

Event: SMBE Satellite Workshop on Pathogen Pangenome Evolution Between and Within their Hosts. Tokyo, Japan. 26-28th November 2024.

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Meeting format

The *SMBE Satellite Workshop on Pathogen Pangenome Evolution Between and Within their Hosts* took place over three days in the auditorium of the National Museum of Nature and Science, Ueno Park, Tokyo, Japan. We hosted 81 in-person attendees and 41 remote attendees.

The meeting had five scientific sessions, described in detail below. Each session had two or three invited speakers (20 minutes each, 14 total) and three to four speakers selected from abstracts (10 minutes each, 17 total). Across both groups we aimed for a balance of topics, gender, career stage and geography. This was achieved by the committee ranking possible speakers and abstracts, then agreeing on a final list with this balance in mind. We were delighted that our community presented and submitted high quality abstracts which naturally fulfilled our criteria of balance with minimal need for redistribution. A talk prize sponsored by the *Microbial Genomics* journal was awarded by the committee to one of the talks submitted from abstracts.

Instead of a poster session, and following on from the previous success of this format, we also had two sessions of lightning talks (2 minutes each, one slide) from 35 further presenters who submitted abstracts. Networking was informally achieved through two extended lunch breaks and numerous shorter coffee breaks. We had a standing dinner and drinks in the museum lounge on the second evening – this format allowed attendees to move around more easily, and was scheduled after most of the presentations but before the very end of the meeting so most people had the chance to catch presenters they wanted to talk to.

Attendees



The meeting aimed to bring together researchers working on the molecular biology and evolution of microbes, particularly to link the new scale of pathogen data with sound evolutionary theory. Previous satellite meetings have also recognised the size and need for this community to be represented beyond the main SMBE symposia, and had a focus on pathogen transmission and within-host variation. This meeting refocused on emerging technologies for capturing pangenome variation, and was also a forum to consolidate knowledge from working on SARS-CoV-2 since the pandemic. We aimed to bring together microbiologists, evolutionary biologists, computational biologists, statisticians and mathematical modellers and communicable disease controllers to collaborate in this field – we achieved good representation across these fields.

A high proportion of the participants had also worked on COVID-19 during the pandemic, and a number of senior researchers commented that this was the first scientific meeting they had attended since the COVID-19 pandemic began. Experiences of this unique period of research across different countries were shared. We were happy to be able to (re)connect this community.

Many meetings in this area focus on a single species, or are specific to either viruses, bacteria or eukaryotes. However the biology and evolution of these organisms, and the techniques used to study them, frequently have a lot in common. Participants commented positively about bringing researchers across these communities together, and consequently being exposed to new ideas and research.

Overall we had 53 ECR (<7 yrs post-PhD) registrations, 8 local (within Japan) registrations, and 20 senior researcher registrations. This was an increase of about 35% over previous satellite meetings in this broad topic area, and the new addition of 41 hybrid participants represented a doubling over previous events.

Demographic breakdown of all in person attendees, speakers and committee

Male: 43 / Female: 38

ECR: 53 / Senior: 28

Europe: 45 / North America: 3 / Asia: 18 / Oceania: 14 / Africa: 1

Scientific sessions

After a short housekeeping presentation from the organisers, Prof Christophe Fraser (University of Oxford, UK) opened the meeting with a presentation on using within-host diversity to understand the transmission of HIV-1, connecting the focuses of pathogen transmission analysis with within-host and pangenome variation.

Session 1: The use of metagenomics for pathogen surveillance ('metagenomics')

Talks in this session included the development of methods to identify variation in mixed populations, and how this information can be used to inform transmission detection. New data modalities such as wastewater monitoring were also discussed. A conclusion from this session is that metagenomic data is becoming commonplace in research studies, and is a powerful tool to extract more genomic information from samples and study evolution of populations – these techniques are also beginning to find uses in public health and surveillance.

Session 2: Analysis and interpretation of selection in pathogen populations ('selection and evolution')

The presenters covered evolutionary constraints on plasmids, surface antigens diversity across different species, new methods to estimate fitness from phylogenies, integrating transcriptome and genomic data, and also cutting-edge transformer methods to understand the gene structure and epidemiology of bacterial pathogens. This session reflected the multi-species direction of the field, with most talks presenting generalised conclusions of methods applicable across many species, and careful consideration of the interactions of mobile elements, pathogen and host genomes.

Session 3: The role of evolutionary analysis in emerging infectious diseases, spanning bacteria and viral species including SARS-CoV-2 ('emerging infectious diseases')

This session had an explicit focus on SARS-CoV-2, with the first invited speakers showing how integrative genome and protein modelling combined with real-time lab work is capable of estimating the growth rate of emerging SC2 lineages in Japan. The last talk of the session showed in detail the approaches used in New Zealand to COVID tracking and elimination using molecular methods. Other talks included work on molecular analysis to identify an unknown Kakapo pathogen, pangenomics of fungal diseases, and genome reduction in a pig pathogen. Overall, the session showed the fundamental importance of both standard and bespoke evolutionary research for controlling emerging and pandemic pathogens.

