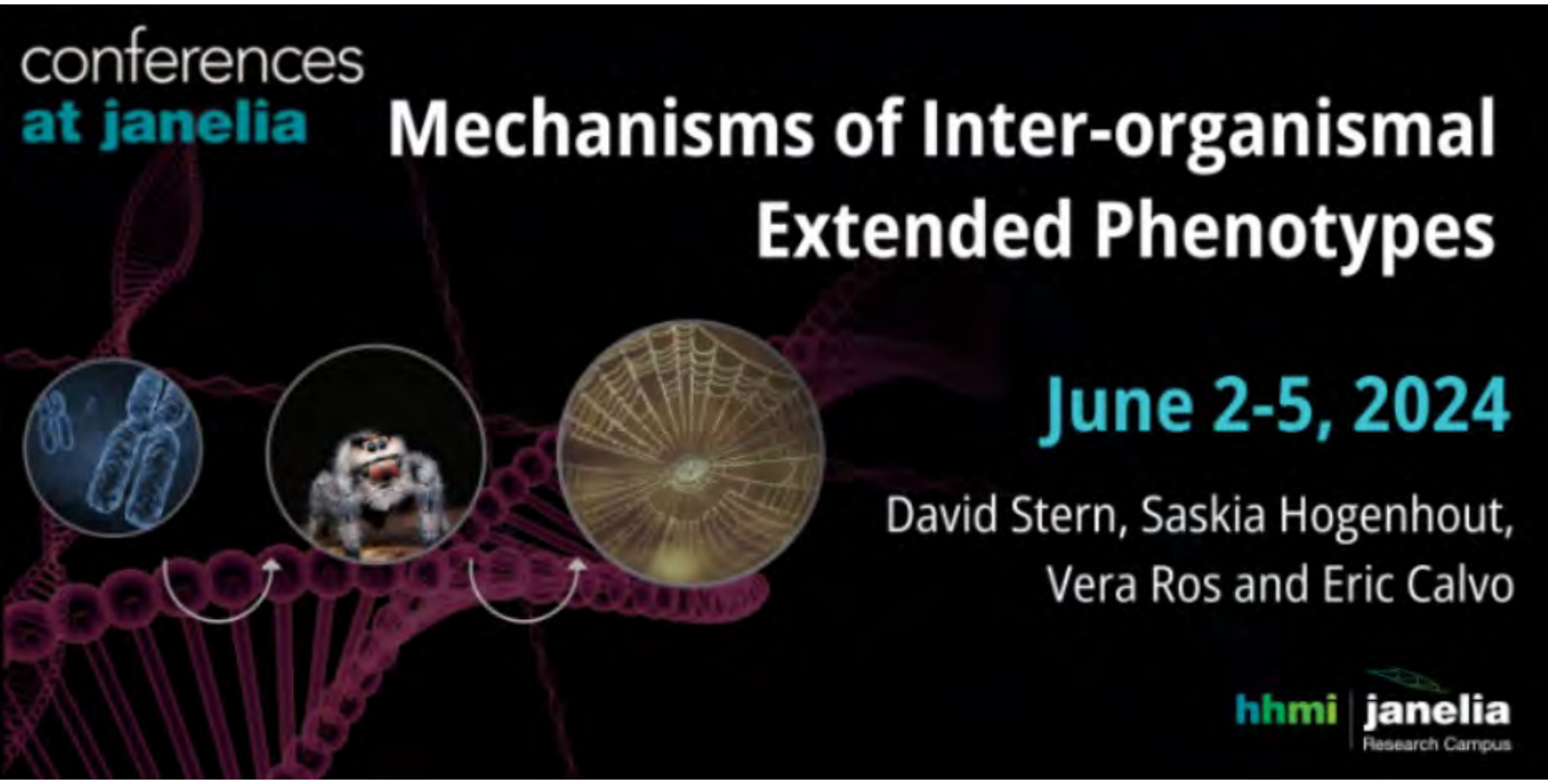
学術変革領域研究 (A)
共進化表現型創発：延長された表現型の分子機構解明
Co-evolutionary Emergence of Extended Phenotypes

CEEP Newsletter

Vol. 1 No. 2 (2024)

Janelia Conference "Mechanisms of Inter-organismal Extended Phenotypes" 参加報告

表紙　Janelia Conferenceに参加した領域メンバーたち　左より陰山、丹羽、佐藤、西川、沓掛、春本、深津、国生、室



（上）Janelia Conference "Mechanisms of Inter-organismal Extended Phenotypes" のウェブサイト等のトップイメージ
（下）参加者集合写真
画像はいずれも Janelia Conferences の好意による

目次

Janelia Conference “Mechanisms of Inter-organismal Extended Phenotypes” への参加の経緯と背景について

深津武馬（産業技術総合研究所）

標記国際会議は、2024 年 6 月 2 日〜5 日に米国バージニア州に所在するハワードヒューズ医学研究所のジャネリアリサーチキャンパスで開催された[1]。標題を見れば一目瞭然であるが、当学術変革領域「共進化表現型創発：延長された表現型の分子機構解明」とほぼ同様のコンセプトのもと、世界の有力な関連研究者に声をかけ、企画されたものである。科学の発展や展開におけるシンクロニシティは、しばしば偶然の共時性というよりは、むしろ技術の進展や先行知見の蓄積により必然的に生じるものである。私たちの研究領域が国際的な観点からも、まさに時機を得たものであったことの証左といってよかろう。仕掛人はジャネリアリサーチキャンパスに所属の Senior Group Leader の David Stern である[2]。大学院生時代の社会性アブラムシの進化生態学的研究を皮切りに、アブラムシの進化発生学を創始し、そこからショウジョウバエの進化発生学の最前線に展開し、近年またアブラムシに回帰して分子遺伝学や虫こぶ形成機構に取り組むという幅の広さをもつ研究者である。加えて昆虫媒介ファイトプラズマによる植物の形態形成異常誘起機構の研究で知られる英ジョン・イネスセンターの Saskia Hogenhout[3]、バキュロウィルスによる鱗翅目幼虫の行動操作研究に取り組む蘭ワーゲニンゲン大学の Vera Ros[4]、そして蚊による病原体媒介機構を専門とする米国立アレルギー感染症研究所の Eric Calvo[5]が本国際会議を企画した（**図 1**）。

