

The 33rd Annual Meeting of the Society of Population Ecology

Meeting Program & Abstracts

Date: Oct. 13(Fri) – 15(Sun), 2017

Venue: Nishijin Plaza, Kyushu Univ. (Fukuoka, Japan)

第 33 回個体群生態学会大会 @九州大学 西新プラザ
プログラム・講演要旨集

主催：第33回個体群生態学会実行委員会
協賛：シュプリンガー



Greetings

大会開催のごあいさつ

福岡にようこそ。

2017年度の個体群生態学会の大会は、福岡で開催することになり、九州大学の会員を中心として準備をすすめてきました。

4つのシンポジウムには、国内外から多数の招待講演者の方々に来ていただけることになり、また多くの参加者をお迎えでき、大変感謝しております。

大会会場も懇親会場も、それぞれ西新と天神のアクセスの便利な場所を選びました。生態学に加えて、秋の福岡を楽しんでいただければと思います。

第33回個体群生態学会大会 実行委員会

巖佐 庸・粕谷 英一・佐竹 暁子・津田 みどり・細川 貴弘・関 元秀

Welcome to Fukuoka!

We, members of the organizing committee, are delighted to extend our warm greetings to numerous participants at the 33rd Annual Meeting of Society of Population Ecology. In four thematic symposia, we will have a number of invited speakers from abroad as well as from Japan. There will also be more than 50 poster presentations.

We chose conference venue and banquet place in the city center of Fukuoka, Nishijin and Tenjin, respectively. We hope that participants will enjoy learning about the recent advancements and discussing the future of ecological sciences.

We also would like to encourage participants to enjoy beautiful Autumn in Fukuoka and Northern Kyushu area.

Organizing Committee:

Yoh Iwasa, Eiiti Kasuya, Akiko Satake, Midori Tuda, Takahiro Hosokawa, Motohide Seki.

Contact us

大会事務局・お問い合わせ先

大会全般に関するご質問は、大会事務局までお尋ね下さい。

第33回個体群生態学会大会事務局

E-mail: populationecology2017@gmail.com

Schedule

日程

October 13 (Fri)

13:00 – 15:50 Symposium I (genomic imprinting)

16:00 – 17:30 General meeting

17:30 – 17:40 Young Scientist Award ceremony

17:40 – 18:30 Award lecture

October 14 (Sat)

9:30 – 12:20 Symposium II (ecological genomics)

12:30 – 14:20 Poster session 1 (odd numbered posters)

14:30 – 17:20 Symposium III (bio-logging and big data)

19:00 – 21:00 Banquet (Pietro Centrale)

October 15 (Sun)

9:30 – 12:30 Symposium IV (evolutionary radiation)

12:30 – 14:30 Poster session 2 (even numbered posters)

Registration fee

参加登録費

	懇親会参加 W/ BANQUET	懇親会不参加 W/O BANQUET
会員・一般 MEMBERS, NON-STUDENTS	JPY 13,000	JPY 7,000
会員・学生 MEMBERS, STUDENTS	JPY 9,000	JPY 5,000
非会員 NON-MEMBERS	JPY 15,000	JPY 8,000

Venues

会場

Conference venue:

九州大学西新プラザ <http://nishijinplaza.kyushu-u.ac.jp/>

Nishijin Plaza, Kyushu University

〒814-0002 福岡市早良区西新 2-16-23

(地下鉄西新駅 7 番出口より徒歩 10 分)

2-16-23 Nishijin, Sawara-ku, Fukuoka 814-0002 Japan

(10 minutes by walk from Exit #7 of Nishijin subway station)



※福岡空港・博多・天神から西新へは、下記行先の電車に乗ってください。

西新・姪浜・筑前前原・筑前深江・西唐津

Please take a train on Fukuoka City Subway Kuko-line (orange) bound for...

Nishijin, Meinohama, Chikuzen-Maebaru, Chikuzen-Fukae, or Nishi-Karatsu.

Banquet place:

ピエトロセントラーレ <http://www.pietro.co.jp/restaurant/fukuoka/1.html>

Pietro Centrale

〒810-0001 福岡市中央区天神 3-4-5 ピエトロビル 1F

(地下鉄天神駅より徒歩約 5 分)

Pietro bldg. 1F, 3-4-5 Tenjin, Chuo-ku, Fukuoka 810-0001 Japan

(5 minutes by walk from Tenjin subway station)



Symposium I

October 13 (Fri) 13:00 – 15:50

The era of genome imprinting: epigenetic inheritance and a paradigm shift in evolutionary ecology

Organizer: Kenji Matsuura (Kyoto Univ.)

Evolutionary biology is in a transitional period. The concept of ‘epigenetic inheritance’ provides the keys to many unsolved puzzles in a wide range of biology by circumventing the limitations of genetic inheritance. Recent empirical studies have revealed that the transfer of epigenetic marks from parents to offspring can influence offspring phenotype independently of DNA sequence. Theoretical studies indicate that epigenetic inheritance acts as an important factor in evolution and that can engender outcomes unanticipated under the traditional genetic model. In this symposium, we are going to feature recent theoretical and empirical studies on epigenetic inheritance, especially on genomic imprinting, and discuss the importance of recognizing and understanding epigenetic inheritance for evolutionary ecology and other relevant fields.

Program:

13:00 – 13:10	Short introduction
13:10 – 13:50	[S1-1] Yoh Iwasa
13:50 – 14:30	[S1-2] Sergey Gavrilets
14:30 – 15:10	[S1-3] Hidetoshi Saze
15:10 – 15:40	[S1-4] Kenji Matsuura
15:40 – 15:50	General discussion

[S1-1]

Genomic imprinting in mammals: success and failure of conflict theory

Yoh Iwasa

Department of Biology, Kyushu University, Japan

In some mammalian genes, the paternally and maternally derived alleles are expressed differently, which is an evolutionary outcome of the conflict between them.

[1] Consider the evolution of gene expression levels for a zygotic gene coding for an embryonic growth factor affecting the amount of maternal resources. Then genomic imprinting evolves easily if females have some chance of multiple partners.

[2] Deleterious mutations in the coding region of the gene disfavor imprinting. Hence not all genes controlling placental development are imprinted, and imprinting in some genes is not conserved between species.

[3] The conflict theory fails to explain the pattern of X-linked imprinting in humans and mice, which evolved to control sex specific gene expression in early embryos.

[S1-2]

Sexually antagonistic epigenetic marks and canalization of sexual development

Sergey Gavrilets

Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, USA

Sex-specific ontogeny can be canalized by the production of epigenetic marks (epimarks) generated during early ontogeny that increase sensitivity of XY embryos to testosterone and decrease sensitivity of XX embryos. I will outline the evidence indicating that such epimarks sometimes carry over across generations and produce mosaicism in which some traits are discordant with the gonad. Such carryover epimarks are sexually antagonistic (SA) because they benefit the individual in which they were formed (via canalization) but harm opposite-sex offspring when they fail to erase across generations and produce gonad-trait discordances. SA-epimarks have the potential to magnify phenotypic variation for many sexually selected traits and to explain some paradoxical human traits.

[S1-3]

Epigenetic regulation of genes and transposable elements in plants

Hidetoshi Saze

Plant Epigenetics Unit, Okinawa Institute of Science and Technology Graduate University, Japan

Plants show stable transgenerational inheritance of induced epigenetic states that are associated with morphologically or physiologically distinctive phenotypes. The epigenetic inheritance is often caused by changes in chromatin modification of transposable elements (TEs) that affect expression of neighboring genes. Because of their negative effects on gene expression, TEs associated with repressive epigenetic modifications are generally excluded from actively transcribed genes. However, our recent studies revealed novel epigenetic mechanisms that masks negative effects of intragenic TEs on gene expression. Epigenetic regulation of genes and TEs, and its impact on plant genome evolution will be discussed.

