastric Cancer in the Japanese Population. ***Genes***, 11(7), 775. doi: 10.3390/genes11070775
4. Satta Y, N. Takahata, (2020) Population genomics on the origin of lactase persistence in Europe and South Asia. ***BioRxiv.*** doi: 10.1101/2020.06.30.179432 Archivo per I' Antropologia e la Entologi Volume CL :99-117.
5. Satta Y, W. Zheng, KV, Nishiyama, RL, Iwasaki, T. Hayakawa, NT. Fujito, N. Takahata, (2019) Two-dimensional site frequency spectrum for detecting, classifying and dating incomplete selective sweeps. ***Genes and Genetic Systems***. 94:283-300. doi: 10.1266/ggs.19-00012
6. Fujito NT, Y. Satta, M. Hane, A. Matsui, K. Yashima, K. Kitajima, C. Sato, N. Takahata, T.Hayakawa, (2018) Positive selection on schizophrenia-associated ST8SIA2 gene in post-glacial Asia. ***PLoS ONE*** 13(7): e0200278. doi: 10.1371/journal.pone.0200278

Molecular Evolution

Study evolution of biological systems, such as vertebrate immune systems and plant reproductive systems, at molecular level.

OTA, Tatsuya
Associate Professor

Research keywords
Molecular evolution, immune system, self-incompatibility, genome analyses, transcriptome analyses.

Career

B.S.,1987, Kyoto University (Department of Agriculture). Ph.D, 1994, The Pennsylvania State University (Genetics). Postdoctoral, 1994-1999, Boston University. Assistant professor, 1999-2006, Sokendai. Associate professor, 2006-, Sokendai.

Membership

Genetic Society of America, Society for Molecular Biology and Evolution, Japanese Society of Breeding, Society of Evolutionary Studies, Japan

To applicants

Graduate university is the starting point of your research life. Why do you try to find research subject/ problem worth for your time in life together?

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Research details

As analyses of omics such as genomes and transcriptomes have been progressed for the increasing number of species, it becomes possible to study an organism as a whole, with recognizing each and every underlying system as product of complexed products of genes expressed. In our laboratory, with emphasizing the viewpoints of molecular evolution and population genetics, a few biosystems have been studied to solve questions such as "How have the mutations of individual genes led to phenotypical changes and become subject to natural selection?" or "How have complex systems been formed through the accumulation of mutations?". With the aims in mind, we are conducting specific research on the followings:

(1) the evolution of vertebrate immune systems such as adaptive and innate immune systems of fishes,

(2) Origin and genomic history of domestication of cultivated plants such as Azuki bean and buckwheat,

(3) the evolution of reproductive systems in Polygonaceae, including buckwheat.

Long-styled flower and short-styled flower of buckwheat

Long-styled flower and short-styled flower of Japanese knotweed

Together with researchers from the Coelacanth Genome Project

Major Publications

❶ A.W. Thompson et al., (2021) The bowfin genome illuminates the developmental evolution of ray-finned fishes. ***Nature Genetics*** 53, 1373-1384. doi:10.1038/s41588-021-00914-y

❷ I. Braasch et al., (2016) The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. ***Nature Genetics*** 48, 427-437. doi: 10.1038/ng.3526

❸ C.T. Amemiya, J. Alföldi, et al. (2013) The African coelacanth genome provides insights into tetrapod evolution. ***Nature*** 496, 311-316. doi: 10.1038/nature12027

❹ T. Ota, J. P. Rast, G. W. Litman, and C. T. Amemiya (2003) Lineage-restricted retention of a primitive immunoglobulin heavy chain isotype within the Dipnoi reveals an evolutionary paradox. ***Proceedings of the National Academy of Sciences USA*** 100, 2501-2506. doi: 10.1073/pnas.0538029100

❺ T. Ota, and M. Nei (1994) Divergent evolution and evolution by the birth-and-death process in the immunoglobulin V(H) gene family. ***Molecualr Biology and Evolution*** 11, 469-482. doi: 10.1093/oxfordjournals.molbev.a040127

Molecular Evolution,Population genetics,Physical Anthropology

Learning human evolution from genetic diversity

GOJOBORI, Jun
Lecturer

Research keywords
Human,Evolution,Adaptation, Genetic diversity, Population History

Humans emerge in Africa and spread around the world

Career

EDUCATION
Mar. 2007 Ph. D,Department of Biological Sciences, Graduate School of Science,University of Tokyo,Japan
Nov. 2003 – Mar. 2006, Visiting Student, Department of Ecology and Evolution, University of Chicago, USA
Mar. 2003 M. Sc. Department of Biological Sciences, Graduate School of Science, University of Tokyo,Japan
Mar. 2001 B. Sc. Department of Biological Sciences, Faculty of Science, University of Tokyo, Japan

PROFESSIONAL EXPERIENCE
2007- Postdoc, University of Tokyo
2008- Postdoc, SOKENDAI
2011- Assistant Professor, SOKENDAI
2016- Lecturer, SOKENDAI

Membership

The Anthropological Society of Nippon,The Genetics Society of Japan,The Japan Society of Human Genetics,Society of Evolutionary Studies,The Molecular Biology Society of Japan

To applicants

We are studying the genetic diversity and demographic history of human using molecular evolution and population genetics. Let's learn and work on various knowledge and techniques for research, from whole genome sequencing to probability- and statistic-based evolutionary theory and to handling genome data on computers.

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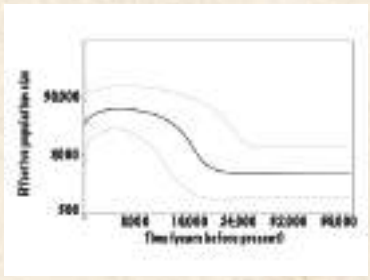
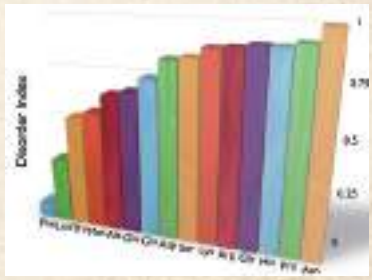
Research details

How our species, Homo sapiens, emerged? To address this question, I take two approaches. One is "to understand the evolution of human specific traits". The other is "to understand the demographic history of human after they appeared in Africa". I study Molecular Evolution and Population Genetics to understand these processes of human evolution at DNA level. One of the current targets is tandem repeat of single amino acids, which is called as homopolymeric amino acid repeat. It is known that unusual length of this repeat causes genetic diseases, which affect central nervous systems and skeletogenesis. These kinds of diseases related to human specific traits such as large brain size or bipedal locomotion. I expect that the evolution of homopolymeric amino acid repeats can be a key to understand human evolution. And there are many projects aim to find markers or genes that are responsible for human genetic disease. As a consequence of these projects, massive amount of human SNP data or human genetic variation data are produced. I apply these medical data to human evolutionary study and try to connect medical and evolutional researches. My interest is not only limited to human evolution but also includes evolution of primates, mammals and vertebrates.



Example of changes in effective population size in humans



Possibility of uncertain regions of single amino acid repeats

Example of a single amino acid repeat

Major Publications

❶ Mizuno F, Gojobori J* et al. (2021) Population dynamics in the Japanese Archipelago since the Pleistocene revealed by the complete mitochondrial genome sequences. ***Scientific reports*** 11:12018-12018.

❷ Nishiyama KV, Satta Y, Gojobori J* (2020) Do Genes Associated with Dyslexia of Chinese Characters Evolve Neutrally? ***Genes*** 11:658.

❸ Gojobori J* et al. (2015) mtDNA diversity of the Zapotec in Mexico suggests a population decline long before the first contact with Europeans. ***J Hum Genet*** 60: 557-559.

❹ Gojobori J and Ueda S*. (2011) Elevated evolutionary rate in genes with homopolymeric amino acid repeats constituting nondisordered structure. ***Mol Biol Evol*** 28:543-550.