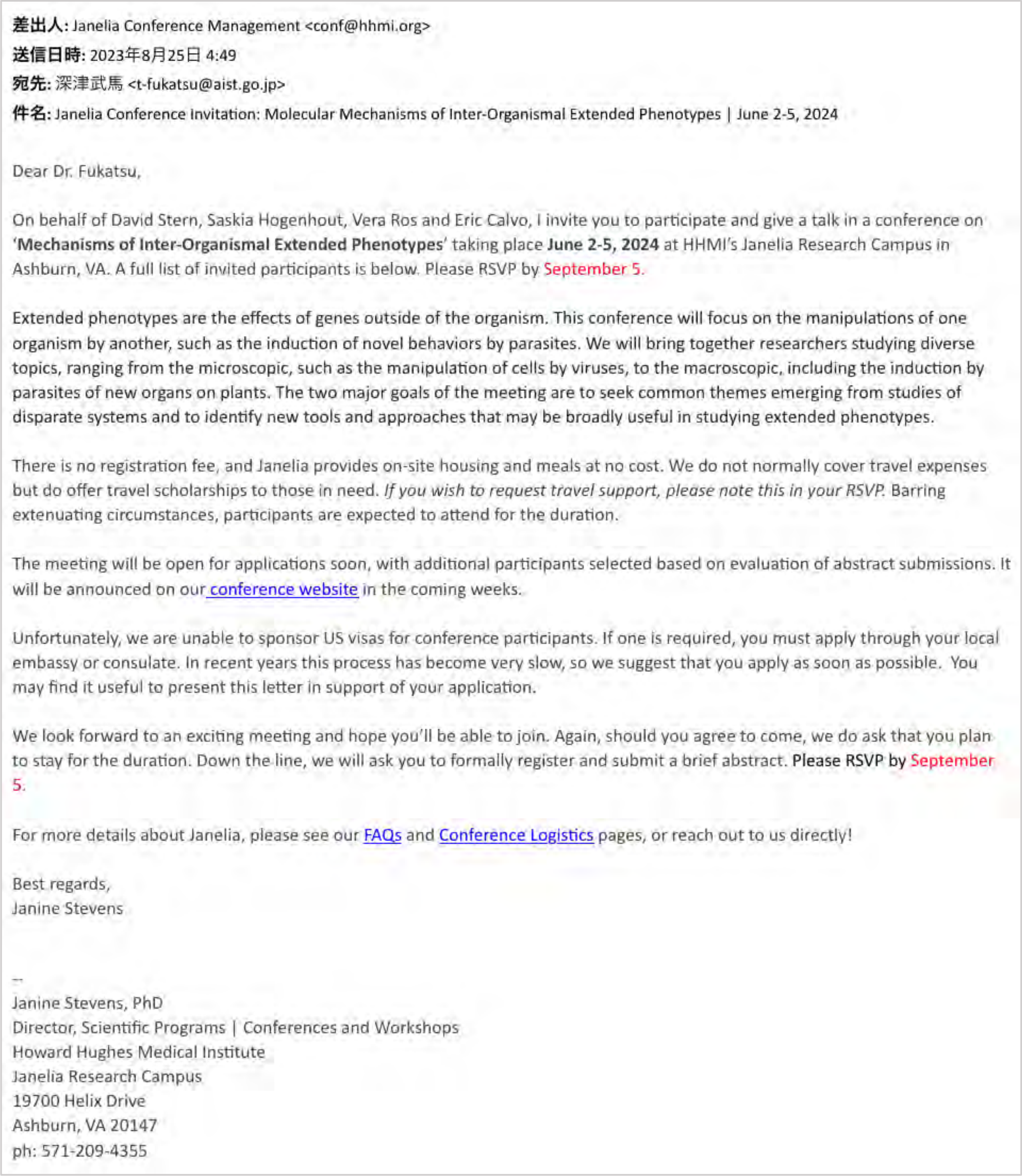
What a fantastic and successful meeting!

David Stern, Saskia Hogenhout, Vera Ros and Eric Calvo

Thank you very much!

図 1：深津の講演の冒頭におけるオーガナイザーへの謝辞スライド。最終日の最終招待講演者として成功裡に終わりつつある本国際会議を企画してくれたことへの感謝の意を述べると、会場は大きな拍手に包まれた。写真は Prof. Sophien Kamoun (Sainsbury Univ., UK) の好意による。

発端は2023年8月25日に深津が受け取った1通のEメールだった。“Mechanisms of Inter-organismal Extended Phenotypes” と題する国際会議を開催するので招待講演をしてもらえないかという内容である。



差出人: Janelia Conference Management <conf@hhmi.org>
送信日時: 2023年8月25日 4:49
宛先: 深津武馬 <t-fukatsu@aist.go.jp>
件名: Janelia Conference Invitation: Molecular Mechanisms of Inter-Organismal Extended Phenotypes | June 2-5, 2024

Dear Dr. Fukatsu,

On behalf of David Stern, Saskia Hogenhout, Vera Ros and Eric Calvo, I invite you to participate and give a talk in a conference on ‘**Mechanisms of Inter-Organismal Extended Phenotypes**’ taking place **June 2-5, 2024** at HHMI’s Janelia Research Campus in Ashburn, VA. A full list of invited participants is below. Please RSVP by September 5.

Extended phenotypes are the effects of genes outside of the organism. This conference will focus on the manipulations of one organism by another, such as the induction of novel behaviors by parasites. We will bring together researchers studying diverse topics, ranging from the microscopic, such as the manipulation of cells by viruses, to the macroscopic, including the induction by parasites of new organs on plants. The two major goals of the meeting are to seek common themes emerging from studies of disparate systems and to identify new tools and approaches that may be broadly useful in studying extended phenotypes.

There is no registration fee, and Janelia provides on-site housing and meals at no cost. We do not normally cover travel expenses but do offer travel scholarships to those in need. *If you wish to request travel support, please note this in your RSVP.* Barring extenuating circumstances, participants are expected to attend for the duration.

The meeting will be open for applications soon, with additional participants selected based on evaluation of abstract submissions. It will be announced on our conference website in the coming weeks.

Unfortunately, we are unable to sponsor US visas for conference participants. If one is required, you must apply through your local embassy or consulate. In recent years this process has become very slow, so we suggest that you apply as soon as possible. You may find it useful to present this letter in support of your application.