[S1-4]

Genomic imprinting and the evolution of caste determination system in termites

Kenji Matsuura

Laboratory of Insect Ecology, Graduate School of Agriculture, Kyoto University, Japan

Is royalty an inherited trait in social insects? There has been a long controversy over the factors determining caste development of individuals in social insects. In *Reticulitermes* termites, parental phenotypes influence on the caste fate of the offspring. This heritable effects on caste propensity has been recognized as an evidence of genetic caste determination. Here we demonstrate that parental phenotypes influence the social status of the offspring not through genetic inheritance but through genomic imprinting. We document a genomic imprinting caste determination (GICD) system in termites, in which queen- and king-specific epigenetic marks antagonistically influence the sexual development of offspring and thus determine their caste fate. The GICD model accounts for all known empirical data on caste differentiation in termites and explains the evolutionary processes underlying diverse reproductive systems.

Symposium II

October 14 (Sat) 9:30 – 12:20

Ecological Genomics and Population Ecology

Organizers: Akiko Satake (Kyushu Univ.), Asano Ishikawa (Natl. Inst. Genet. Jpn.)

Progress in the field of Ecological Genomics has contributed to draw the history of evolutionary alterations of genetic architecture for environmental responses in plant and animals inhabiting geographically diverse environments. This symposium will feature the recent and exciting progresses in this young field of research in diverse organisms. How the interaction of the environment and the genome is shaping ecological speciation and parallel divergence in fish and leaf beetles and how plants respond to seasonal environmental change and their genotypes influence microbe communities will be presented. We will discuss the usefulness of this trans-disciplinary approach to impart a new perspective to old and challenging ecological and evolutionary questions.

Program:

9:30 – 9:35	Overview
9:35 – 10:05	[S2-1] Mark Ravinet
10:05 – 10:30	[S2-2] Asano Ishikawa
10:30 – 11:00	[S2-3] Scott Egan
11:00 – 11:30	[S2-4] Thomas Mitchell-Olds
11:30 – 11:55	[S2-5] Akiko Satake
11:55 – 12:15	[P54] [†] Shinnosuke Kagiya
12:15 – 12:20	General discussion

[†]The speaker was chosen from the list of poster presentations.

[S2-1]

The evolution of human-commensalism in Eurasian *Passer* sparrows

Mark Ravinet^{1*}, Tore Oleide Elgvin^{1,2}, Cassandra Trier¹, Angelica Cuevas¹,
Anna Runemark^{1,3}, Fabrice Eroukhmannhoff¹, Glenn-Peter Sætre¹

¹Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway

²Natural History Museum, University of Oslo, Oslo, Norway

³Department of Biology, Lund University, Lund, Sweden

The evolutionary history of *Passer* sparrows, including the house sparrow, a ubiquitous commensal bird species, is poorly understood. We re-sequenced the genomes of 17 species, covering nearly the entire *Passer* genus. Reconstructing this phylogeny places the evolution of commensalism in context. We used population genomic data from across the distribution of Eurasian species to examine their recent evolutionary history. We show clear evidence of introgression between House and Spanish sparrows in Europe. Furthermore, a divergent house sub-species occurring in Western Asia probably split from the main house lineage prior to the evolution of commensalism. Comparing commensal and wild populations of house sparrows, we identify phenotypic differences and strong signatures of selection in the house sparrow genome. Our findings point towards candidate traits and genes that may be involved with adaptation to a commensal niche.

[S2-2]

A key role for an omega-3 fatty acid desaturase gene in stickleback freshwater colonization

Asano Ishikawa^{*}, Jun Kitano
National Institute of Genetics, Japan

Colonization of empty niches can trigger adaptive radiation and phenotypic diversification. However, not all lineages have taken advantage of the ecological opportunities. Here we focused on two stickleback species, *Gasterosteus aculeatus* and *G. nipponicus*, to investigate a genetic factor that underlies the different ability to colonize new niches: the former has colonized novel freshwater habitats and diversified, but the latter could not. We identified a copy and paste transposition of omega-3 fatty acid desaturase gene that occurred in *G. aculeatus*, which we consider facilitated their freshwater colonization. In aquatic ecosystems, freshwater prey items generally lack polyunsaturated fatty acids, while marine prey items contain a lot. Thus, the copy number increase of this gene likely enables a more efficient use of freshwater food resources and trigger adaptive radiation into freshwater habitats.

[S2-3]

Ecological speciation among herbivorous insect populations

Scott Egan

Department of Biosciences, Rice University, USA

In 1859, Charles Darwin described the evolution of new species as the “mystery of mysteries”. Over 150 years later, biologists have made incredible progress in understanding the forces that promote, maintain, and constrain biodiversity. Ecology has always played a pivotal role, however, only recently has the role of ecology been the subject of intensified research. Using evidence from leaf beetles, gall wasps, and fruit flies, I will present research focused on three core areas in field of ‘ecological speciation’: (1) the ecological sources of divergent selection, (2) the evolution of ecologically based barriers to gene flow, and (3) the potential role of the genome in mediating this process based on how the genes under selection are embedded and arrayed across the genome.

[S2-4]

Biotic and abiotic influences on balancing selection in nature

Thomas Mitchell-Olds

Department of Evolutionary, Ecological and Agricultural Functional Genomics,
Duke University, USA

Although many studies provide examples of evolutionary processes such as balancing selection or deleterious polymorphism, the relative importance of these processes for phenotypic variation is unclear. To understand the evolutionary forces that influence variation in a wild relative of *Arabidopsis*, we are studying genes that control complex traits and fitness in nature. We performed a Genome-Wide Association Study (GWAS) for ~100 traits, using sequenced genotypes from 430 populations across the species range. Among the significant results, we focus on a gene that is widely polymorphic and experiences heterogeneous selection among natural populations in the Rocky Mountains. Field experiments show that this polymorphism is influenced by fitness tradeoffs in nature.

[S2-5]

**Coordinated timing of gene expression in response to
seasonal environmental change in trees**

Akiko Satake

Department of Biology, Faculty of Science, Kyushu University, Japan

Significant advances have been achieved in understanding the genetic pathways that stringently regulate the timing of transition to flowering by integrating environmental cues and developing the state of plants. However, when and at what levels these genes are expressed in nature is still poorly understood. To uncover the dynamic aspect of gene regulatory network for flowering time, we performed target-gene or global gene expression analyses using trees inhabiting temperate and tropical rainforests. Our analyses unraveled the non-intuitive relationship between seasonal environment and expression profiles of genes involved in photoperiod and circadian clock pathways and the relationship between flowering and nitrogen and carbon metabolic pathways. A mathematical model that describes regulatory dynamics of key flowering-time genes unraveled differential responses to environmental signals between species.

Symposium III

October 14 (Sat) 14:30 – 17:20

Bio-logging and big data: automated simultaneous tracking of many individuals and its impact on field ecology

Organizers: Eiiti Kasuya (Kyushu Univ.) and colleagues

Many of unsolved questions in ecology can be answered if spatial positions of animal individuals that comprise a population or other types of groups are recorded continuously in the field. The continuous recording of the position of individuals in the field also help to tackle themes that have not been studied because of difficulty of obtaining relevant data in the field. The continuous recording in the field, however, has been “a dream of field ecologists” in most cases. Recent advances of technology, including sensor arrays for sound or visual image and miniature radio frequency tags (RFID), begin to enable the continuous recording of the position of individuals in the field. These techniques provide a huge quantity of data including simultaneous and continuous recording of spatial positions of many individuals at the short interval of time. Identities of the individuals can be recognized in these data. The data will readily show the personality of individuals, interactions among them, and their consequences at the level of populations. Possible impacts of applications of these techniques in ecology in the field will be discussed.

Program:

14:30 – 14:45	[S3-1] Eiiti Kasuya
14:45 – 15:30	[S3-2] Shizuko Hiryu
15:30 – 15:40	Break
15:40 – 16:30	[S3-3] Henrik Baktoft
16:30 – 17:15	[S3-4] Fumiaki Y. Nomano
17:15 – 17:20	Discussion

[S3-1]

Introduction: impact of recent advances in technology on ecology in the field

Eiiti Kasuya

Department of Biology, Kyushu University, Japan

Knowing spatial positions of animal individuals in the field is a prerequisite to answer many questions in field ecology. When performing this task by one or small number of human observers, which has been usually the case in past studies, this is often tiring and is a main limiting factor to obtain sufficient data to solve the questions. Recent advances in technology offer opportunities to overcome this by enabling the recording of automated determination of positions of many individuals. These advances can give a major impact on ecological studies by solving previously intractable problems and solving questions in higher precision by obtaining big data.