❺ Gojobori J, Tang H, Akey JM, Wu CI*. (2007) Adaptive evolution in humans revealed by the negative correlation between the polymorphism and fixation phases of evolution. ***PNAS*** 104:3907-3912

Molecular Cytogenetics・Chromosome Biology

Spatial visualization of chromosomes within the cell nucleus by multi-color FISH techniques

TANABE, Hideyuki
Associate professor

Research keywords

Chromosome,chromosome territory, FISH technique,3D-FISH,multi-color FISH,spatial positioning, cell nucleus,genome evolution, nuclear architecture

Career

Graduated from the Department of Anthropology,Faculty of Science, the University of Tokyo,and entered the Graduate School of Science, obtained doctor' s degree in 1998 (Hokkaido University). After engaged as a senior staff scientist at the Division of Genetics and Mutagenesis, National Institute of Health Sciences, became an associate professor at the School of Advanced Sciences, Sokendai. Studying abroad for Prof. Thomas Cremer' s laboratory, LMU, Munich(1999-2001).

Membership

The Society of Chromosome Research, The Japan Society of Human Genetics, The Genetics Society of Japan, Society of Evolutionary Studies,Japan, Japan Society for Cell Biology,The Molecular Biology Society of Japan, Japanese Cancer Association, The Japanese Society for Regenerative Medicine,The Japanese Coral Reef Society

To applicants

I was fascinated by the multicolored world with FISH technique,then I entered the research field for analysis of chromosome structure and function in terms of evolution. Humans and primates were the first subjects, but observations are expanding to mammals,birds,reptiles,amphibians, fish,and marine invertebrates. Chromosomes are the basis of the genome and the bridge between molecules and live cells. Why don't you first look at the chromosomes of the species of your interest?

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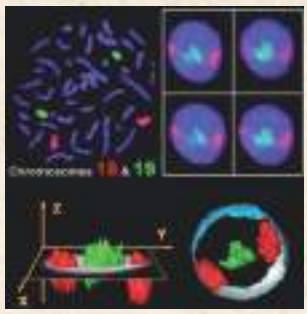
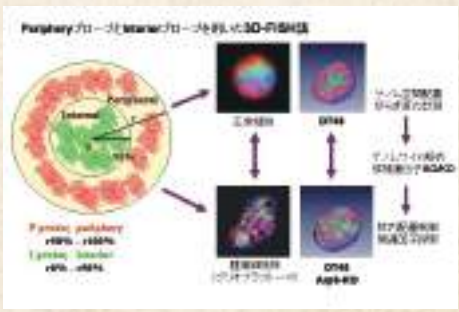
Research details

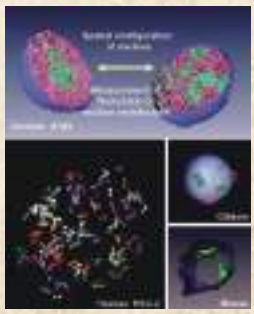
By observing the chromosomes, we can see the history and evolution of life as well as the whole set of genome of the species. I have been examined how the spatial arrangement of chromosomes and genes is organized within the cell nucleus by FISH techniques and molecular biological approaches using various cultured cells. Chromosome territories (CTs) in the interphase nucleus have a radial positioning depending on the gene density and chromosome size. Spatial positioning of CTs shows dynamics and is affected by the gene expression status due to the process of development and cell differentiation, physiological environmental changes, aging and tumorigenesis, and so on. The hierarchical structures from CTs to DNA are as follows: Compartments, TADs (Topologically Associating Domains), and chromatin structures. The mechanism of how spatially regulated of each structure is unknown in many parts. Therefore, I am trying to elucidate the molecular basis of how CTs, compartments, TADs, chromatin are spatially organized by making full use of 3D-FISH and genome editing techniques.



Overview of 3D-FISH analysis



Overview of Two-color FISH analysis of radial nuclear positioning



Measurement of fluctuation of nuclear architecture

Major Publications

1. Tanabe H, Kusakabe KT, Imai H, Yokota SI, Kuraishi T, Hattori S, Kai C, Koga A* (2021): The heterochromatin block that functions as a rod cell microlens in owl monkeys formed within a 15 million year time span. ***Genome Biology and Evolution*** Feb 3:evab021. doi: 10.1093/gbe/evab021.
2. Shioda N*, Yamaguchi K, Onozato M, Yabuki Y, Li Y, Shimbo H, Kurosawa K, Tanabe H, Okamoto N, Kondo T, Inoue H, Era T, Sugiyama H, Wada T*, Fukunaga K*(2018): Targeting G-quadruplex DNA as cognitive function therapy for ATR-X syndrome. ***Nature Medicine*** 24: 802-813.
3. Koga A*, Tanabe H, Hirai Y, Imai H, Imamura M, Oishi T, Stanyon R, Hirai H: Co-opted megasatellite DNA drives evolution of secondary night vision in Azara's owl monkey. ***Genome Biology and Evolution*** 9: 1963-19702 doi: 10.1093/gbe/evx142.
4. Nakaya M, Tanabe H, Takamatsu S, Hosokawa M, Mitani T*(2017): Visualization of the spatial arrangement of nuclear organization using three-dimensional fluorescence in situ hybridization in early mouse embryos: A new “EASI-FISH chamber glass” for mammalian embryos. ***Journal of Reproduction and Development*** 63: 167-174. doi: 10.1262/jrd.2016-172
5. Omori S, Tanabe H, Banno K, Tsuji A, Nawa N, Hirata K, Kawatani K, Kokubu C, Takeda J, Taniguchi H, Arahori H, Wada K, Kitabatake Y*(2017), Ozono K: A pair of maternal chromosomes derived from meiotic nondisjunction in trisomy 21 affects nuclear architecture and transcriptional regulation. ***Scientific Reports*** 7: 764.
6. Kono M*, Tanabe H, Ohmura Y, Satta Y, Terai Y*(2017): Physical contact and carbon transfer between a lichen-forming Trebouxia alga and a novel Alphaproteobacterium. ***Microbiology*** 163: 678-691. doi: 10.1099/mic.0.000461

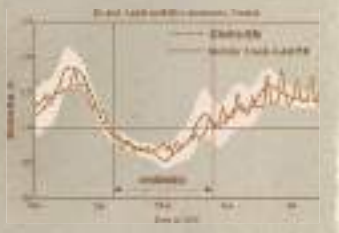
Theoretical Biology

Evolutionary Projection, Evolutionary Dynamics, Diversity

SASAKI, Akira
Professor

Research keywords

mathematical biology,
host-pathogen coevolution,
theoretical immunology,
infectious disease,
speciation, spatial ecology



Career

Ph.D. (1989)
Assistant Professor at Kyushu University (1989-1996)
Associate Professor at Kyushu University (1996-2007)
Professor at SOKENDAI (2007-present)
President of Japanese Society for Mathematical Biology (2017-2018)
Journal of Theoretical Biology, Editor-in-Chief (2020-present)

Membership

The Ecological Society of Japan
Society of Evolutionary Studies, Japan
Japanese Society for Mathematical Biology

To applicants

I welcome any student who is interested in studying biological phenomena theoretically.