We look forward to an exciting meeting and hope you’ll be able to join. Again, should you agree to come, we do ask that you plan to stay for the duration. Down the line, we will ask you to formally register and submit a brief abstract. **Please RSVP by September 5.**

For more details about Janelia, please see our FAQs and Conference Logistics pages, or reach out to us directly!

Best regards,
Janine Stevens

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Janine Stevens, PhD
Director, Scientific Programs | Conferences and Workshops
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図 2: Janelia Conference よりの招待講演依頼メール。

当時の状況は、勝間領域代表を中心に申請書をまとめ、学術変革領域（A）に申請したものの、まだヒアリングに進めるかどうかの通知も来ていない段階であった。しかしどう見ても私たちの領域のめざすところと共通したコンセプトのもとで開催される最重要の国際会議であ

り、招待講演者も錚々たる顔ぶれである。この会議に参加すれば、当該研究分野における世界の現状がすべて把握できるに違いない。ぜひ皆で参加すべきではないかという議論が盛り上がり、その機運は 9 月 26 日にヒアリング対象研究領域に選定されたという通知によりさらなる熱を帯びた。2024 年 1 月初旬の参加申込・要旨提出の締切までに、計画研究代表者の大部分が参加登録をおこない、勝間領域代表は残念ながら都合がつかず参加を見送ったものの、研究室の若手研究者 2 名を派遣することで対応し、提案研究領域の総力をあげた参加により、国際的な情報収集および発信にとりくむ体勢を構築した。幸いにして本研究領域「共進化表現型創発：延長された表現型の分子機構解明」は採択に至り、2024 年 6 月開催の Janelia Conference において以下のメンバーが参加、発表をおこなうことで日本における新規プロジェクト “Co-evolutionary Emergence of Extended Phenotypes” の発足を世界に向けて発信することができた。次頁以降に発表要旨を収録する。

招待講演：深津武馬（産総研）

口頭発表：陰山大輔（農研機構）

ポスター発表：佐藤拓哉（京都大）、西川義文（帯広畜産大）、春本敏之（京都大）、沓掛磨也子（産総研）、丹羽隆介（筑波大）、國生龍平（東京大）、室智大（東京大）

本号は Janelia Conference “Mechanisms of Inter-organismal Extended Phenotypes” 参加報告として、本国際会議の概要について記録、報告するものである。当該 Conference の website[1]および agenda[6]も併せて参照いただきたい。

References

[1] https://www.janelia.org/you-janelia/conferences/mechanisms-of-inter-organismal-extended-phenotypes

[2] https://www.janelia.org/people/david-stern

[3] https://www.jic.ac.uk/people/saskia-hogenhout/

[4] https://www.wur.nl/en/persons/vera-ros-1.htm

[5] https://www.niaid.nih.gov/research/eric-calvo-phd

[6] https://www.dropbox.com/scl/fi/2ei0cz1whrmhs76me33yj/Janelia-2024-Extended-Phenotypes-Conf-AGENDA.pdf?rlkey=wf6hcw6yezo9le4eiruc4xso7&dl=0

Takema Fukatsu
National Institute of Advanced Industrial Science and Technology (AIST)

Co-evolutionary Emergence of Extended Phenotypes

Takema Fukatsu

In nature, intimate inter-organismal interactions often entail “extended phenotypes”, where genetic information of an organism is expressed as phenotypes of another organism. Such “extended phenotypes” are particularly common in coevolutionary interactions across closely associated organisms as observed in endoparasitism/endosymbiosis. The drastic phenotypes emerging via close inter-organismal interactions have attracted profound interest of scientists as well as general public. However, molecular mechanisms underlying the “extended phenotypes” have been poorly understood in most cases. This is mainly because such phenomena are mostly found among interactions between non-model organisms. Recent technological advancement, represented by high-throughput DNA sequencing, RNA-seq, MS-driven omics, CRISPR-Cas9 genome editing, etc., has enabled us to overcome these conventional difficulties. Here I overview recent advancement in understanding of molecular mechanisms underpinning “behavioral manipulation”, “reproductive manipulation”, “morphological manipulation”, “developmental manipulation” and “symbiotic phenotype alteration” achieved by Japanese researchers, and introduce our “Co-evolutionary Emergence of Extended Phenotypes” project.

Daisuke Kageyama
National Agriculture and Food Research Organization

Maternally transmitted male-killing symbionts in insects: biological diversity, mechanisms, and evolutionary significance

Kageyama, D., Nagamine, K., Harumoto, T., Watada, M., Shintani, Y., Herran, B., Sugimoto, T.N., Arai, H., Hayashi, M., Hornett, E.A. and Hurst, G.D.D.

In insects, various vertically transmitted symbionts reside in the cytoplasm. Because they are transmitted exclusively by females, males are a dead end for the cytoplasmic symbionts. To circumvent this problem, some symbionts manipulate host reproduction in several ways, such as cytoplasmic incompatibility, feminization, thelytokous parthenogenesis, and male killing. Among them, male killing is employed by the most diverse symbionts. Here we show (1) our attempt to investigate the mechanism of male killing by using male insect cell culture, (2) recent discoveries of male-killing viruses from distantly related taxa, and (3) the rapid spread of host suppressors against male killing, which may trigger an evolutionary arms race between symbionts and hosts.

Maternally transmitted male-killing symbionts in insects: biological diversity, mechanisms, and evolutionary significance

Daisuke Kageyama

Institute of Agrobiological Sciences,
National Agriculture and Food Research Organization (NARO)
Tsukuba, Japan