[S3-2]

**Tracking of 3D flight paths and ultrasounds
—Laboratory and field studies on acoustic navigation of bats—**

Shizuko Hiryu*, Emyo Fujioka

Faculty of Life and Medical Sciences, Doshisha University, Japan

To investigate sophisticated sonar system of bats, we developed several measurement techniques to track 3D flight path and ultrasound broadcasts of individual bats according to their navigation scale. Especially, the most advanced performance of echolocation can be seen during foraging in the field. Using the microphone array system, we revealed that the aerial foraging bats controlled their flight and sonar directions to plan future suitable approach paths for consecutive capturing. Furthermore, by surrounding the entire patch with the arrays, we also acoustically determined the foraging duration, the number, the timing and 3D position of prey capture by individual bat in the field. These information will bring a novel perspective for understanding ecology of bat's acoustic navigation.

[S3-3]

Fish telemetry and big data—applications, challenges and prospects

Henrik Baktoft

National Institute for Aquatic Resources, Technical University of Denmark, Denmark

Field studies of spatial behaviour of fish is inherently challenging due to the difficulties of observing the fish in their natural habitat. To overcome this, several telemetry techniques have been developed and used to study fish movement behaviour during the last decades. These range from simple presence/absence to continuous monitoring of tagged individuals. I will give an introduction to fish telemetry with focus on acoustic positional telemetry using hydrophone arrays. This methodology enables researchers to obtain sub-meter accuracy positioning of many tagged fish (and other aquatic animals) in near real-time. While this method holds great promises for answering ecological questions, its use entails challenges in both field application and subsequent data analyses and statistics. Examples of applications, challenges and potential for future studies will be presented.

[S3-4]

Decoding animal society at the central place: a case study in a cooperative breeder

Fumiaki Y. Nomano

Graduate University for Advanced Studies, Japan

Members of cooperatively breeding groups engage in a range of collective activities. Key group activities in cooperatively breeding societies are not necessarily accessible by conventional observation techniques. Offspring provisioning is the primary helping behaviour provided by non-breeding members in chestnut-crowned babblers, *Pomatostomus ruficeps*, but is not easy to quantify. The difficulty was overcome by the PIT-tag decoder that electronically detects ID tags at the nest entrance. This system is increasingly used in other species and has a potential to further expand the scope for studying group activities. I will present the data obtained from the PIT-tag system that have implications for fitness benefits of provisioning by non-breeders and communal roosting in *P. ruficeps*.

Symposium IV

October 15 (Sun) 9:30 – 12:30

Is adaptation a harsh mistress of diversity? —adaptive and non-adaptive causes of radiation—

Organizers: Kei Matsubayashi (Kyushu Univ.), Ryo Yamaguchi (Tokyo Metro. Univ.)

Biological diversification sometimes includes a pattern of rapid lineage splitting. This ‘radiation’ is an arena to generate novel species, and further phylogenetic cluster. Radiation accompanied with ecological diversification, so called ‘adaptive radiation’ has been a central issue in evolutionary biology. In the symposium, speakers provide various evidences of adaptive and non-adaptive radiations from theoretical and empirical studies, especially focusing on the ecological and genetic mechanisms. Finally, we will argue about the delimitation of the mechanism of adaptive radiation against non-adaptive radiation, which provides novel insight into rapid and complicated biological diversification.

Program:

9:30 – 9:40	Overview (Ryo Yamaguchi)
9:40 – 10:10	[S4-1] Ryo Yamaguchi
10:10 – 10:40	[S4-2] Kotaro Kagawa
10:40 – 11:10	[S4-3] Joana Meier
11:10 – 11:40	[S4-4] Satoshi Chiba
11:40 – 12:10	[S4-5] Kei Matsubayashi
12:10 – 12:30	Closing remarks (Kei Matsubayashi)

[S4-1]

Mathematical modeling of an evolutionary radiation and its patterns caused by non-adaptive processes

Ryo Yamaguchi

Department of Biological Sciences, Tokyo Metropolitan University, Japan

Adaptive radiation has been defined as a pattern of species diversification in which a lineage of species rapidly occupies a diversity of ecological niches. Alternatively, reproductive isolation accumulates slowly as a result of non-adaptive processes such as genetic incompatibility, and ecological differentiation happens later. Many radiations are likely to contain elements of both adaptive and non-adaptive diversification. Our current study uses a mathematical model, which derives predictions about recurrent speciation based on geographic isolation, to explore the importance of non-adaptive process in the radiation. Similar adaptive patterns can be reproduced in non-adaptive radiations. We discuss how the pattern of radiation is affected by the manner in which populations diverge.

[S4-2]

Theoretical studies of adaptive radiation caused through hybridization

Kotaro Kagawa

Swiss Federal Institute of Aquatic Science and Technology (EAWAG), Switzerland

Understanding the mechanisms of rapid adaptive radiation has been a central problem of evolutionary ecology. Recently, there is a growing recognition that interspecific hybridization can facilitate adaptive radiation by creating novel phenotypes. However, the plausibility of this hypothesis remains unclear because hybridization can also negate pre-existing species richness. Here, I theoretically investigated whether and under what conditions hybridization promotes adaptive radiation by using an individual-based model to simulate genome evolution following hybridization between two allopatrically evolved lineages. Simulation results demonstrate that hybridization can promote adaptive radiation and shed light on conditions where hybridization contributes to evolutionary diversification.

[S4-3]

**Adaptive radiation fueled by hybridization—Genomic insights
from Lake Victoria cichlid fishes**

Joana Meier^{1,2}

¹Institute of Ecology & Evolution, University of Bern, Switzerland

²Swiss Federal Institute of Aquatic Science and Technology (EAWAG), Switzerland

The African Lake Victoria region harbors 700 cichlid fish species that evolved through adaptive radiation in multiple lakes in only 150,000 years. Recently, we showed that they all originate from a hybrid swarm between two divergent cichlid lineages. This hybridization event provided functional genetic polymorphisms that subsequently recombined and sorted into many new species. With over 400 sequenced genomes, we show that cichlids mostly cluster by lake suggesting independent adaptive radiations. Within Lake Victoria, the genomic structure generally reflects ecological similarity and hybridization played important roles in the emergence of new species and entire guilds.

[S4-4]

Adaptive and non-adaptive radiation in island snails

Satoshi Chiba

CNEAS, Tohoku University, Japan

Evolutionary radiation often gives rise to ecologically and morphologically similar species that are distributed allopatrically in a mosaic pattern of numerous congeneric species. Examples of such diversification, termed non-adaptive radiation, commonly occur on oceanic islands as well as in continental regions. Endemic land snails of the oceanic Ogasawara Islands provide excellent models to address the cause of different radiation patterns. I provide examples of adaptive and non-adaptive radiation in endemic snails of Ogasawara. By comparing ecology, morphology and habitat use between the island endemics and their mainland relatives, I suggest that phylogenetic constraint play a role in the generation of different patterns of radiation.

[S4-5]

Adaptive radiation and evolution of isolation barriers caused by specialization to different host plants in a phytophagous ladybird beetle

Kei Matsubayashi

Faculty of Arts and Science, Kyushu University, Japan

Adaptive radiation is rapid diversification in a lineage correlating to ecological divergences. Nonetheless of the impact on biodiversity, the ecological and genetic mechanism of such rapid diversification remains unclear. To elucidate evolutionary causes of adaptive radiation, we detected the isolating barriers involved in the earliest stage of adaptive radiation of a phytophagous ladybird beetle, *Henosepilachna diekei*. Beetle populations collected from 4 host plant species showed highly specialized food acceptance and survivorship on the original host plant irrespective to the phylogenetic relationships. As these populations exhibited relatively weak isolating barrier other than host plant uses, we suggest that divergent host adaptation directly causes adaptive radiation in the species.