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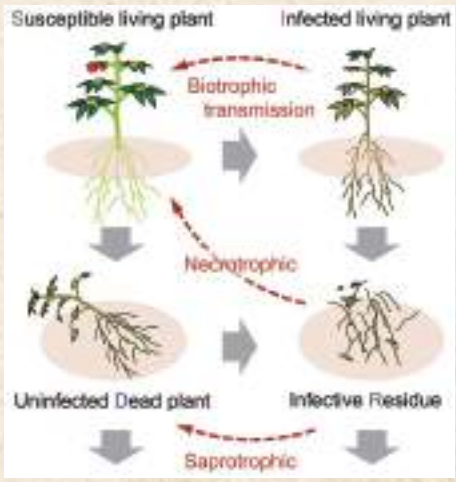
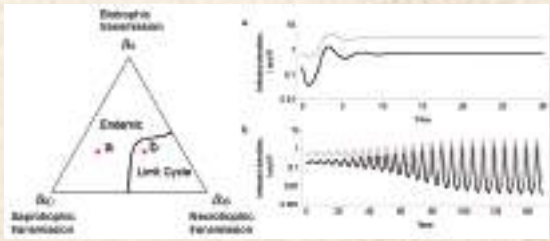
Research details

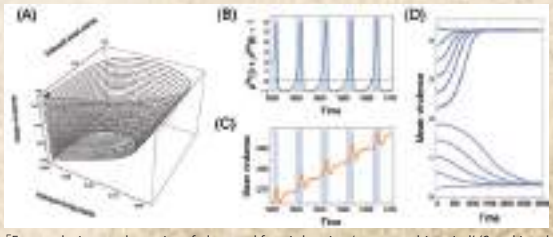
Pathogens like human immune deficiency virus and Trypanosoma brucei, the causative agents of AIDS and sleeping disease, are known to repeatedly change their cell surface coat proteins, thereby escaping the host immune response and enabling their persistent infection. To predict such rapid and complicated evolutionary processes of pathogens, we need to develop mathematical models to describe the evolution of pathogen's cell surface protein and immune response within an infected host. With these mathematical models, I have been studying, for example, the antigenic drift of HIV and influenza viruses to escape host immune system, the evolution of pathogen virulence with host spatial structure or metapopulation heterogeneity, the evolution of viral mutation rates, and the optimal strategies for vaccination and drug therapy. Other topics I am studying intensively include Müllerian mimicry and formation of spatial mosaic, coevolutionary cycles and their geographical asynchrony, species packing and sympatric speciation, the evolution of division of labor in mutualism, and the evolutionary fragility of mutualist systems.



Fungi eat plants in three different ways: biotrophically, necrotrophically, and saprotrophically (From Suzuki and Sasaki 2019 Am Nat)



Ecological dynamics of plants and fungi with given proportions of biotrophic, necrotrophic, and saprotrophic infections reveal that the system is destabilized when the proportion of necrotrophic infection exceeds a threshold (From Suzuki and Sasaki 2019 Am Nat)



「Eco-evolutionary dynamics of plant and fungi showing 'necrotrophic spiral' (Suzuki and Sasaki 2019 Am Nat). The virulence of fungi against infected plants increases evolutionarily only when plant-fungi ecological dynamics show sustained cycles. The increased virulence, then, further promotes ecological cycles — there is no way back once fungi become necrotrophic.

Major Publications

❶ Ito H, Sasaki A (2023) The adaptation front equation explains diversification hotspots and living-fossilization. ***American Naturalist*** (in press).

❷ Lion S, Sasaki A, Boots M (2023) Extending eco-evolutionary theory with oligomorphic dynamics. ***Ecology Letters*** 2023:00 1-25 doi:10.1111/ele.14183

❸ Kumata R, Sasaki A (2022) Antigenic escape accelerated by the presence of immunocompromised hosts ***Proceedings of the Royal Society B: Biological Sciences*** 289 20221437 doi:10.1098/rspb.2022.1437

❹ Uchiumi Y, Sato M, Sasaki A (2022) Evolutionary double suicide in symbiotic systems. ***Ecology Letters*** 26 87-98 doi:10.1111/ele.14136

❺ Sasaki A, Lion S, Boots M (2022) Antigenic escape selects for the evolution of higher pathogen transmission and virulence. ***Nature Ecology and Evolution*** 6 51-62 doi:10.1038/s41559-021-01603-z

Mathematical Biology

Revealing rules behind biological phenomena and exploring universal principles of life through mathematical analysis

OHTSUKI, Hisashi
Associate professor

Research keywords

evolution, mathematical models, simulations, sociality, game theory, cooperation, punishment, human behavior, life history, ecology, diversity, cultural evolution,evolutionary dynamics

Career

B.S., Univ. of Tokyo (2001); M.S.,Univ. of Tokyo (2003); PhD (Science), Kyushu Univ. (2006); JSPS researcher (PD) (2006, 2008); Post-doctoral Fellow, Harvard University(2007-2008); PRESTO researcher, JSPS (2008-2012); Assistant Prof. (2011-2015), Lecturer (2015-2019) and Associate Prof. (2019-) at the Graduate Univ. of Advanced Studies, SOKENDAI.

Membership

Japanese Society for Mathematical Biology,Human Behavior & Evolution Society of Japan,

To applicants

There are various principles behind evolution, as several laws exist in physics. Mathematical methods allow us to study any species and any biological phenomena.
We routinely read scientific papers, construct mathematical models, and study them with mathematical analyses and computer simulations to unveil the mystery of life. This field is suitable for those students who like to think deeply and logically.

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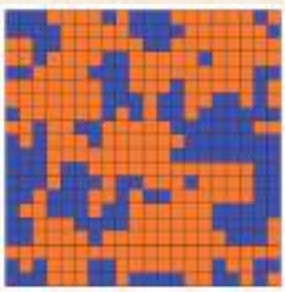
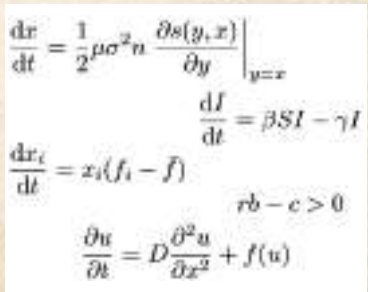
Research details

When starved, cells of slime mold, Dictyostelium discoideum, aggregate and some of them die to form stalks in order for others to disperse to a better location. In most eusocial insects such as bees and ants, queens dominate reproduction whereas workers are specialized in various labors in the colony. Reciprocal cooperation forms a basis of human society. Cooperation is ubiquitous in biology, yet its evolutionary origin is paradoxical because one can expect the emergence of "social parasites" which do not pay the cost but enjoy the benefit of cooperation. One of my main goals is to theoretically unveil the origin of cooperation. My research topics include: kin recognition in microorganisms, dynamic optimization in ant colonies, generalization of inclusive fitness theory, interplay between population structure and evolutionary dynamics, indirect reciprocity in humans, evolution of punishment and reward, and evolution of dominance hierarchy. I also work on modeling of animal behavior, species diversity, cultural evolution, social networks, human life-history evolution, and cancer progression. In addition, I study mathematical foundations of evolutionary game theory and adaptive dynamics theory.

Conceptual diagram of a social network



Lattice simulation of cooperation and non-cooperation



Various mathematical formulas that appear in mathematical biology

Major Publications

❶ Ohtsuki H, Rueffler C, Wakano JY, Parvinen K & Lehmann L (2020) The components of directional and disruptive selection in heterogeneous group-structured populations. ***Journal of Theoretical Biology*** 507,110449. doi: 10.1016/j.jtbi.2020.110449

❷ Parvinen K, Ohtsuki H & Wakano JY (2020) Evolution of dispersal in a spatially heterogeneous population with finite patch sizes. ***Proceedings of the National Academy of Sciences of the United States of America*** 117(13): 7290-7295. doi: 10.1073/pnas.1915881117

❸ Kobayashi Y, Wakano JY & Ohtsuki H (2018) Genealogies and ages of cultural traits: An application of the theory of duality to the research on cultural evolution. ***Theoretical Population Biology*** 123: 18-27. doi: 10.1016/j.tpb.2018.04.007

❹ Uchiumi Y, Ohtsuki H & Sasaki A (2017) Evolutionary emergence and maintenance of horizontally transmitted mutualism that do not rely on the supply of standing variation in symbiont quality. ***Journal of Evolutionary Biology*** 30:2211-2221. doi: 10.1111/jeb.13187

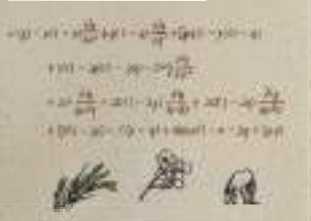
❺ Ohtsuki H & Innan H (2017) Forward and backward evolutionary processes and allele frequency spectrum in a cancer cell population. ***Theoretical Population Biology*** 117: 43-50. doi: 10.1016/j.tpb.2017.08.006

Population genetics

Understanding the mechanisms of molecular evolution

INNAN, Hideki
Professor

Research keywords
Population genetics,
Genome evolution,
Theory



Career

Hideki Innan received Doctor degree in 1999 at University of Tokyo Graduate School of Science. After working as a postdoctoral fellow at Rochester University and University of Southern California, he became Assistant Professor at University of Texas at Houston in 2002. He was appointed to be Associate Professor at SOKENDAI, the Graduate University for Advanced Studies, from 2006 to 2018, and Professor from 2018. For his accomplishment, he received Alfred P Sloan Award (from U.S.A.),JSPS Prize and Japan Academy Medal (from Japan).