NARO 農研機構

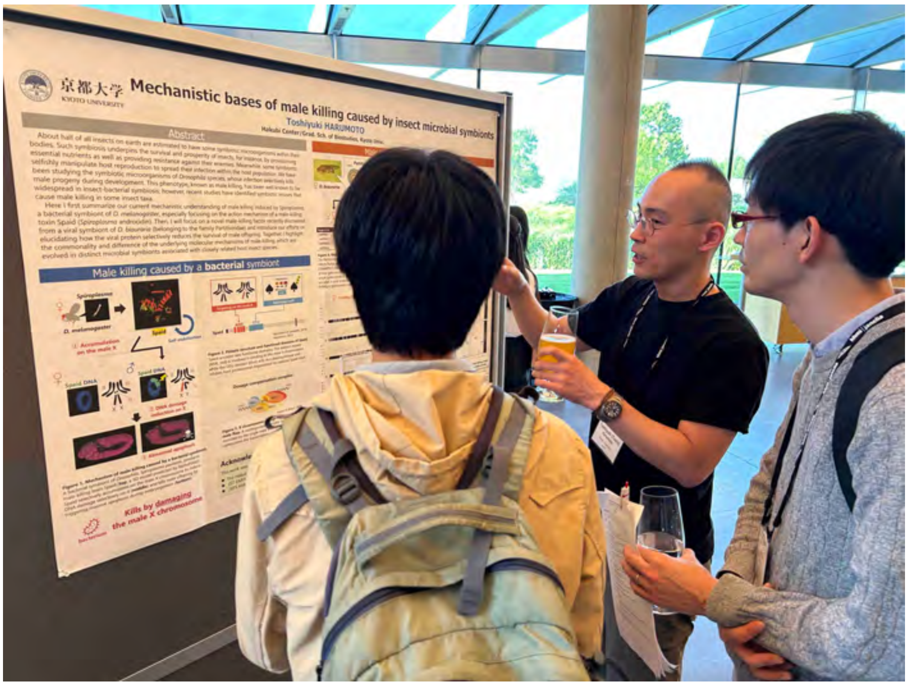
Toshiyuki Harumoto
Kyoto University

Mechanistic bases of male killing caused by insect microbial symbionts

Harumoto, T.

About half of all insects on earth are estimated to have some symbiotic microorganisms within their bodies. Such symbiosis underpins the survival and prosperity of insects, for instance, by provisioning essential nutrients as well as providing resistance against their enemies. Meanwhile, some symbionts selfishly manipulate host reproduction to spread their infection within the host population. We have been studying the symbiotic microorganisms of Drosophila species, whose infection selectively kills male progeny during development. This phenotype, known as male killing, has been well known to be widespread in insect-bacterial symbiosis; however, recent studies have identified symbiotic viruses that cause male killing in some insect taxa.

In the first part of this presentation, I would like to summarize our current mechanistic understanding of male killing induced by Spiroplasma, a bacterial symbiont of *D. melanogaster*, especially focusing on the action mechanism of a male-killing toxin Spaid. Next, we will focus on a novel male-killing factor recently discovered from a viral symbiont of *D. biauraria* (belonging to the family Partitiviridae) and will introduce our efforts on elucidating how the viral protein selectively reduces the survival of male offspring. Together, we highlight the commonality and difference of the underlying molecular mechanisms of male killing, which are evolved in distinct microbial symbionts associated with closely related host insect species.

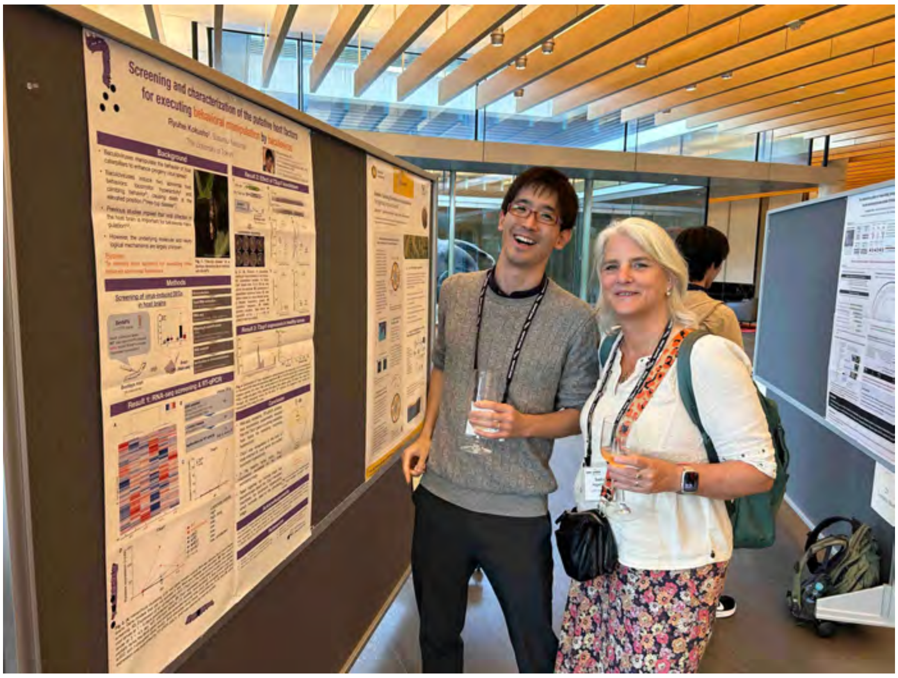


Ryuhei Kokusho
University of Tokyo

Screening and characterization of the putative host factors for executing behavioral manipulation by baculovirus

Kokusho, R. and Katsuma, S.

Pathogens and parasites sometimes manipulate host behavior to enhance progeny production or dispersal. Baculovirus is a classic pathogen whose infection causes abnormal behaviors (locomotor hyperactivity and climbing behavior) of host caterpillars — known as “Wipfelkrankheit” from over 100 years ago. Although some baculoviral genes have been identified as critical factors for manipulating host behavior, it is largely unknown which host gene plays a significant role in executing these virus-induced abnormal behaviors. We used Bombyx mori nucleopolyhedrovirus (BmNPV) and its host, Bombyx mori (the domesticated silkworm), as the model system to identify host gene(s) for executing baculovirus-induced behaviors. RNA-seq analysis using brains from uninfected and BmNPV-infected B. mori larvae identified 56 differentially expressed genes (DEGs) that were significantly up- or down-regulated only in the brains of locomotor-hyperactivated larvae. Of these, the expression changes of 13 DEGs were verified by RT-qPCR analysis using another set of time-course brain samples. To examine whether these DEGs are involved in inducing locomotor hyperactivity, we generated recombinant BmNPVs expressing downregulated DEGs and those expressing antisense RNA of up-regulated DEGs for attenuating the DEG expression changes. The locomotor assay revealed that when infected with the BmNPV expressing antisense RNA of an up-regulated DEG (here named as T3up1), B. mori larvae showed lower locomotor activity than those infected with the control BmNPV. This result suggests that T3up1 is a strong candidate host gene for executing locomotor hyperactivity. T3up1 is a lepidopteran-specific gene whose protein product has a signal peptide but no putative conserved domains. T3up1 expression was low in the brains of feeding-stage larvae, whereas it increased at the wandering stage. This implies that BmNPV hijacks the host’s wandering machinery for activating locomotion. We are now examining neuroanatomical characteristics of T3up1-expressing cells.