Award lecture

October 13 (Fri) 17:40 – 18:30

Sex as a maintenance mechanism of biodiversity

Kazuya Kobayashi

Hokkaido Forest Research Station, Field Science Education and Research Center,
Kyoto University, Japan

Biodiversity has long been a source of wonder and scientific curiosity. Thus, determining the factors that sustain biodiversity is one of the core challenges of ecology. Here I show that the mating competition can be the key to maintaining biodiversity. Under high density condition, natural selection favors traits that increases mating success even at the expense of population growth rate. At low density, such negative effect on the growth rate is mitigated due to less competition over mating. This negative density-dependent effect on the growth rate allows co-occurrence of competitive species. Models incorporating this mechanism demonstrate that hundreds of species can co-occur over 10,000 generations, and reproduces the species rank abundance distributions observed in nature.

Poster sessions

October 14 (Sat) 12:30 – 14:20

October 15 (Sun) 12:30 – 14:30

外国人の参加者が多いことから、シンポジウムの発表はすべて英語にします。ポスター発表についても英文もしくは日英併記での作成をお願いします。

ポスターボードは 14 日（土）の 9:00 までに準備されます。ポスターは 14 日の 9:30 までに貼ってください。また 15 日（日）の 14:30 には取り外してください。

ポスター発表の説明時間は、ポスター番号によって 2 つに分かれています。

奇数番号のポスター：14 日（土）12:30 – 14:20

偶数番号のポスター：15 日（日）12:30 – 14:30

ポスターボードのサイズは横 90cm × 縦 210cm です。

All posters must be written either in English or in both Japanese and English, for the sake of foreign participants.

Poster boards will be ready before 9:00 of the 14th (Sat). Poster presenters should display their posters before 9:30 on the 14th, and remove them by 14:30 on the 15th (Sun).

Presentation time:

Odd numbered posters: 12:30 – 14:20 of the 14th (Sat)

Even numbered posters: 12:30 – 14:20 of the 15th (Sun)

Size of a poster board will be 90 cm wide and 210 cm high.

[P01]

Evolution of male mate choice for conspecific females in *Mnais* damselflies

Yoshitaka Tsubaki
Kyoto University

Two *Mnais* damselflies distribute in Japan: *M. costalis* exists in allopatric in northern area while sympatric with *M. pruinosa* in southern area of Japan. Males of *M. costalis* show wing color polymorphism in allopatry (orange-winged territorial males and clear-winged non-territorial males), while this species often lose clear-winged male (or significantly decreased frequency of clear-winged male) in sympatry. Moreover, females of this species are monomorphically clear-winged in allopatry while they often show pigmented (amber colored) wings (some populations show wing-color polymorphism) in sympatry. Common garden experiments were conducted on mating behavior of *Mnais* damselflies to test the evolution of male mate choice for conspecific females in sympatry.

[P02]

Tadpoles intensify cannibalism of future predator, but this means the coming of predation threat

Kunio Takatsu^{1*}, Osamu Kishida²
¹Shizuoka University
²Hokkaido University

Because predators can consume large prey after growing into enough large size (i.e., recruitment into larger predatory stage), investigating what factors affect the predator recruitment is fruitful to better understand dynamic nature of interaction between growing predator and prey. Our experiment using *Hynobius retardatus* salamander larvae (growing predator) and *Rana pirica* frog tadpoles (large prey) showed that frog tadpoles highly enhanced growth of salamanders by intensifying cannibalism among salamanders at hatchling stage and consequently, the frog tadpoles were exposed to predation pressure by the well-grown salamanders in the subsequent period. The result indicates that future large prey itself can be a factor increasing likelihood of recruitment of its large predator.

[P03]

**Mutual wing eating in the mating pair of the subsocial wood-feeding cockroach:
Conditions where they accept or refuse attempts of the wing eating by the partner**

Haruka Osaki*, Eiiti Kasuya
Kyushu University

Several wood-feeding cockroaches make biparental care. A female and a male of them eat their wings each other when they make a pair. In species with the biparental care, giving damage on the body of the partner of a pair may be maladaptive because the damage may reduce the ability of parental care by the partner. We recorded the wing eating behavior of *Salganea taiwanensis ryukyuanus* by video cameras in the laboratory to describe details of the behavior. They showed behaviors of acceptance and refusal of attempts of eating their wings by their partner: they leaned the body to the partner or wagged the body violently. We analyzed the videos with several hypotheses on these behaviors to clarify the condition that the acceptance or refusal occurs.

[P04]

Comparison of echolocation behavior of two bat species, *Rhinolophus ferrumequinum* Nippon and *Miniopterus fuliginosus*, while flying with conspecifics

Toma Tatsumi*, Takara Miyamoto, Yasufumi Yamada,
Kohta I. Kobayasi, Shizuko Hiryu
Doshisha University

Echolocating bats are divided into two types according to time-frequency structure of ultrasound pulses, which is thought to reflect the adaptations to the constraints imposed by their habitat in context of echolocation. In this study, we compared the echolocation behavior of two bat species with different type of ultrasounds, *Rhinolophus ferrumequinum* Nippon and *Miniopterus fuliginosus* while flying by pairs in a chamber. We found that *R. f.* emitted pulses toward both their own flight direction and the other bat whereas *M. f.* aimed only toward their own flight direction. *M. f.* shortened interpulse interval, changing the frequencies of the pulses when the individual distance was closer. Our findings suggest that these bat species have different echolocation strategies during group flight.

[P05]

Night Heron rises: resolving conflicts between residents and heron colonies in urban areas

Miyuki Mashiko^{1*}, Yukihiro Toquenaga²

¹National Institute for Land and Infrastructure Management

²University of Tsukuba

Heron colonies are often formed in residential areas in Japan. Grey Herons lead such colony formation, and we used this property to move a colony causing a conflict with residents over disgusting smell and noises. For reducing colony site fidelity, we removed nest materials of Grey Herons and repelled coming herons with explosive noises allowing minimum reduction of standing trees. As a result, the colony was abandoned but three new ones were formed nearby. Only one of them included Grey Herons and the other two included Black-crowned Night Herons that have lead colony formation before Grey Heron invasion in the Kanto Plain. Our removal act waked the potential habit of Night Herons for colony formation, which should be seriously concerned while resolving those conflicts.

[P06]

Searching strategy when a mating pair gets separated in termites

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Kyoto University

Animal movement is shaped by its efficiency to encounter searching objects. In mate search, both males and females can mutually optimize their movement patterns. Here we show that termite dealates show sexually dimorphic movements context-dependently to maximize their encounter rates. Before encounters, both males and females moved actively and diffusively. On the other hand, when they are separated after encounters, termites showed distinct sexually dimorphic movements, where females stopped and males moved around thoroughly. Computer simulations demonstrated that such sexually dimorphic movements can be optimal for each other when a mate is near but its location is uncertain. Our results emphasize the importance of considering mutual optimization in random search problem.

[P07]

Same-sex sexual behavior mitigates male–male competition in the field cricket

Takashi Kuriwada
Kagoshima University

Males compete against rival males to increase their mating success. Because male-male contest is risky behavior, the aggressiveness is expected to be mitigated depending on external and internal factors. When rival males are relatives, reduced aggressiveness to the males leads to inclusive fitness benefits. To mitigate male-male contest, same-sex sexual behavior may be used. I investigated how relatedness affect the male-male contest and same-sex sexual behavior in the cricket *Teleogryllus occipitalis*. Relatedness had no significant effect on the male-male contest and occurrence of the same-sex sexual behavior. However, when same-sex sexual behavior was observed, the intensity of male–male contest was weakened. Same-sex sexual behavior has an adaptive significance by mitigating risky behavior.

[P08]

Automatic tracking reveals temporal organization in ant colony

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Most organisms exhibit a periodic activity of about 24 hours. This circadian rhythm can be entrained by various kinds of social interactions. In social insects, workers perform different tasks to achieve a highly organized colony. However, how ant behaviors are organized by various social interactions remains unknown. In this study, we collected time series data on the movement of individual ants in a colony using an automatic tracking system (Bug tag) in *Diacamma* sp. In solitary condition, most ants showed circadian rhythms. However, in colony condition (i.e. under social interactions), they exhibited clearly different behaviors; all workers show no circadian rhythms. We will discuss temporal organization of colony from the perspective of social interaction and related behavioral changes.