Membership

The Genetics Society of Japan

To applicants

Population genetics is to understand the mechanism of molecular evolution theoretically. We use mathematics and computer simulation to describe the process of evolution.
This research requires logical thinking, which is a crucial ability that can be used in a variety of areas.

E-mail
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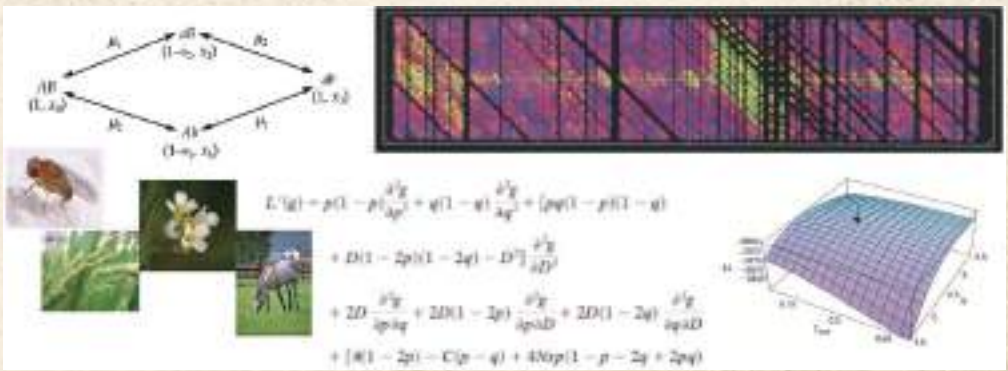
URL
https://sites.google.com/view/innanlab
https://researchmap.jp/hinnan

Research details

We aim to theoretically understand the mechanism of molecular evolution. The genetics-based theory can be applied to a wide range of species. Genomic polymorphism data are analyzed to understand how and when Darwinian selection worked in the genome.

Thoroughbred Genome Research
(Blast Onepiece)



Examples of changes in the effective population size of humans

Major Publications

❶ Sakamoto, T., and H. Innan, (2019) The evolutionary dynamics of a genetic barrier to gene flow: from the establishment to the emergence of a peak of divergence. ***Genetics*** 212: 1383-1398. doi:10.1534/genetics.119.302311

❷ Fawcett, J. A., and H. Innan (2016) High similarity between distantly related species of a plant SINE family is consistent with a scenario of vertical transmission without horizontal transfers. ***Mol. Boil. Evol***. 33: 2593-2604 doi:10.1093/molbev/msw130

❸ Innan, H., and F. Kondrashov, (2010) The evolution of gene duplications: classifying and distinguishing between models. ***Nat. Rev. Genet***. 11: 97-108. doi:10.1038/nrg2689

❹ Gao, L. Z., and H. Innan, (2004) Very low gene duplication rate in the yeast genome. ***Science*** 306:1367-1370. doi:10.1126/science.110 2033

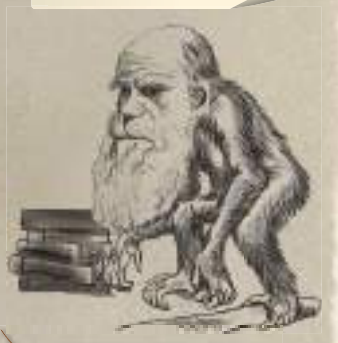
❺ Innan, H., (2003) A two-locus gene conversion model with selection and its application to the human RHCE and RHD genes. ***PNAS***. 100: 8793-8798. doi:10.1073/pnas.1031592100

History of science and technology

Let's think about the landscape of knowledge.
What do we know and what don't we know? Why?

IIDA, Kaori
Associate professor

Research keywords
History of science, genetics, radiation, breeding, tobacco, Japan, 20th century



Career

After graduating from Tsukuba Univ., I went to the U.S. as a Japanese language instructor at college. I received PhD in Genetics from Pennsylvania State Univ. and PhD in History of Science and Technology from Johns Hopkins Univ. I joined SOKENDAI in 2010.

Membership

History of Science Society of Japan (HSSJ), Biological Unit of the HSSJ, History of Science Society, International Society for the History, Philosophy and Social Studies of Biology

To applicants

Being able to think critically and flexibly about various issues including those related to science and society is important for all of us to help make the world a better place.

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URL
https://researchmap.jp/iida_k

Research details

My main interests are in history of biology in Japan. I have examined how genetics developed in Japan from the 1920s to 1960s through dynamic social contexts such as modernization, imperial expansion, postwar reconstruction /democratization, and Cold War. My current interests include how concepts of radiation and its effects were shaped after the war and what roles the Japanese community played in that shaping.

US National Academy of Sciences

National Taiwan Univ.

Major Publications

❶ Iida, K. (2021) Postwar reconstruction of Japanese genetics: Kihara Hitoshi and the Rockefeller Foundation Rice Project in Cold War Asia. ***Historia Scientiarum*** 30 no.3: 176-194.

❷ Iida, K. (2020) Peaceful atoms in Japan: Radioisotopes as shared technical and sociopolitical resources for the Atomic Bomb Casualty Commission and the Japanese scientific community in the 1950s. ***Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological & Biomedical Sciences*** 80, article # 101240. doi: 10.1016/j.shpsc.2019.101240

❸ Iida, K. and R.N. Proctor. (2018) 'The industry must be inconspicuous': Japan Tobacco's corruption of science and health policy via the Smoking Research Foundation. ***Tobacco Control*** 27: e3–e11. doi: 10.1136/tobaccocontrol-2017-053971

❹ Iida, K. (2015) A controversial idea as a cultural resource: The Lysenko controversy and discussions of genetics as a 'democratic' science in postwar Japan. ***Social Studies of Science*** 45 no.4: 546-569. doi: 10.1177/0306312715596460

❺ Iida, K. (2015) Genetics and 'breeding as a science': Kihara Hitoshi and the development of genetics in Japan in the first half of the twentieth century. In D. Phillips and S. Kingsland eds. ***New Perspectives on the History of Life Sciences and Agriculture*** (Cham, Switzerland: Springer I nternational), pp. 439-458. doi: 10.1007/978-3-319-12185-7_21

Philosophy of Science

Analyzing the nature of science and scientific knowledge

ONISHI, Yukinori
Lecturer

Research keywords
scientific realism, scientific representation, model, confirmation, epistemology

Career

Graduated from Kyoto University, Graduate School of Literature (Ph.D.) in 2015.
Joined SOKENDAI in the same year. Visited University of Miami in 2013-2014 as a Fulbright scholar.

Membership

Philosophy of Science Association, Philosophy of Science Society Japan, Japan Association for Philosophy of Science

To applicants

One of the unique features of our department is that it has both scientists and the science & society scholars. We welcome those who are willing to take advantage of this exciting environment and study philosophy of science based on the actual scientific practice.