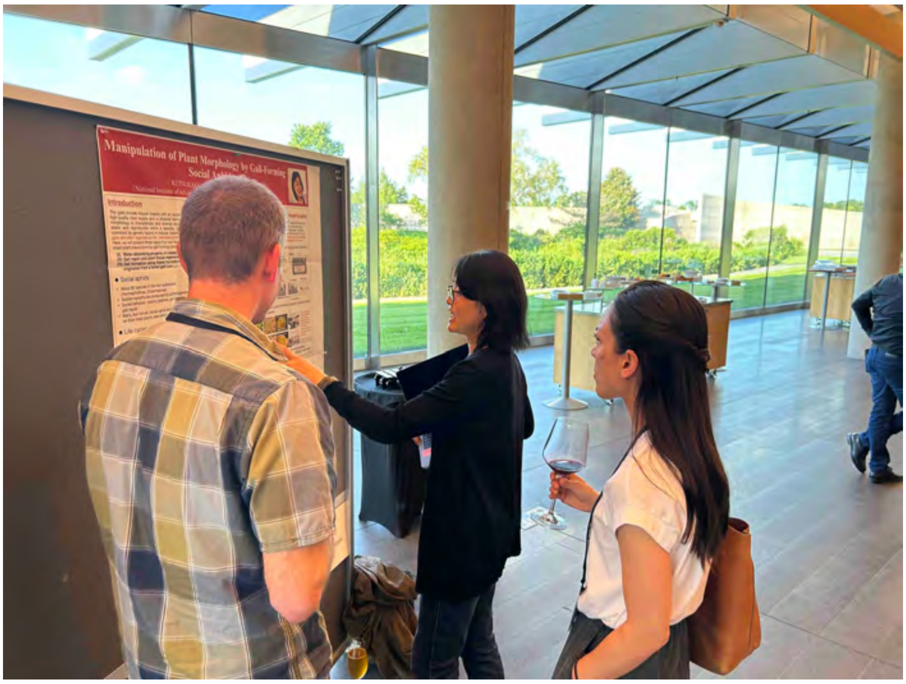
Mayako Kutsukake
National Institute of Advanced Industrial Science and Technology (AIST)

Manipulation of plant morphology by gall-forming social aphids

Kutsukake, M. and Fukatsu, T.

The galls provide inducer insects with an isolated and exclusive habitat, a constant and high quality food supply and a physical barrier against predators and parasites. Interestingly, gall morphology is characteristic and diverse depending on insect species, but it remains stable and reproducible within a species, suggesting that gall formation is precisely controlled by genetic factors in inducer insects. Therefore, the morphological traits of the galls are often regarded as the "extended phenotypes" of the inducer insects.

Here, we will present several intriguing cases from our findings of sophisticated insect-plant interactions related to gall-forming social aphids. In the social aphid *Nipponaphis monzeni*, when the gall is damaged, altruistic individuals known as soldiers promptly repair the hole on the gall wall by discharging and plastering their body fluid. Subsequently, the soldiers continuously stimulate the wound site around the breach, leading to the proliferation and regeneration of plant tissue, ultimately restoring the inner gall wall. This phenomenon represents one of the most sophisticated plant-insect interactions in a social context. We will show another study regarding a novel plant phenotype to solve a waste problem in completely closed galls. *N. monzeni* forms completely closed galls containing over 2,000 individuals, but surprisingly, no accumulation of honeydew is observed in the gall. We found that honeydew is absorbed by the inner gall wall and this property is determined by aphids, which can be regarded as extended phenotype and 'indirect social behavior' of the social aphids. Recently, to gain insight into the molecular mechanisms of gall formation, we are focusing on *Ceratovacuna nekoashi*, whose banana-shaped galls exhibit an intriguing phenomenon known as "late flowers" originating from failed galls. While much remains to be explored, we would like to present some results obtained from field experiments and transcriptome analyses conducted so far.

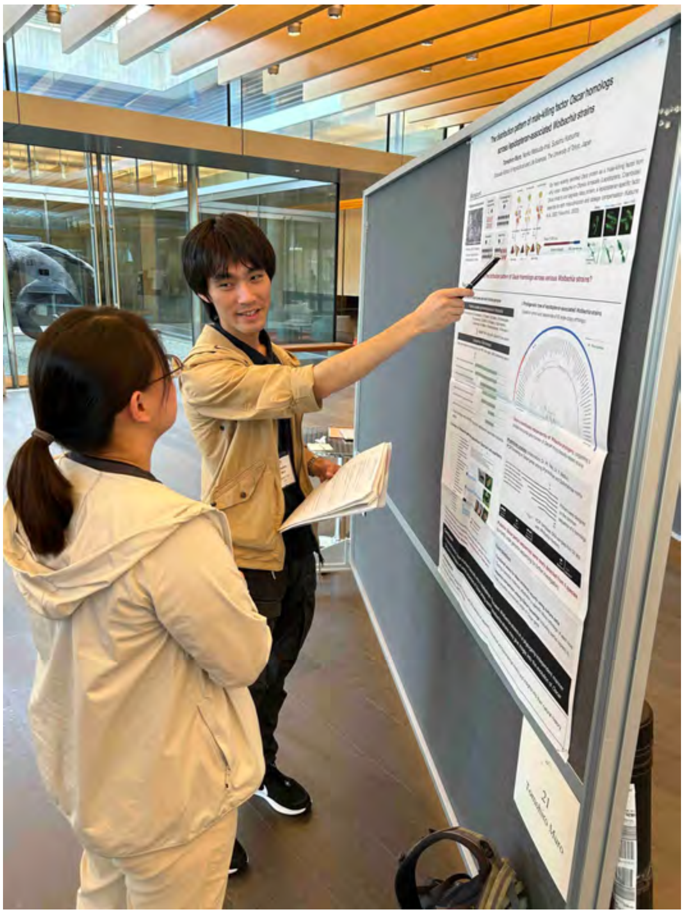


Tomohiro Muro
University of Tokyo

The distribution pattern of male-killing factor Oscar homologs across lepidopteran-associated *Wolbachia* strains

Muro, T., Matsuda-Imai, N. and Katsuma, S.