[P09]

Path control of group flying bats for collision avoidance

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¹Doshisya University

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Bats have a highly developed sonar system which can help them fly in complex situations such as flying with other conspecifics. In this study, we investigated how the group flying bats adapt their flight paths in an experimental chamber. When a bat joined a group flight with circular path, it tended to follow its own flight altitude and direction with other individuals. We found that “the phase difference” between successive bats was kept stable while flying on the same circular path. In other cases, when the bat rotated in opposite directions, it flew at lower altitude than the others to separate flight distance. These results suggest that the mutual control of the altitude and the phase is important for group flight in a restricted space.

[P10]

Quantitative observation of numbers of flashings by fireflies *Luciola parvula*

Tetsuro Konishi

Chubu University

A new systematic method for quantitatively observing numbers of flashings of fireflies is introduced. The method is based on capturing images by digital still cameras and image processing by softwares. The method is successfully applied to flashings of *Luciola parvula*, a kind of firefly, and time series for their flashing activity are obtained. Examples of such time series confirm two interesting properties, both of which are known by visual observations. First, the flashing activity varies greatly for intervals of minutes or several tens of minutes. Second, main part of the activity begins at midnight. Implication of this method is discussed.

[P11]

Minimalized Boids: Can bird-brained organisms swarm together?

Yukihiko Toquenaga
University of Tsukuba

As shown in impressive swarms of starlings, swarming organisms show specific and functional adhesiveness. Boid algorithm coined by Reynolds (1987) and its matrix expression by Couzin et al. (2002) have been used for implementing flocking birds, schooling fish and swarming insects and artificial materials. Here I propose another novel algorithm by blunting sensors of swarming organisms: each organism can only detect signal strength emitted from other organisms. No direction, no velocity, no distance of other organisms in matrix expressions are required for making adhesive flocks, schools, and swarms. This algorithm can be applied to realize swarming of lightweight robots that have limited capability of sensors and computational abilities as well as primitive natural organisms.

[P12]

**Irreversibility of social organization arises from cooperation cost
in the social amoeba**

Yuka Shirokawa*, Masakazu Shimada, Satoshi Sawai
University of Tokyo

The social amoeba switch between nutrient-rich solitary growth and starved adhesive social state involving spores and dead stalk that altruistically supports spores. Solitary transition during social differentiation is suppressed by social interaction. Fed differentiating cells was localized in stalk position because of relative adherence weakness. From our empirical result, we considered sequential cell fate determination by adherence and evolution of adhesion degradation. To investigate robustness of social state, we hypothesized a suppression-breaking mutant, Withdrawer, which has individual benefit but abandons social traits. The model showed Withdrawer could not invade because the intermediates becoming dead stalk fell into a fitness valley before reverting to adaptive solitary state.

[P13]

Sinistral snails warn a predator snake

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Southeast Asian snail-eating snakes specialize in predation on dextral majority in shelled snails by soft-body extraction. Snails have countered the snakes' dextral-predation by recurrent coil reversal, which instantaneously generates a sinistral species because interchiral mating is rarely possible. We found that *Pareas carinatus* living with abundant sinistrals avoids approaching or striking at a sinistral that is more costly to handle than a dextral. Whenever it strikes, however, the snake succeeds in predation by handling dextral and sinistral prey in reverse. This indicates that the snake recognizes prey handedness. The novel warning, instead of sheltering, effect of sinistrality benefitting both predators and prey could further accelerate single-gene ecological speciation in snails.

[P14]

**Evolution of sexual difference in the induction of pupal diapause
in temperate flesh flies**

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Multivoltine flesh flies overwinter in pupal diapause induced by a short day photoperiod. The overwintering generation adults show a male-biased sex ratio despite the 1:1 primary sex ratio. The bias is due to the longer critical daylength in males than in females. This phenomenon has been explained as an outcome of selection pressure to minimize the diapause duration in females subject to harmful effects of diapause. However, it explains nothing as to why males enter diapause earlier than females. We constructed a Leslie matrix and considered evolutionary stable diapause rate of males with the reproductive values. The result revealed that sexual differences in the critical daylength depends mainly on the degree of generation overlap in males and not on the deleterious effects of diapause.

[P15]

Advantage for the sex changer who retains the gonad of the nonfunctional sex

Sachi Yamaguchi^{1*}, Yoh Iwasa²

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²Kyushu University

Among coral fish that exhibit bidirectional sex change, some retain the gonad of the nonfunctional sex as well as the current sex, while others exhibit the gonad of the current sex only. A game-theoretic model was developed to investigate under what conditions we might expect a bidirectional sex changer should keep the gonad of the nonfunctional sex. The frequency of sex change opportunity, the time required to reconstruct the gonad, and the maintenance cost all affect the evolution of gonad retention. A quantitative parameterization of the model for well-studied species concluded that the cost for a male to keep a female gonad must be much smaller than the cost for a female to retain a male gonad.

[P16]

Flower constancy by pollinators drives ecological speciation of flowering plants

Gaku Takimoto

University of Tokyo

Pollinator's flower constancy may mediate assortative mating and can cause speciation in angiosperm. To test this idea theoretically, we develop a population genetic model and examine whether and what degree of flower constancy can cause ecological speciation of flowering plants when subjected to divergent natural selection from the growth environment. We find that speciation is facilitated when pollinator's flower constancy to plants adapted to the local growth environment is stronger than constancy to locally-maladapted plants. Moreover, realistic levels of flower constancy can cause speciation. These results suggest that flower constancy can play key roles in angiosperm speciation when acting jointly with other agents of natural selection.

[P17]

**Stability analysis of ratio-dependent community dynamic model
of Batesian mimicry**

Hayato Kato^{*}, Takenori Takada
Hokkaido University

Batesian mimicry has been researched for a long time, but there are only a few population dynamic models on the mimicry. Yamauchi (1993) proposed a mathematical model on the dynamics of model- and mimicry-species where mimicry effect was regarded as ratio-dependent. This is not only a model on mimicry, but also one of the basic models that have both density- and ratio-dependent effects. Actually, this model includes ratio-dependent predator-prey model of Haque (2009). While Yamauchi and Haque provided several theorems about the behavior of solutions and conducted numerical calculations, the stability and bifurcation analysis are not completed yet. We analyzed this model in detail. In some cases, the system showed bistability of equilibria of coexistence and mimicry alone.

[P18]

Predator character divergence driven by prey diversity under character release

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²Kyoto University

Body size is related to various fitness components, but relative importance of different selection pressures in body size are seldom evaluated. In *Carabus japonicus*, of which larvae prey on earthworms, adult body size is related to presence/absence of larger congener and habitat temperature. In sympatry, *C. japonicus* exhibits smaller body sizes facilitating avoidance of interspecific mating, but in allopatry it shows a marked size variation unrelated to temperature. In the absence of the congener, the body size was larger where larger prey occurred. This pattern is adaptive because larger females produce larger larvae, which can subdue larger prey. With experimental and field evidences, we demonstrate how conflicting selection pressures have played roles in the predator size variation.

[P19]

Loss of circadian rhythm in population of *Tribolium castaneum* reared long-term

Takahisa Miyatake*, Kentarou Matsumura
Okayama University

Locomotor activities and circadian rhythms of long-reared (more than 35 years) and wild populations of *Tribolium castaneum* (Coleoptera: Insect) were compared. We found significantly higher percentages of arrhythmic individuals in the long-reared population compared to the population caught in the wild (Okayama Prefecture). Only males were compared because no difference between the sexes was found in the percentage of arrhythmic beetles. Next, comparison of the circadian rhythms of wild and long-reared beetle populations showed no significant difference between the populations. The result suggests that the circadian rhythm in *T. castaneum* has been lost during long-rearing under an artificial condition. We will discuss arrhythmicity in organisms.

[P20]

Do pathogens promote invasion of alien species?

Kengo Nagata*, Yoh Iwasa
Kyushu University

Invasion of a foreign species can be promoted by being accompanied by a pathogen that infects both invaders and residents, if the pathogen was absent before the invasion. This is called disease-mediated invasion (DMI). In this study, we established mathematical model of the competition between the introduced frogs: *Polypedates leucomystax* and the native frogs of Japan: *Rhacophorus viridis*, taking into consideration the influence of the nematode: *Raillietnema rhacophori* discovered from *P. leucomystax*. As a result of analysis, we found that there exists an intermediate level of virulence that favor the invasion of alien species and there are cases where coexistence conditions do not exist.