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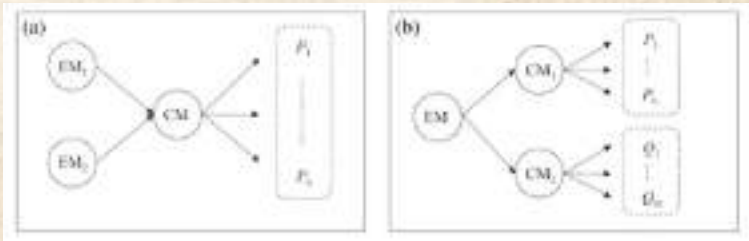
Research details

Today, science and technology have a profound impact on every aspect of our lives. While it brings us tremendous benefits, the emergence of new science and technology can also lead to unprecedented disasters and ethical challenges. Therefore, the relationship between science and society has been actively discussed from various aspects and using knowledge from various fields. Philosophy of science is one of these fields.

To fully understand the relationship between science and society, it is first necessary to understand more deeply what science is. For example, what characteristics of science make it special and distinguish it from other activities called "pseudoscience"? Is science affected by social values? If individual scientists are not influenced by the specific social and cultural context in which they conduct their research, how is this possible? If they are, does this undermine the authority and rationality of science? These questions have been discussed in the philosophy of science.

My own interest in this area is mainly in the analysis of scientific knowledge. In particular, I have been studying the "scientific realism controversy" (the controversy over the approximate truth of what scientific theories say about the world, including unobservable things) and have attempted to apply various theories in epistemology (theory of knowledge, justification or warrant) to this controversy. In addition, I am interested in various issues related to scientific representations (how scientific theories represent the world), such as the relationship between so-called "models of data" and raw data.



Major Publications

❶ Yukinori Onishi and Davide Serpico (2022 Co-first). Homeostatic property cluster theory without homeostatic mechanisms: Two recent attempts and their costs. ***Journal for General Philosophy of Science*** 53, 61-82. doi: 10.1007/s10838-020-09527-1

❷ Otávio Bueno and Yukinori Onishi (2020). The likelihood ratio measure and the logicality requirement. ***Erkenntnis***, 87:459-475. doi: 10.1007/s10670-019-00202-6

❸ Yukinori Onishi.(2019) “Philosophy of science and research integrity.” Journal of Japanese Geotechnical Society, Vol. 67-9: 52-59, 2019.

❹ Yukinori Onishi.(2017) Defending the selective confirmation strategy. ***Studies in History and Philosophy of Science***, Part A. Vol. 64: 1-10. doi: 10.1016/j.shpsa.2017.07.001

❺ Yukinori Onishi.(2012) “Analyzing the scientific realism debate from the contextualist's point of view,” Kagaku Tetsugaku Vol. 44: 65-81, doi: 10.4216/jpssj.44.2_65

MATSUSHITA, Atsuko
Lecturer

Technical Support
for Microscopy
Fine neuroanatomy

The properties of neural processing depend on anatomical factors such as the number and shape of synapses, which can be investigated by electron microscopy(EM). I take a comparative approach at the EM level to elucidate diversity and general principles of neural functions.

Career

Doctor of Science, Yokohama City University. I have been working on research projects on the sensory system of various species, such as insects, mammals, and weakly electric fish, by using electron microscopy for a long time. It is fun to observe any morphologies in terms of comparative studies. Appointed to SOKENDAI in 2008.

To applicants

People often look at things through "colored" spectacles. Shall we reconsider the importance of capturing subjects correctly through careful observation? (I am in charge of the 'electron microscopy' of the Laboratory of Basic Biology.)

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URL
https://researchmap.jp/am9p

研究詳細 QR

Communal Microscope Facility
https://rcies.soken.ac.jp/html/equipments.html

Communal Microscope Facility

The RCIES provides the microscope facility for promoting collaborative research. Here we introduce our unique pieces of equipment with state-of-the-art techniques.

1 Transmission electron microscope

Technical supports

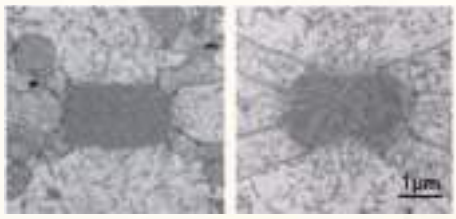
From biological sample preparation for conventional electron microscopy and immunocytochemistry, to image acquisition

Specimen examples

Insect compound eyes; optic lobes, antennal lobes, and central brains; Butterfly wing scales; electro-sensory region of midbrain in weakly electric fish; reproductive organ of mice

Hitachi H-7650

Graphium sarpedon *Parnassius glaciaris*



Butterflies' photoreceptive site, rhabom

2 Scanning electron microscope

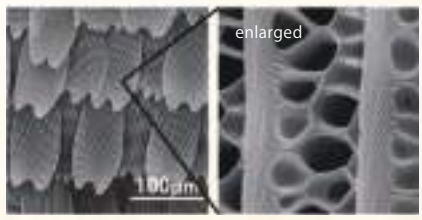
Technical supports

From biological sample preparation to image acquisition

Specimen examples

Insect wing scales, compound eyes, antennal sensilla; Archaeological animal/plant remains and their replicas, and extant species for comparative studies

JEOL JSM-6490LV



Papilio wing scale

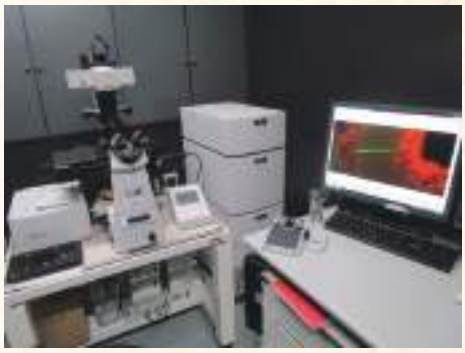
3 Confocal laser-scanning microscope

Applications

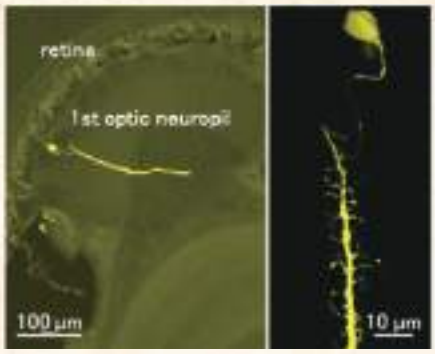
2D/3D multicolor/DIC imaging, in vivo imaging,time series imaging, spectral analysis, photo-activation imaging, etc.

Specimen examples

Tissues of echinoderms(nervous system, developmental processes); Insect brains (cockroach, butterflies)



Nikon A1Rsi



Large monopolar neuron in 1st optic neuropil in *Papilio*

Overview and Features of the Course's Education

The Integrative Evolutionary Science course is one of only a few programs in Japan specializing in evolution. We offer a unique and innovative program to foster scientists with broad perspectives who can address questions such as “What current advances in life science contribute to our society?” and “How should we as humans beings deal with the issues surrounding these advances?”

Every living organism is the product of a long evolutionary history. Furthermore, organisms do not exist in isolation but rather are interrelated via the biosystems that they form together. Evolution is the key to understanding the history and diversity of organisms. Unfortunately, conventional biology has narrowly focused on extremely segmented and specialized areas, making it hard to form a unified picture of biological phenomena.