Wolbachia is one of the most widespread endosymbionts found in arthropods and nematodes. To facilitate infection prevalence through maternal transmission, *Wolbachia* induces several types of reproductive manipulations to its hosts. Male killing, one of such reproductive manipulations, is known for some coleopteran, dipteran, and lepidopteran insects, where male progenies are selectively killed in *Wolbachia*-infected lineages. Recently, Oscar was identified from wFur strain *Wolbachia* as a responsible factor for male killing in a crambid moth *Ostrinia furnacalis*. Here, we surveyed a distribution pattern of Oscar homologs across publicly available *Wolbachia* genome sequences as well as in-house generated genome assemblies. Besides previously reported strains (male-killing strains in *Ostrinia*, *Homona*, or *Hypolimnas* moths/butterflies), at least 3 lepidopteran-associated strains were found to possess Oscar homologs. Altogether, Oscar homologs were identified in Wolbachia strains derived from 3 lepidopteran superfamilies: Tortricoidea, Papilionoidea, and Pyraloidea. Additionally, we found that a strain other than lepidopteran-associated ones has an apparently truncated copy of Oscar. The strains with Oscar homologs did not necessarily form a cluster phylogenetically, indicating a possible horizontal gene transfer among distant strains. These results characterize the evolutionary property of Oscar genes in *Wolbachia* endosymbionts.



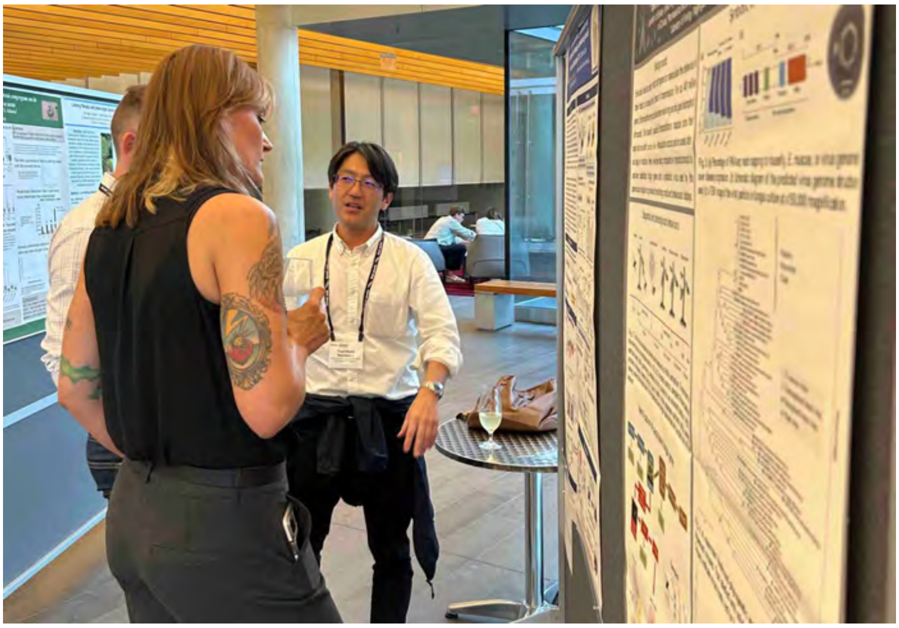
Yoshifumi Nishikawa
Obihiro University of Agriculture and Veterinary Medicine

Brain manipulation of mammalian host by intracellular parasite, *Toxoplasma gondii*

Nishikawa, Y.

Many parasitic organisms have distinctive life cycles, and one of their unique parasitic strategies is the phenomenon of host manipulation. Our research focuses on *Toxoplasma gondii* as a host-manipulating parasite. *Toxoplasma* is a commensal intracellular parasitic protozoan that uses felines as its definitive host and most of warm-blooded animals including humans as intermediate hosts. It is estimated that about one-third of the world's population is infected with T. gondii, making it the most successfully spread pathogen. When *T. gondii* infects an intermediate host, it migrates into the brain and muscles of that host, eventually forming dormant cysts and establishing chronic infection. Dormant parasites are not pathogenic in hosts with normal immune systems, but can sustain infection for the lifetime of the host. Because chronic *Toxoplasma* infections rarely show clinical signs, the effects of infection on the central nervous system have been neglected. However, studies in recent decades have reported that chronic *Toxoplasma* infection increases the risk of developing human psychiatric disorders and alters rodent behavior. However, mechanism of brain manipulation by *T. gondii* is largely unknown.

Therefore, we established a mouse model of toxoplasmosis and analyzed behavioral changes in hosts during the acute, chronic, and reactivation phases of infection. In mice during the acute and reactivation phases of infection, the appearance of core symptoms of "depression" dependent on activation of the kynurenine pathway was observed. On the other hand, in chronically infected mice, abnormal neurotransmitter production and neuronal dysfunction in the brain were inferred, and impairment of the ability to fix fear memories was confirmed. These results suggest that T. gondii infection disrupts the central nervous system. Future detailed studies will elucidate Toxoplasma's parasitic strategy and reveal the true significance of host manipulation by this parasite.



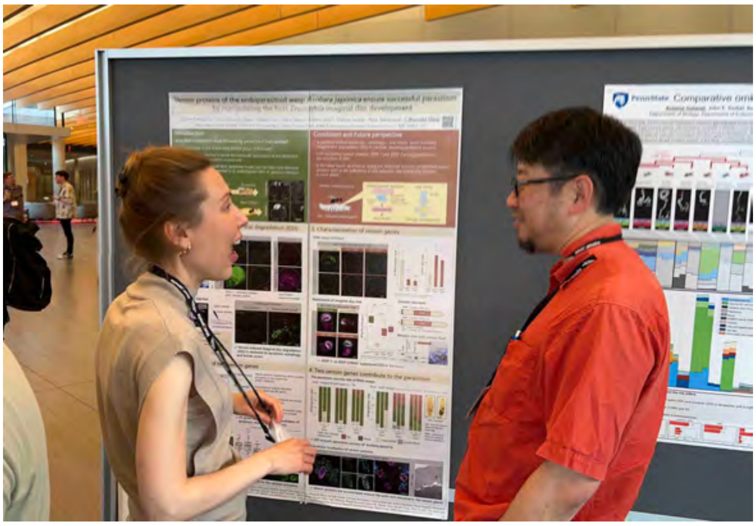
Ryusuke Niwa
University of Tsukuba

Venom proteins of the endoparasitoid wasp *Asobara japonica* ensure successful parasitism by manipulating the host *Drosophila* imaginal disc development

Kamiyama, T, Shimada-Niwa, Y, Tani, N., Takasu, A., Mori, H., Senda, T., Nakamura, A., and Niwa, R.