[P21]

Population genetic model on three alleles at the same locus on X-chromosome for the colour vision polymorphism in the New World monkeys

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Colour vision is an important feature of primates. In New World monkeys, 2–6 alleles coding for different opsins are observed in a locus on the X-chromosome; coupled with an autosomal opsin, this genetic system provides all males dichromatic vision (but multiple types) while it gives females di- or trichromatic vision. Overdominance in females is thought to keep the allelic polymorphism, but no modelling study has focused on this specific topic. We developed an X-chromosomal n -allele genetic model assuming an infinite population. In the case of $n = 3$, a biologically feasible tri-allelic equilibrium is found. However, comparison between the model outcomes and field data using Bayesian statistics suggests that overdominance, by itself, can hardly explain the observed allelic frequencies.

[P22]

Genetic structure and potential environmental determinants of local genetic diversity in Japanese honeybees (*Apis cerana japonica*)

Teruyoshi Nagamitsu

Forestry and Forest Products Research Institute

Declines in honeybee populations have been a recent concern, and environmental factors may be responsible. We estimated the genetic structure of *Apis cerana japonica*, and environmental determinants of local genetic diversity in nuclear microsatellite genotypes of fathers and mothers, inferred from workers collected at 139 sites. The genotypes showed weak isolation by distance and negligible genetic structure. The local genetic diversity was high in central Japan, decreasing toward the peripheries, and depended on the climate and land use characteristics of the sites. The findings suggest that *A. cerana japonica* forms a single population connected by gene flow in its main distributional range, and that climate and landscape properties potentially affect its local genetic diversity.

[P23]

The genetic causes for albinisms in the migratory and desert locusts

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¹National Agriculture and Food Research Organization

²Shimane University

Our laboratory has maintained several genetic mutants including an albino *Locusta migratoria* mutant and an albino *S. gregaria* laboratory strain. We investigate the causes for albinisms for these locusts. A neuropeptide, corazonin (Crz), is responsible for darkening in these locusts. Sequencing analysis showed that the albino *L. migratoria* and *S. gregaria* have a defect in Crz and Crz receptor genes, respectively. RNAi-mediated knockdown of these genes markedly reduces the intensity of black patterning in the treated nymphs. The pattern of deletion in LmCRZ of the albino suggests that the mutation was generated by the mutagenic DNA double-strand break repair. The locusts in the field might suffer from DNA double-strand breaking and possibly carry many mutations in their genome.

[P24]

**Extinction driven by reproductive interference between native species in field
—a case study of two spined loaches—**

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²Ishikawa Prefectural University

Studies of reproductive interference in the field have been limited to between invasive species and native species. The biggest reason is because they had already experienced interspecific interactions including reproductive interference in their evolutionary history. Artificial environmental changes, however, can trigger the reproductive interference between native species, which are not interacting in the present day, and it may drive to population extinction. In this study, we surveyed the spatio-temporal dynamics of parents and juveniles of two native spined loaches (*Cobitis magnostrata* and *C. minamorii oumiensis*). From these results, we discussed effects of the reproductive interference and it reflected current distribution of two native spined loaches.

[P25]

**Reproductive interference can explain host plant partitioning
on two oriental fruit flies**

Daisuque Kitano^{1*}, Nobuyuki Fujii¹, Sujiono², Shigemasa Yamaue¹,
Tasuku Kitamura³, Atsushi Honma¹, Morio Tsukada³, Takayoshi Nishida¹,
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Closely related two oriental fruit flies, *Bactrocera carambolae* and *B. dorsalis* (Diptera: Tephritidae), substantially partition host plants but the reason has never been understood. In this study, we tested the sexual interaction between species, i.e. reproductive interference, as a driving factor of the host partitioning. We observed reproductive behaviors and the effect of the coexistence with heterospecific individuals on reproductive success of females. Results showed that *B. dorsalis* males did not discriminate species of females in mating and this decreased the females' mating success of *B. carambolae* only. These suggested that *B. dorsalis* superior in the reproductive interference can occupy a high-quality host plant and inferior *B. carambolae* are forced to use the other.

[P26]

The application of eDNA technique for the monitoring of marine fish species

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Environmental DNA (eDNA) is DNA molecules that organisms shed into the environment. Analysis of eDNA extracted from the environmental samples (e.g. soil and water) enables us (i) detecting species difficult to find, (ii) determining species composition or (iii) evaluating their spatial or temporal variations. In this presentation, we introduce our recent development of eDNA techniques and its applications to marine fish species. Frequent, multi-site eDNA monitoring would in the future provide highly resolved data of marine fish community and its dynamics, which is not only beneficial to the applied ecology related to natural resource management and biodiversity conservation, but also catalyzes rapid growth of population to community ecology as a data-driven science.

[P27]

The density dependent suppression of juvenile growth may destabilize the population under status-dependent strategy

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In salmonids, some juveniles migrate to the ocean and come back to their natal river (migrant tactic), whereas others mature in the river without migration (resident tactic). There is a trend that larger one becomes a resident. This trend is explained by the status-dependent-strategy model (SDS), in which fitness functions of both tactics are functions of status, and the status where both fitness functions intersect is a threshold at which tactic changes. A density dependence of growth is documented. We incorporate the growth suppression of juveniles into the SDS, and explore how it affects the dynamics of alternative tactics and the evolution of threshold size. We demonstrate that the growth suppression can destabilize the population and cause bistability of evolutionary outcomes.

[P28]

The relationship between seasonal migration and subpopulation structure of the sika deer population in Hokkaido

Shoko Morimoto^{*}, Takashi Saitoh

Hokkaido University

Prior analysis of microsatellite DNA showed that the sika deer population in Hokkaido consisted of two subpopulations. The sika deer has a biological feature of seasonal migration. It was reported that the distance of seasonal migratory reached more than 100 km. However, few study investigated the relationship between seasonal migration and subpopulation structure. I added samples collected from Hokkaido in 2016–2017 to samples used in prior researches. I estimated spatial genetic structure of the sika deer population in Hokkaido in summer and winter by using GENELAND based on microsatellite DNA data of summer (Jul.–15 Oct.) sample ($n = 240$) and winter (Jan.–Mar.) sample ($n = 298$). In this poster presentation, I'll consider the relationship between seasonal migration and subpopulation structure.

[P29]

**Analyzing elasticity of Leslie matrix with phenotypic plasticity
in the parasitic wasp, *Anisopteromalus quinarius***

Masakazu Shimada*, Yasuko Nagase, Minoru Kasada
University of Tokyo

From evolutionary demographic point of view, an experimental system with the *Callosobruchus* seed beetle and two closely related parasitoid species, *Anisopteromalus quinarius* and *A. calandrae* is very interesting to analyze elasticity of the Leslie matrix with phenotypic plasticity. *A. quinarius* shows great phenotypic plasticity of life history parameters, provided with either none, honey only or honey + collagen peptide. On the other hand, *A. calandrae* does not have any plasticity of life history parameters because they suck host with straw they made using the ovipositor. Counting their daily-based fecundities and daily-based survival rates, integrating the two life history parameters to the Leslie projection matrices, and we estimated elasticity structures of the two species.

[P30]

Conditions of the prevailing slope ($1 < b < 2$) in the temporal Taylor's law

Takashi Saitoh
Hokkaido University

Taylor's law (TL) is an empirical rule describing the relationship between the variance and the mean of population density: $\log_{10}(\text{variance}) = \log_{10}(a) + b \times \log_{10}(\text{mean})$. I used a second-order autoregressive model of population dynamics to analyze the temporal TL of gray-sided vole populations. Extensive simulations using various combinations of model parameters for environmental variability and density dependence demonstrated that sustainable populations could satisfy the form of TL. When environmental variability was low and density dependence was intermediate, simulated time series showed higher probabilities for $1 < b < 2$. In general, slopes became steeper with the increase of environmental variability and with the decrease of density dependence coefficients.