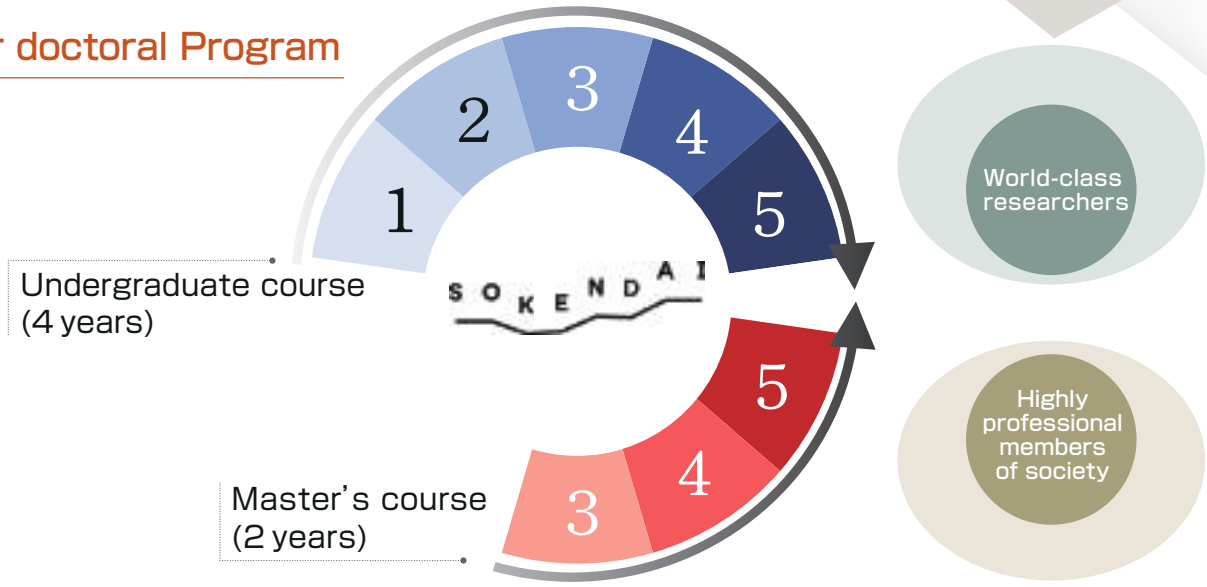
This course, therefore, emphasizes the importance of obtaining both depth and breadth of knowledge, so that our graduates can view biological phenomena within a wider evolutionary framework.

Our course welcomes prospective students not only from science majors - including biology engineering and agriculture - but also from humanities majors such as psychology, sociology, and philosophy. Introductory courses are provided for those from humanities majors so that they may acquire the fundamental biology skills and knowledge required for study at the graduate level. The course also offers programs for “Social Studies of Science”.

Students write a paper (“sub-thesis”), the aim of which is to develop a broad perspective to understand the relationship between science and society. We expect that our graduates will become researchers, curators, and professionals in media and other intellectually intensive industries and will serve as contacts between life science and society bridging the conventional disciplinary boundary between “science” and “humanities.”

5 year doctoral Program

3 year doctoral Program



Educational Characteristics

Our educational program is structured so that individuals can establish their own perspective on life and is aimed at developing professionals who can be employed in the future development of society. The biggest feature is that all faculty members are involved in the management of learning and research processes for all students, and a number of novel initiatives are engaged in that are not found in conventional graduate school education.

The Collective Leadership System

Every teacher pays attention to the progress of each individual student's learning and research as they instruct them. Students may request research guidance and advice not only from instructors (one supervisor and two sub-supervisors) but also from other faculty members.

The Sub-Thesis System

In order to cultivate the broad perspective that is also the philosophy of this university, the submission of sub-theses as well as degree papers in specialized fields (main papers) is required for the conferral of degrees.
Students who write their primary thesis in the Biosciences write their sub-thesis on the theme of Science and Society, while students who write their primary thesis in the field of Science and Society write their sub-thesis on a theme from Biosciences. Faculty members in the relevant field will provide guidance and support for research on sub-theses.

Pioneering Scientific Research

We invite researchers who are active at the forefront of various fields, such as Biosciences and Chemistry and Society, to give guest lectures, holding eight seminars a year. Students can learn the latest research trends and historical context while having direct discussions with lecturers.

Comprehensive Support for Students

We will support students' research activities and presentations of their results Perhaps expand on what you mean by this.

The Research Assistant (RA) Employment System

We will provide payment up to an amount equivalent to the annual tuition fee to RAs.

Laptop Rentals

All students will be lent a laptop for use in research and learning.

Support for Overseas Travel Expenses

The government will provide support for the presentation of research results overseas, as well as travel and accommodation expenses associated with research activities and the collection of materials at overseas research institutes.

Support for Domestic Travel Expenses

We will provide support for travel and accommodation expenses for those taking Programs in other major fields of study or other graduate schools, as well as for the presentation of research results at Japanese academic societies, and experiments at institutions and shared laboratory facilities.

SOKENDAI Publication Grant for Research Papers

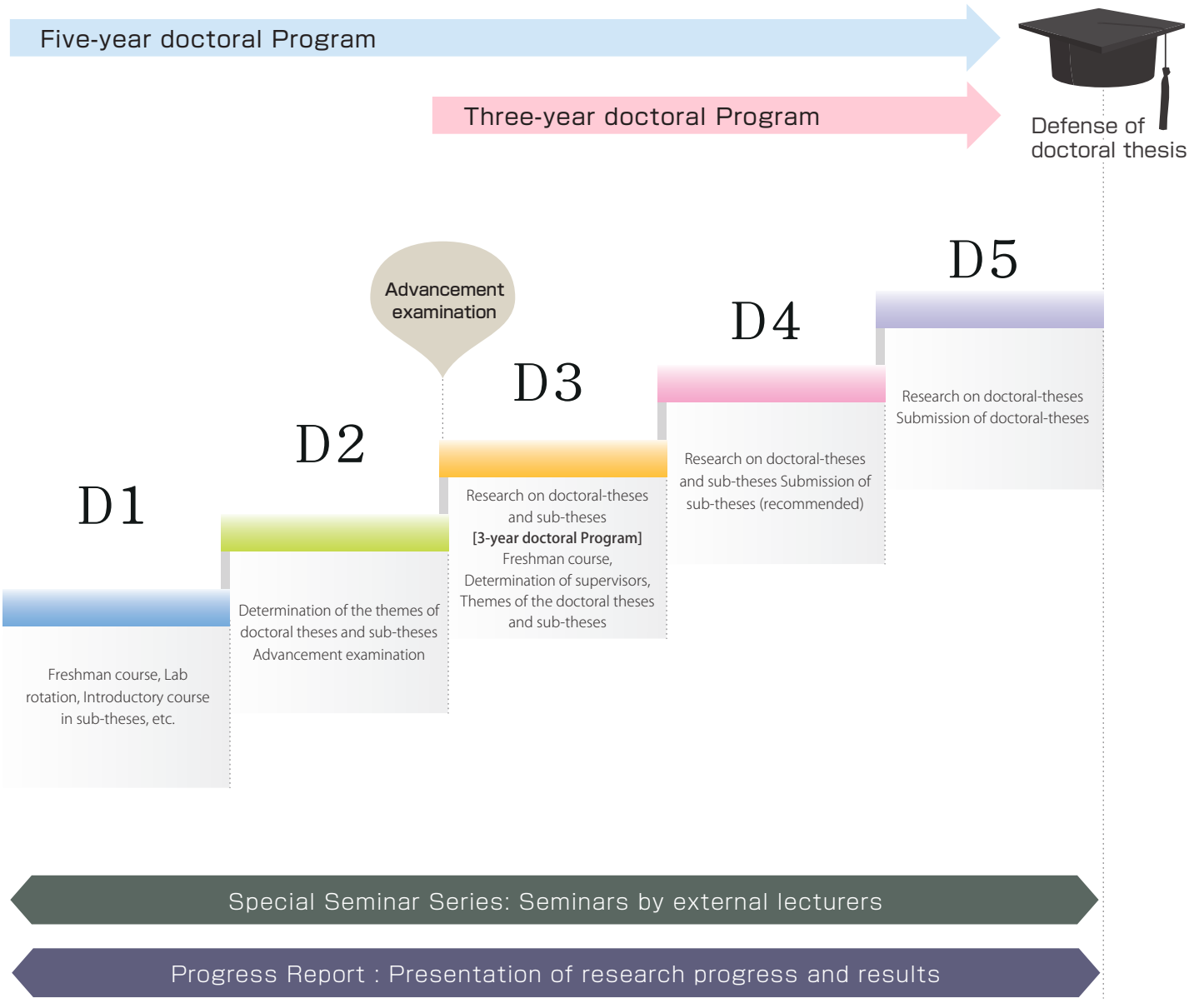
We will cover expenses necessary for the publication of research papers, etc.

SOKENDAI Student Dispatch Program

We will support long-term collaborative research in Japan and overseas.