Parasitoid wasps, one of the most diverse groups of animals, are hymenopteran insects that develop inside or on the bodies of host organisms and ultimately kill them. Among the wasps, a group of endoparasitoid wasps inject various venoms to manipulate the host's development and physiology to achieve successful parasitism. However, the molecular mechanisms of venom-induced host manipulation at the molecular and cellular level remain largely unexplored. To address this issue, we use *Asobara japonica*, a Braconidae endoparasitoid wasp, and the host species *Drosophila* as a model for endoparasitoid wasp-host interaction. The adult wasp injects a single egg along with venoms into the larval body of the host *Drosophila*. The wasp larva preys on its host body only after the host becomes a pupa. Eventually, the adult wasp emerges from the host fly pupal case.

We found that *A. japonica*'s venom, when injected into the host *Drosophila*, rapidly induces imaginal disc degeneration (IDD), mediated by apoptosis, autophagy, and inhibition of cell proliferation. In contrast to IDD, other tissues appeared intact. To identify the responsible venom components, we performed whole-genome sequencing of *A. japonica* [Kamiyama et al. DNA Res. 2022]. Transcriptomics, proteomics, and comparative genomics approaches allowed us to narrow down 63 candidate genes that are predominantly expressed in the *A. japonica* venom gland. We then assessed these candidates by double-stranded RNA injection-based gene knockdown. We eventually identified two candidate venom genes, both of which encode novel secretory proteins. RNAi of either of these two venom genes almost completely abrogated the venom-induced apoptosis, autophagy, and inhibition of cell proliferation in the host imaginal discs, thus significantly suppressing IDD. Notably, the RNAi wasps exhibited a lower parasitism success rate than the control wasps. Our study highlights a novel hijack strategy of the endoparasitoid wasp, contributing to successful parasitism by manipulating host metamorphosis.



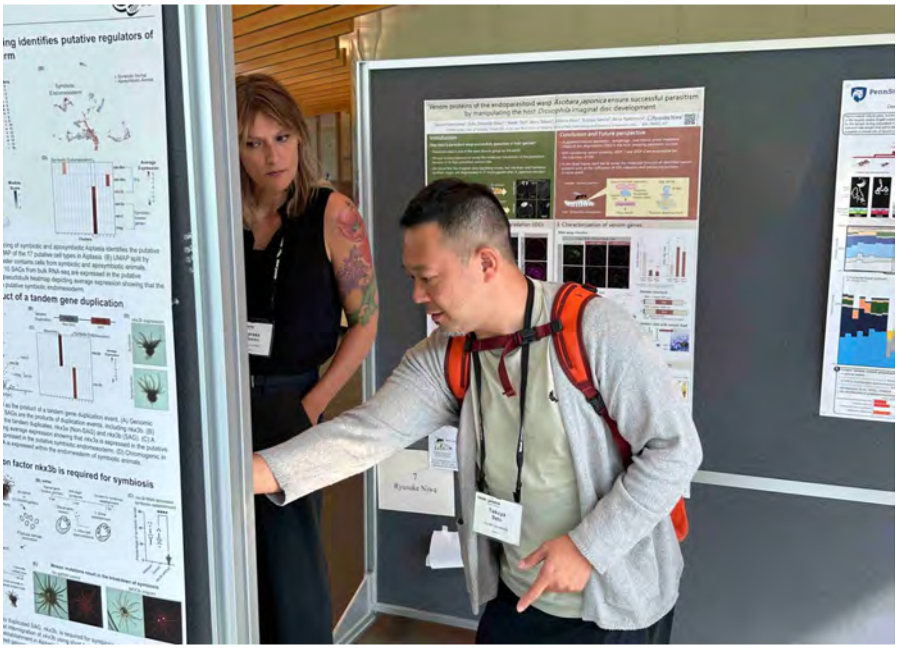
Takuya Sato
Kyoto University

Proximate mechanisms and evolution of nematomorph-driven behavioral manipulation of mantids

Sato, T., Mishina, T., Chiu, M-C., Iwatani, Y., Okada, R., Hashiguchi, Y., Takeshima, H. and Sakura, M.

A wide range of parasites manipulate the behaviours of their hosts in order to complete their life cycle, in a well-known example of the “extended phenotype”. Recent studies have explored the proximate and ultimate mechanisms of such manipulation of host behavior, including potential molecular mechanisms and their genome evolution. However, we still have very few empirical examples to fully understand the behavioral manipulation by parasites.

Nematomorph parasites have evolved the ability to induce their terrestrial insect hosts to enter bodies of water, where the parasite reproduces. This is one of the most fascinating examples of the extended phenotype of parasites, but the key mechanisms triggering the hosts' entry into water have long been wrapped in mystery. A previous report argued that parasite-induced positive phototaxis can increase the encounter rate of hosts and water bodies. However, luminous environments are ubiquitous in nature, and thus a simple alteration of the response to light intensity may not be sufficient for hosts to effectively find water. The reflection of sunlight from water bodies is horizontally polarized, which is used by many arthropods to seek out water habitats. In this talk, we will first show our experiments demonstrating that the induced positive polarotaxis explained entering water of a mantid host infected by a nematomorph parasite. We then present our recent discovery that a nematomorph has many genes likely acquired by horizontal gene transfer (HGT) from its mantid hosts, and that the candidate HGT-derived genes were frequently up-regulated during the behavioral manipulation. It is currently unclear whether and how these many candidate HGT-derived genes cause behavioral manipulations, including induced polarotaxis. However, our findings provide a new avenue of research focusing on the general role of HGT-derived genes in the molecular mechanisms of host manipulation, as well as in the genome evolution of manipulative parasites.