[P31]

Variation of the upper molar form that is a morphological identification feature for *Myodes rex* and *Myodes rufocanus*

Arisa Fujiwara*, Takashi Saitoh
Hokkaido University

Myodes rex has similar morphology and ecology to those of *Myodes rufocanus*, but they can be distinguishable based on enamel forms of the upper 3rd molar. *M. rufocanus* and *M. rex* has a simple and complex form, respectively. In addition, *M. rufocanus* is distributed throughout Hokkaido, whereas *M. rex* has been found in limited areas of Hokkaido (Nakara et al. 2015). However, the distribution survey of *M. rex* has not been carried out extensively. The object is to discover new distribution areas. I captured 33 voles in northern Hokkaido. Based on enamel forms, 6 samples were identified as *M. rex*, while 27 as *M. rufocanus*. However, 13 of 27 *M. rufocanus* showed an intermediate feature of the enamel form. I will discuss the appearance reason in this form and a relationship with their distribution.

[P32]

How each life history parameter affects demography and elasticity in tree- and ground-squirrel populations

Iori Tanio*, Takenori Takada
Hokkaido University

Various impacts on wild animals by human activities, such as degradation of habitat and competition with alien species, are being problems. To solve these problems, grasping the basic knowledge at the population-level is very important. Squirrels are distributed throughout the world and some species have decreased in number. However, how each factor strongly affects their population dynamics are still little known. Matrix population models (MPMs) are the widely used demographic tools to examine population characteristics. We examine (1) reproductive value, and sensitivity and elasticity of population growth rate by each parameter, (2) fast-slow continuum of tree- and ground-squirrels to know the difference in ecological characteristics by using MPMs data in open access database, COMADRE.

[P33]

Does the development of insecticide resistance affect the virulence to resistant rice varieties in the brown planthopper, *Nilaparvata lugens*?

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Kyushu Okinawa Agricultural Research Center, NARO

The brown planthopper *Nilaparvata lugens* is the most important pest on rice throughout Asia. We compared the virulence to five resistant rice varieties, Mudgo, ASD7, Rathu Heenati, Babawee, and Balamawee, between two imidacloprid (a neonicotinoid insecticide) resistant strains (Res-PH and Res-VN) and two control strains (Con-PH and Con-VN). Survival rates on Mudgo and ASD7 in two resistant strains were similar to those in two control strains. However, survival rates and body weights of survived insects on Rathu Heenati, Babawee and Balamawee in two resistant strains were lower than those in two control strains, respectively. These results suggest that the development of imidacloprid resistance might affect some physiological performances on three resistant rice varieties.

[P34]

**Is global eradication of the pest possible if sterile insects are locally released?
An individual-based model**

Yusuke Ikegawa
Ryukyu Sankei Co. Ltd.

Sterile insect technique (SIT) is one of pest control methods by releasing sterilized pests to wild pest populations. As the entire target region becomes too large, efficiency of pest control reduces because abundance of released insects per unit area is diluted. Therefore, SIT often targets spatially limited areas, and after the pest is locally eradicated there, then shift the adjacent new areas. Repeating this process, one aims to eradicate the pest from the entire target region. However, immigrants of pests from adjacent non-released areas may interrupt local eradication of pests in the released area. In this study, I constructed multi-patch individual-based model comprised of pests and sterile insects, and examined whether sequential local releases can attain regional eradication.

[P35]

**Comparative demography of invasive and native plant populations
based on inter-stage flows of individuals**

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³Institute of Statistical Mathematics

⁴Oregon State University

Several processes likely act to change demographic rates of introduced species and these in turn could cause changes in inter-stage flows of individuals. We compared inter-stage flows of invasive and native plant populations using flow matrices. We obtained projection matrices for native and introduced populations from the COMPADRE plant matrix database. We then derived flow matrices from projection matrices and stable stage distributions. We found that native and introduced populations differed in their demographic flows. This suggests that demographic evolution might have occurred in introduced species after their introduction.

[P36]

**TomboWatch! Entertainment web based gaming system
for the dragonfly survey as a tool of citizen's science**

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²Tottori University

³University of the Ryukyus

We developed a web-application, TomboWatch, which includes an entertainment gaming function to compete dragonfly observations among participants. The user is only required to send an email with the photograph taken by the cellular phone. After receiving the email, the system can recognize who, when and where the photo is taken. We conducted citizens' observation events of dragonflies in seven educational institutes in 2016 and had 338 contributions from 52 participants. Though the number of contributions was not so many as we have expected, there were continuous self-contributions after the events. We hope that the entertainment flavor in our TomboWatch will work properly to enhance the motivation of public contributors.

[P37]

Management of Japanese macaque using Bayesian inference and Monte Carlo simulation

Hiroyuki Hirayama*, Yasutaka Kishimoto, Hironori Seino, Mami Saeki
Wildlife Management Office Inc.

[P38]

Impact of avian collisions caused by wind farms on the population variability of golden eagles

Hiroyuki Matsuda
Yokohama National University

Japanese golden eagles (*Aquila chrysaetos japonica*) are endangered. I evaluate the increment of extinction risk of the eagles' population caused by wind farms. I use an individual-based model that incorporates the carrying capacity, age structure and monogamy. If a wind farm is established in close to eagles' habitat, the mortality rate of juvenile and adult eagles increase. If a habitat in close to eagles' nests is artificially closed as mitigation measures, the carrying capacity decreases. The impact of habitat closure on the extinction risk of eagles is comparable with the impact of avian collisions.

[P39]

Why do we overlook the threat of invasive species? Comparison of tractability to toxic prey toads between original and novel predators

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Hokkaido University

Although *B. japonicus* toad originally distributed in Honshu was introduced into Hokkaido at least 30 years ago, no one has documented impact of the invasive toad. In this year, our team found lethal toxic impact of the larval invasive toad on native amphibian predators, larval *Rana pirica* frog and *Hynobius retardatus* salamander (Muto and Kishida, unpub.). Present study gives one explanation for the question “Why have people overlooked the threat of the invasive toad in Hokkaido?” We experimentally showed that consumption of the toad is not harmful for *Rana ornativentris* and *Hynobius nigrescens* which are original predators for *B. japonicus* toad in Honshu. Adaptation of original interacting partner of an invasive species can give people wrong impression about impact of the invasive species.

[P40]

Invasive clonal plants population management by spatial arrangements of competitors

Shin Fukui
Waseda University

Invasive alien species is of great concern at global scale. For invasive alien plants, clonal reproduction is common feature. The occupation of space is important for clonal plants because their new born individual needs a space to establish. In this study, the management of invasive species by competitive plants was considered using the spatially explicit individual based (SEIB) model. For the plants in the model, the colonization–competition trade-off was assumed. With several spatial arrangements, the population dynamics of invasive species were simulated. The result suggests the spatial arrangements of competitors that is able to prevent the spread of invasive species.

[P41]

Empirical dynamic modelling revealed the area-wide herbivore-induced interaction between the two rice planthoppers

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A tradition says “outbreaks of the white-backed planthopper, *Sogatella furcifera* (*Sf*), produces a rich rice harvest in autumn.” Experimental studies have inferred possible mechanisms underlying this tradition: feeding by *Sf* in early summer increased host resistance against the brown planthopper, *Nilaparvata lugens* (*Nl*), which can be more serious pest. However, the story has been anecdotal so far since the two pests show noisy and complicated dynamics. In this study, we disentangle the effect from noisy but extensive trap catch records over 50 years in Kyushu island with the empirical dynamic modelling (EDM) approach. In summary, the EDM results showed the area-wide negative effect with time-delay of *Sf* on *Nl*, which corresponds to our hypothesis of the herbivore-induced adverse interaction.

[P42]

Dynamic linkages between consumer and resource assemblages in rocky intertidal shore

Yuki Kanamori*, Takashi Noda

Hokkaido University

Focusing on consumer–resource interactions is an effective approach to understand food web dynamics. Especially, how temporal variability differs between adjacent trophic levels is fundamental question. Since species traits, e.g. mobility and generation time, are generally different between assemblages of different trophic levels, the statistical features in community property, such as temporal coefficient of variation and temporal distance decay, are likely to be different between trophic levels and correlate to each other involving time lag. We tested these hypotheses for rocky intertidal molluscan herbivore and sessile algae by analyzing 16-year census data obtained from 25 plots along the Pacific coast of eastern Hokkaido, Japan.