The Model of the Study Process

	Five-year doctoral Program	Three-year doctoral Program
D1 (1st grade)	Through “lab rotation” (research experience in multiple laboratories) and taking an introductory course in sub-theses, the themes of the thesis and sub-thesis are determined; research plans are prepared; and supervisors are decided upon.	
D2 (2nd grade)	Research begins in earnest. An advancement examination is held at the end of the second year.	
D3 (3rd grade)	Research advances on doctoral-theses and sub-theses.	The supervisors, the themes of the thesis and sub-thesis are determined; Research advances
D4 (4th grade)	A sub-thesis is submitted at the end of the fourth year (recommended).	Research advances on theses and sub-theses. The sub-thesis is submitted at the end of the fourth year (recommended).
D5 (5th grade)	The doctoral-thesis is submitted. It is reviewed for the conferral of the degree.	The doctoral-thesis is submitted. It is reviewed for the conferral of the degree.



2023 Open Campus Information session on the Academic Program

We held open-campus events and information sessions on the academic program.
In addition, for those who so desire, we accept requests for trial enrollment, consultations on admissions, and laboratory visits at any time.

2023 On-line Session

◎ **May 13, 2023《Held online》**

“ Research Frontline :
Let’ s study at graduate school!”
lecture meeting
Entrance Examination information Session

Briefing Session Flow

Overview of Sokendai and the program
▼
Curriculum/Explanation of Admissions
▼
Individual Discussions

◎ **November 11, 2023**

Information Session on the academic program
For details, please refer to the following URL.
https://ies.soken.ac.jp/en_index.html

◎ **January 5, 2024**

Open Campus (Implementation method undecided)

Please note: on the HP site For more information. https://ies.soken.ac.jp/

- Listening to the Real Voices of Students at the Hayama Campus -

Interview with Graduates

INTERVIEW

March 24 Completion

Dr. IWASAKI, Risa

What is your day-to-day like?

Sometimes I come in in the morning and suddenly begin reading papers, and other times I proceed with analysis. If I get stuck in my analysis, I leave it to the side for a moment and might go to the lounge to make tea. There is a kitchen, so I would also bring in ingredients, make bread with tea in it with my friends, and even make popcorn.

— What was your motivation for entering SOKENDAI ?

Some time ago, I read a book called “Guns, Germs, and Steel” and thought it interesting to see humans from various perspectives: archaeologically, anthropologically, and historically. When I identified the keywords I wanted to look at, words like “evolution” and “receptors” emerged, and I chose this major because I was originally interested in people and because there were a wide range of fields in which I could do research.

— What was your research life like ?

There is only a small number of students, but I am glad I got along with people from various fields. In ordinary universities, people in different fields attend different campuses and never meet each other, but at SOKENDAI, because there are people from different fields on the same floor or nearby, I was glad to be able to casually ask them, “What are you doing now?” or something like that. In the “student's room,” where students are housed, it seems as though people have been intentionally placed so that those from different laboratories are mixed up together, so that they may interact with each other.

— What does it mean to be like SOKENDAI?

I think it is a good idea not to be bound by a narrow and entrenched perspective but to proceed with one’s research while recognizing the potential for things to emerge from the flanks. From high school, we are divided between students in the liberal arts and those in the sciences. As a researcher of humans, I like both ways of thinking. I was invited to participate in a lecture on the arts at SOKENDAI, and through this experience, I realized a variety of things. For one lecture, I went to a museum in Hokkaido and was shown their exhibits; for another, a folklore teacher led me to visit museums in Shikoku. Although it is difficult to connect these experiences directly to my own field of research, my perspective expanded greatly.

—What is research?

It is hard for anyone to know from the start how they insert what they want to do into a framework. When I started out, I realized what I could not do; I understood what I could do; and I felt that I began to make sense of things little by little through trial and error. It was a feeling that what was hazy formed a single image and that the resolution improved.

— How was the Hayama Campus?

When I first arrived, I got on the bus, and it went into the mountains, so it was kind of thrilling (haha!). As I engage in research, there are many times when it is tough because I do not get results, so in order to be stimulated and release the stress, I need to come down from the mountains. If you take a walk, the sunset is beautiful, which is good for changing your mood. I liked the compact environment.

— What will you do when you are finished ?

I find human diversity interesting. It is an interesting trait of humans that both genetic diversity and cultural diversity are intertwined. It is extremely interesting to look at why humans have so widened their habitats around the world and expanded them to the greatest extent of all primates, despite their very low levels of genetic diversity. I would like to continue my research in this vein in the future.

Do you have a few words for those who aim to enroll at SOKENDAI?

Even if you have decided on what you want to do or a theme, it is not easy to bring it to tangible form in accordance with the framework of academia. The process is often difficult and disheartening. But beyond that, things that are exclusively your own will appear, so I want you to enjoy the process.

Message to you

March 24 Completion

A palace of the Habsburg family that houses a research institute. As part of the international project of collaborative research hosted by a leading institute, even students have an opportunity to engage in collaborative research with prominent scholars from abroad.

Dr. SATO, Masato

Hayama campus has been very fulfilling, a place for me to grow as a person, and a source of strength for my future.
I would like to express my gratitude for the opportunity to continue my original research in a unique and special environment.

— What was your motivation for entering SOKENDAI?

Since my childhood, I have been interested in how organisms evolve. When I graduated from my undergraduate program and went on to graduate school, I was particularly interested in the theory of evolution, and when I thought about where I could study this theory in Japan, I decided that it was at SOKENDAI. There is really nowhere else that you can study the theory of evolution specifically.

− What was your research life like?

When I first decided on the theme of my research after entering university, the research theme that I had brought with me was accepted. I believe that my greatest achievement was my ability to proceed with research into that topic and have it published in The American Naturalist, a famous international journal that I really admired.

− What kind of research did you engage in?

There is a strange creature called a vestimentiferian that lives in the deep sea, and it coexists with bacteria in the body. I was researching the theoretical model of the evolution of the symbiotic relationship by which the bacteria co-operate with the host. I submitted it when I was in my second year, and after lengthy proofreading, it was published in D5. It took quite a long time (haha!).

− What was your greatest challenge?

I was allowed to proceed at my own pace; I had good relationships with my teachers and other researchers, and, honestly, I did not have any real hurdles to overcome. When I was in D4, while it had nothing to do with my research, I was stung by a hornet and spent about two weeks in bed. I was in the process of proofreading the first paper I submitted for publication.

− What are the merits of SOKENDAI?

Since there is no undergraduate program here, my time is rarely taken up by classes, and it is really great that I can feel free to engage in casual discussions with faculty members and senior students. You do not have to worry about time, and even if you go to their room, they will make sure to listen to you.

− What is your greatest memory?

When I was in D4, I stayed at a Viennese research institute in Austria, the IIASA (International Institute for Applied Systems Analysis) for about two weeks and then had the chance to engage in collaborative research with prominent researchers. From the point of view of my career as a researcher, I was able to train myself to discuss research in English, for which I was glad.

− How was the Hayama Campus?

As an environment in which to engage in research, it was a really great one. There are also no surrounding temptations (haha!).
There were also many events with people on campus often making hot-pot, having a mochi-pounding party, and holding barbecues in spring and autumn, among other events. At such times, we chit-chatted or talked about research.
There are teachers from various different fields on this small campus, so through talking with teachers and more senior classmates from different fields, I got a sense of the cultural differences in each field, which I think was a good stimulus.
I felt as if my research and my everyday life were loosely connected in some way.