Janelia Conference 参加記

室 智大（東京大学大学院農学生命科学研究科博士課程3年）

2024年6月2–5日、アメリカ合衆国ジャネリア研究キャンパスにて開催された国際会議“Mechanisms of Inter-Organismal Extended Phenotypes”に参加した。今回、参加記を執筆する貴重な機会をいただいたので、学会の様子を振り返りたいと思う。

ジャネリア研究キャンパスでは生命科学分野の多岐にわたるテーマの国際会議が次々に開催されており、ウェブサイトを覗くと総覧できる。これら国際会議は、比較的小規模の人数で開催され、参加者同士の密度の濃い情報交換、議論、交流を促進するというスタイルのようだ。今回の会議は参加者50人程度であり、確かに4日間の開催期間でほとんど全員の顔と研究内容が十分頭に入るくらいであった。筆者は日本人参加者の中で唯一の学生であったが、会議全体で見ても学生はかなり少数派で、分野を牽引するベテラン研究者から新進気鋭の若手PI、ポスドク研究者が参加者の多くを占めていた。その分、講演内容も充実しており、学生の身分からすると大変に贅沢な時間であった。

今回の会議は、筆者にとって2回目の国際学会参加であった。1回目は、ちょうど約1年前の2023年夏にギリシャ・クレタ島で開催された国際ボルバキア会議（The 11th *Wolbachia* Conference）である。国際ボルバキア会議は、主としてボルバキア（昆虫や線虫にみられる細胞内共生細菌）という研究対象を同じくする研究者が一堂に会する機会であり、その分、自身の研究分野にほど近い発表が多く行われ、楽しくありながらもある意味で緊張しっぱなしの日々であったことを覚えている。一方、今回の会議は、そのスコープが大変に広かったことが対照的である。会議が本格的に始まった6月3日には、吸血性昆虫と宿主、また媒介される病原微生物の相互作用を中心としたセッションに始まり、さまざまな昆虫における寄生者（寄生蜂や病原微生物）による行動操作のメカニズム研究、アリと好蟻性昆虫、昆虫と共生微生物の間で生じる現象など、次々に異なる対象生物・系・現象の話題が展開されて、わくわくが止まらなかった。翌6月4日は植物が関わる生物間相互作用の講演が目白押しであり、植物吸汁性昆虫、植物病原微生物、寄生性植物、そして虫こぶ形成といった、前日に引けを取らない広範な話題提供が行われた。参加者数のコンパクトさも相まって、（行動操作や虫こぶの研究者が比較的多かったほかは）類似の研究対象をもつ研究者自体が少ないほどで、「延長された表現型」研究の最大の魅力である（と筆者は考える）自然界の圧倒的な多様性をよく象徴する会議であった。筆者はチョウ目昆虫におけるボルバキアのオス殺

し因子 Oscar についてのポスター発表を行なったが、（日本人参加者では陰山さん（農研機構）や春本さん（京都大学）が該当する）生殖操作の海外研究者はいなかったため、新鮮な観点から意見や質問をいただくことができた。会議の目指していた「多様なトピックを扱う研究者が集まり、異なる系の共通項や、延長された表現型の研究に有用なツール、アプローチを見出す」というコンセプトの一助になっていれば幸いである。

学会の学術的内容も大変に刺激的であったが、それに加えて印象的だったのはジャネリア研究キャンパスの環境である。ゲスト向けの宿泊施設はメインの建物（Landscape Building）と繋がっており、部屋に入ると全面の窓で池を望む開放的な景色が広がっていた（写真：窓枠外側には幾多のオニグモが網を構えていて風流であった）。施設内にはパブ（Bob’s pub）が備わっているほか、最上階から外に出て少し歩くと Carriage House という離れがあり、開催期間は毎夜、ドリンクを片手に参加者同士交流する時間が設けられていた（筆者も毎日のように夜遅くまで楽しんだ）。これら宿泊や飲食の費用はすべて主催側が負担しており、（研究者同士の交流も含めて）科学の発展のためにコストを惜しまないジャネリアの理念を垣間見ることができた。開催期間中、Landscape Building を見学する 1 時間程度のツアーがあり、オーダーメイドの機械部品をつくるための工作室やショウジョウバエ遺伝資源を無人で管理するマシーンなど研究をバックアップする強力な設備・施設があること、また研究者を研究に専念させるためのジャネリアのシステム（内部資金でファンドされ外部資金獲得を必要としないなど）について知ることができた。建物内は至るところに生命科学、特に神経科学にまつわる絵や写真（顕微鏡像や蛍光画像）が作品として飾られており、科学へのモチベーションが自然と盛り上がるようなおしゃれな空間が作られていた。一方、建物の周辺は緑も多く、初日到着後の空いた時間を過ごすのにも気持ちの良い環境であった（写真：周辺を散策して見られた昆虫類の一部も記念に掲載）。最終日の朝には、前日の講演にも登場した虫こぶを佐藤さん（京都大学）が周辺で発見し、沓掛さん（産総研）に案内するということで、折角の機会に（筆者と同研究室所属・國生さんと

一緒に）自分も同行した。虫こぶの専門家である沓掛さんによる解説ありの観察会となり、これもまた豪華な時間を送ることとなった（写真）。ところで、会議が開催された本年 2024 年は、周期ゼミ（素数ゼミ）の 2 集団が 221 年ぶりに同時発生することで界隈が大いに賑わっている年である。周期ゼミにおいても寄生者（マッソスポラ）による「ゾンビ化」が知られており、「延長された表現型」の雑談のネタとして大活躍であった（ちょうど開催地が米国東部で、あわよくば一方の集団の個体は現地で見られるのではないかと密かに期待していたが、それは叶わなかった）。

ここまで、本国際会議や現地の様子について述べてきた。きっと、会議の充実ぶりが伝わったことと思う。惜しむらくは、まだまだ自身の英語能力が不足していて、質問にしても交流にしても、（言葉だけの問題ではないが）コミュニケーションを満足にとりきれなかった反省がある。魅力的な材料や現象を対象としたハイレベルな講演を聴くにつけ、純粋な科学の議論をこの人たちと同じ土俵で楽しみたいという思いが強くなった。博士課程のこの時期に、科学研究に対するモチベーションを一層増進させ、外に広がる環境に目を開かせてくれる機会を享受させていただいたことにひとえに感謝する次第である。

末筆ながら、自身が参加できない代わりにぜひ参加したらどうかと本国際会議への出席を提案してくださった勝間進教授（東京大学）には、大変貴重かつ有益な経験を踏ませていただいたことに感謝いたします。また、開催期間中は学術変革領域「共進化表現型創発」の構成メンバーである日本人研究者の皆様に大変お世話になりました。さらに、深津武馬首席研究員（産総研）には、本稿を執筆する貴重な機会をご提案いただきました。重ねて感謝申し上げます。

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