[P43]

Community dynamics of stag beetle in lowland tropical rainforests in Borneo

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The community dynamics of insects show dynamic change even in aseasonal tropical rain forests. To elucidate the underlying mechanisms of community fluctuations, long-term data and a method analyzing nonlinear dynamics are necessary. We analyzed the long-term time series data for stag beetle community dynamics monitored in Lambir National Park in Sarawak, Malaysia. By analyzing the community data using convergent cross mapping in conjunction with rainfall and temperature data, we estimated causal relationship between environmental factors and the community dynamics examined the possibility of change in community dynamics before and after large-scale drought that occurred during monitoring. Our analysis was successful to unravel species specific sensitivities to environmental factors.

[P44]

Do grasshoppers dislike red leaves because they cannot see red color?

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A grasshopper *Atractomorpha lata* does not prefer red or purple leaves to green leaves. Because most insects hardly recognize red color, *A. lata* may be difficult to find red leaves. If this is true, *A. lata* do not eat red leaves not because they dislike red things but because they cannot find red leaves. Then, I investigated color preference of *A. lata* under a condition that they certainly find leaves. I covered the bottom of a container with purple perilla leaves, and another container with green perilla leaves. I put an *A. lata* in the container and measured latent period for *A. lata* of feeding the leaves. *A. lata* took significantly longer time to start feeding when they were on the purple leaves, and this result showed that they hesitated feeding purple leaves even if they noticed them.

[P45]

Different effects of land use change on mutualistic and antagonistic interaction networks

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Land use changes have been reported to affect the structure of species interaction networks, but most previous studies have focused on only a single type of interaction. We compared herbivory and pollination networks in semi-natural grasslands formed in differently managed rice fields (abandoned, managed in the traditional way, intensively managed) to test the prediction that land use change would affect two types of networks in a different way. We found that herbivores in intensively managed sites were less generalized (fed on fewer plant species), while pollination networks showed low generality in abandoned sites. The difference also appeared in the robustness of networks, which highlights the importance of multiple types of interactions in the conservation viewpoints.

[P46]

Estimating geographic structure of species abundance from repeated detection–nondetection observations

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The species abundance distribution, SAD, is a fundamental property of biodiversity. Although SADs have been explored in local-scale studies, knowledge of macro-scale SADs is incomplete: logistical limitations prevent us from examining absolute number of individuals for many species over a large spatial extent. We propose a hierarchical model that estimates species-specific tree density at the regional level, based on replicated species detection–nondetection observations which can be more easily collected within a broad area. By integrating a large dataset of vegetation plots and multiple sources of natural history collection data scattered across the entire region of Japan, we infer SADs over a broad geographical area.

[P47]

Understanding ecosystem using Virtual ECOSYSTEM

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We (including startup company) would like to develop a tool which promotes our understanding “ecological interactions” and “population dynamics” through web application. The web application, called Virtual ECOSYSTEM, accumulates and collects “Big data” simultaneously with progress of our research. For example, population dynamics and player's action like weeding, treatment, and sowing are recorded at our database as time-series dataset. We are going to develop this tool as education supporting tool on “ecology” and “epidemiology”. Please visit our Virtual ECOSYSTEM, <http://ecoepi.jp/>.

[P48]

Population cycles driven by hybrid effect of multiple interaction types

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Population cycle is outstanding widespread phenomenon across many taxa. Antagonistic interaction, such as predation has been well known as a driving force of cycling. However, in nature, diverse types of interaction coexist, leaving an answered question of how multiple interaction types affect to population cycles. Here, using a simple four-species model, we show that the hybrid of major interaction types, antagonism, competition and mutualism, can drive cycling. Stronger interactions easily cause cycling, and even when sub-modules with possible combinations of two interaction types are stabilized by weak interactions, the hybridity of all interaction types cause unstable population oscillations. We propose a novel mechanism of population cycles: hybridity of multiple interaction types.

[P49]

**Bacterial coexistence is determined by initial substrate-user
under competitive conditions**

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To manifest mechanisms of bacterial coexistence, a synthetic microbial ecosystem using phenol-degraders strains P-10 and R2 was constructed under chemostat conditions with phenol as sole carbon and energy source. The population density of P-10 was higher than that of R2 under coexistence. The expression of genes encoding phenol hydroxylase (LmPH) was only observed in P-10, indicating that P-10 did not share phenol as an initial carbon source with R2. These results suggested that R2 would be a scavenger using metabolites from P-10. When R2 became dominant at the lowest phenol-loading rate, the expression of genes encoding LmPH was only observed in R2 and the coexistence was ruined. These results suggested that the metabolic connection is indispensable for coexistence in the ecosystem.

[P50]

Adapting mechanism of bacterial ecosystem to disturbance

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To investigate adapting mechanisms of microbial ecosystem to disturbance, paddy soil-born bacterial communities were enriched by transferred batch cultures with phenol as sole carbon source. These communities were also enriched with phenol and supernatant to disturb bacterial relationships. Bacterial communities were compared with deep sequence techniques targeting 16S rRNA genes, indicating that bacterial community showed succession and then dynamic equilibrium in both cultures. Variation cumulative values of minor populations were higher than those of major populations, reflecting dynamics of bacterial communities. It was unknown why fluctuation of dynamic equilibrium was different but these results suggested that minor population played important role in adapting process to disturbance.

[P51]

Relaxed selection against mutational load in social insect workers facilitates the evolution of their sterility

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Sterility of social insect workers is still an evolutionary conundrum. In eusocial Hymenoptera, workers have an ability of produce their own sons and the realization of the ability should be favored by natural selection. Here we show that the complete sterility of workers can be achieved by accumulation of deleterious mutations attacking genes that are functional only in queens, not in workers and males. Such genes avert mutational load in workers, and worker reproduction allows for accumulation of the queen-specific deleterious mutations. Extensive simulations also revealed that the effectiveness of this mechanism depends on mutation rates.

[P52]

Divergence of male sexual ornaments and female mate preference in speciation driven by joint action of natural and sexual selection

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University of Tokyo

In the speciation model by van Doorn et al. (2009), natural and sexual selection worked in concert to drive the evolution of male's sexual ornaments and female's mate preference, leading to ecological speciation between populations using divergent ecological niches. However, divergence in male ornaments or female preference was precluded in the van Doorn et al.'s model, where speciation ended up daughter species expressing the same ornaments and preference. Here, we construct a model in which ornaments and preference can diverge. We find that ornaments and preference can diverge between daughter species after coordinated evolution between ornaments and preference has reached at certain level. We also investigate the influence of model parameters on whether sexual traits can diverge or not.

[P53]

Superorganismal adaptation explored in the nest size of clonal ants

Naoto Idogawa*, Shigeto Dobata
Kyoto University

The obligatory thelytokous ant *Monomorium triviale* is expected to have some nest-level traits that maximize the productivity of their nests. We focused on the nest size as a candidate trait that would show nest-level adaptation. A partial correlation analysis among nestmate numbers suggested that the number of brood in a nest is mediated by workers, not by queens. The total number of brood produced by a nest was saturated as the worker number increased, indicating the existence of an upper-limit of brood care. Moreover, there were few field nests with worker numbers that exceeded the minimum (or threshold) number resulting in the brood saturation. These observations suggest that a nest reaching the threshold worker number shows fission to maintain efficient reproduction at the nest level.

[P54]

Spatial mosaic of $G \times G$ interactions in trees-bacteria mutualisms: does the mismatch between genetic variation in hosts and partners act as selection?

Shinnosuke Kagiya*, Shunsuke Utsumi
Hokkaido University

In mutualisms, genetic variation in partner species influenced performances of host species. High levels of genetic diversity in mutualistic partners were observed in natural ecosystems. However, a few studies unraveled why high genetic diversity of mutualists was maintained in wild. The benefits of mutualisms were also different among genotypes of hosts. Thus, genetic variation in both partners and hosts may be important to understand coevolution in mutualisms. To test whether $G \times G$ interactions between partners and hosts affect the consequence of mutualisms, we performed common garden experiments, using mutualisms between *Alnus hirsuta* and *Frankia* spp., which are nitrogen-fixing bacteria. As results, $G \times G$ interactions in mutualisms influenced performances of *A. hirsuta*.

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