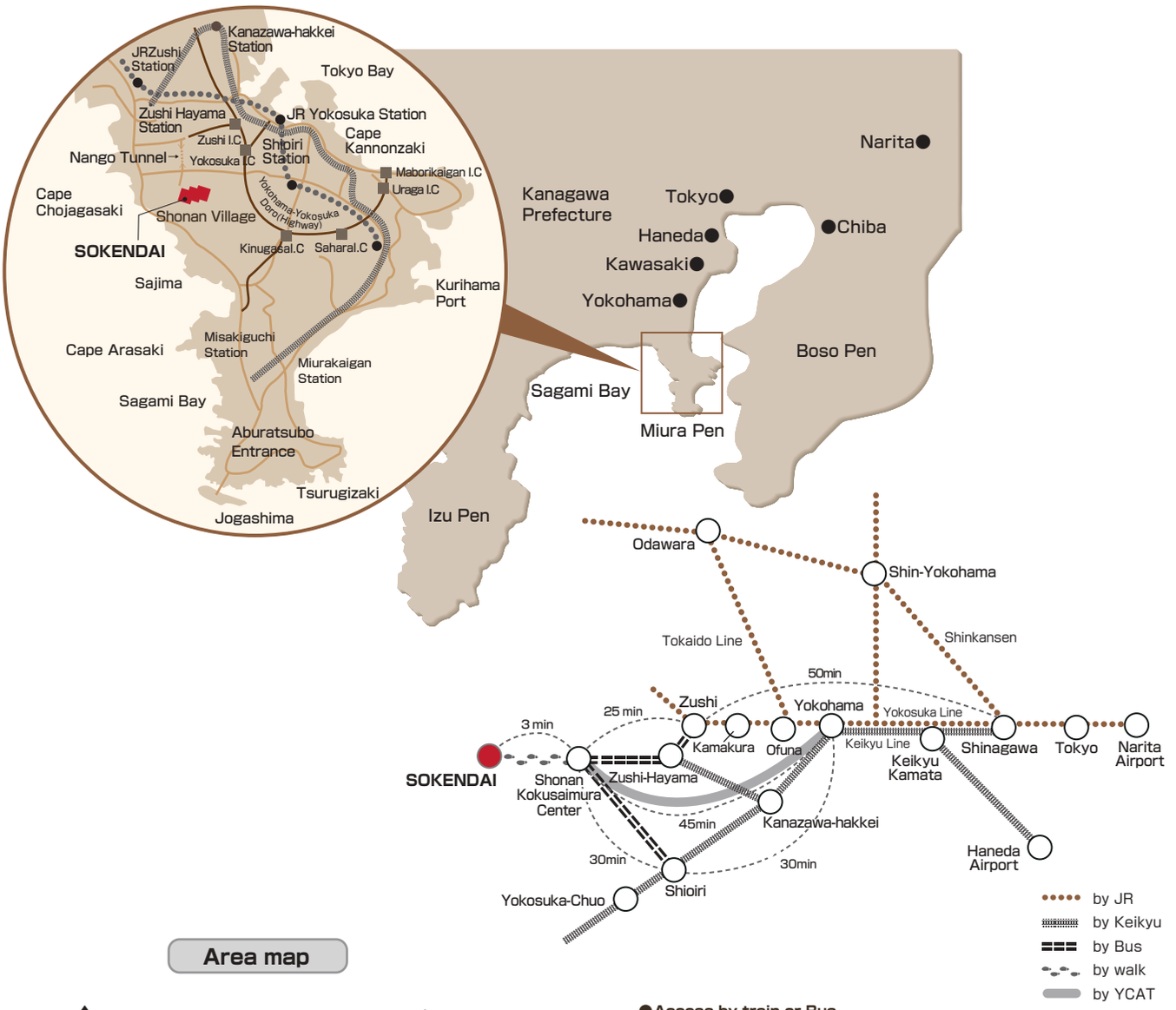
Do you have a few words for those who aim to enroll at SOKENDAI?

I am glad I came here, but of course I cannot guarantee what other people think. Those who think it is best to come here so that they may do what they want to do should definitely come.
Basically, in the doctoral course, the goal is to become a fully independent researcher. I think that if you have that kind of mindset, you can be happy.

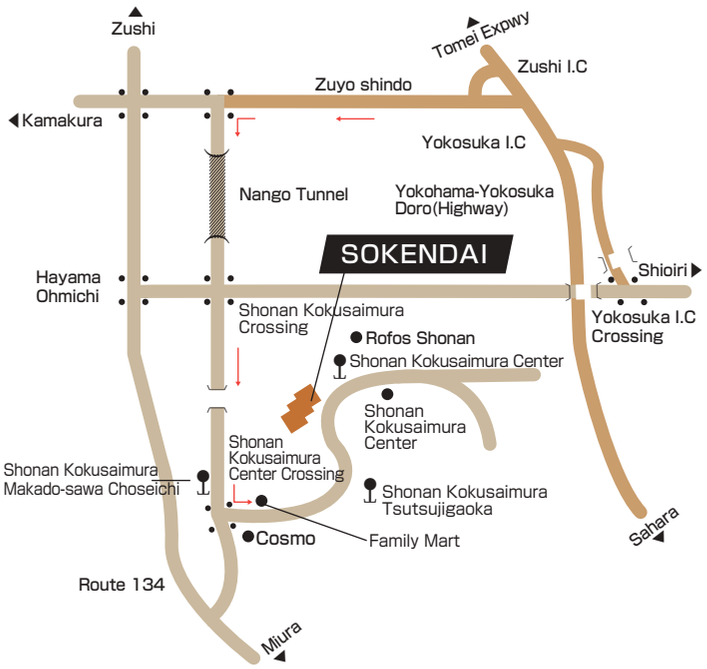
A desk on campus. In summer, you can stay here all the way from 6 A.M. to 8 P.M., with breaks.

Mr. Masato won the 6th SOKENDAI Award. Commemorative photo with the President.

Access to Hayama Campus



Area map



★ From "Shonan Kokusaimura Center Mae." 3 minutes on foot
★ From "Shonan Kokusaimura Tsutsujigaoka." 8 minutes on foot .
★ From "Shonan Kokusaimura Makado-sawa Choseichi." 10 minutes on foot .

●Access by train or Bus

- **From Zushi Station of JR Yokosuka Line (East Exit)**
  - ▶Take the Keikyu Bus No. 16 or 26 bound for "Shonan Kokusaimura" on Track # 1 and qget off at "Shonan Kokusaimura Center Mae." Approx. 25 min.
  - ▶Take the Keikyu Bus bound for "Shonan Sajima Nagisa No Oka" on Track # 2 and get off at "Shonan Kokusaimura Makado-sawa Choseichi." Approx. 20 min.
- **From Zushi-Hayama Station of Keikyu Zushi Line (South Exit)**
  - ▶Take the Keikyu Bus No. 16 or 26 bound for "Shonan Kokusaimura" on Track # 1 and get off at "Shonan Kokusaimura Center Mae." Approx. 23 min. Cost: 350 yen.
  - ▶Take the Keikyu Bus bound for "Shonan Sajima Nagisa No Oka" on Track # 1 and get off at "Shonan Kokusaimura Makado-sawa Choseichi." Approx. 18 min.
- **From Shioiri Station of Keikyu Line**
  - ▶Take the Keikyu Bus No. 16 bound for "Shonan Kokusaimura" on Track # 2 and get off at "Shonan Kokusaimura Center Mae." Approx. 30 min.
- **YCAT(Highway Bus)**
  - ▶Take a bus bound for "Denryoku Chuo Kenkyujo" (For Yokosuka West Side) on Track # 6 of Yokohama City Air Terminal and get off at "Shonan Kokusaimura Center Mae." Approx. 45 min..
    Note) 3-minute walk from "Shonan Kokusaimura Center Mae." or 10-minute walk from "Shonan Kokusaimura Makado-sawa Choseichi." 8-minute walk from "Shonankokusaimura Tsutsujigaoka to the University"

●Access by car

- **From Zushi Interchange of Yokohama-Yokosuka Road (toll way)**
  After going out of the exit of Zuyo-Shindo Route (toll way), turn left at the first intersection. Through the Nango Tunnel, go straight on the street for about 5 minutes. Then, turn left at the "Shonan Kokusaimura Center Iriguchi" intersection and keep driving for about 1 minute to the University.

Keikyu Bus

YCAT Highway Bus

★Information as of 1 April 2021.
Please refer to the bus companies' websites for details.

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