Session 4: New tools for evolutionary and pangenome analysis, including genome graphs ('pangenomes and tools')

In the pangenomes session, methods to build pangenomes from chromosomes and plasmids were presented, along with recent applications. Plasmid data was a common theme – they are now broadly represented in sequence databases, evolutionary distances are now possible to accurately estimate, and these can be used to aid nosocomial outbreak investigation. Talks

looked at different scales of pangenome evolution: one talk looked at broad patterns of pangenomes across all bacteria; another at the microevolution of the pangenome and structural variation in an outbreak lineage. Pangenome analysis is a mature research theme in the field, and has benefitted from high quality open source methods being published and maintained by our community. But there are still major evolutionary questions surrounding the pangenome which will require new methods which accurately determine gene gain and loss at the huge scale of data now available.

The talk prize of £150, sponsored by the *Microbial Genomics* journal, was awarded to Daria Frolova for her talk on 'Applying rearrangement distances to enable plasmid epidemiology with [pling](#)' in this session

Session 5: The union of evolutionary and epidemic modelling for inferring outbreak and epidemic dynamics ('modelling')

The meeting concluded with a session on using mathematical modelling techniques to describe surveillance data and evolutionary experiments. Presentations included repurposing population genetic tools such as IBD for pathogens, formally combining epidemic and evolutionary models in phylodynamic frameworks, the use of mutational spectra (first applied in cancer) to track niche adaptation and identify specific transmission routes. The final talk showed the rapid structural dynamics of the pangenome resulting from phage and environment, and cautioned us against static representations of the pangenome representing all genomic and phenotypically relevant information. The use of mathematical and statistical modelling remains central for unifying epidemiological and evolutionary information when working with molecular data.



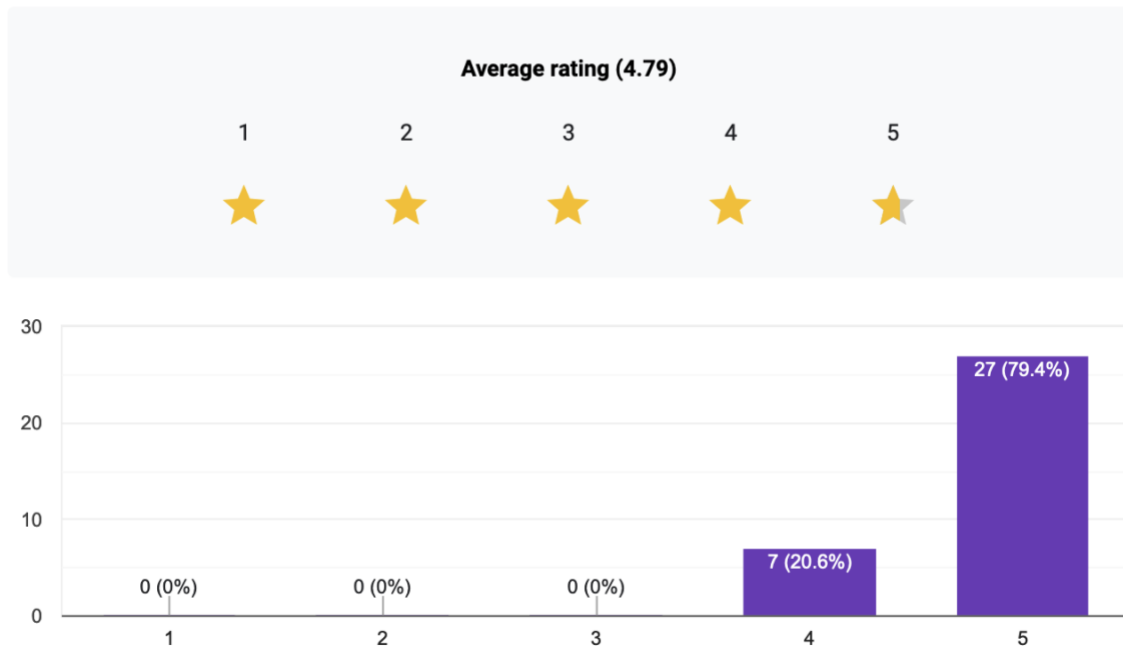
Participant feedback

After the event we collected feedback from the participants, asking for an overall score, scores for each session, points on the balance aspects, as well as one point of improvement, and one element they particularly liked. The meeting was very highly ranked by participants, with the overall high quality of the talk programme being the main positive highlighted.

How would you rate the meeting overall?

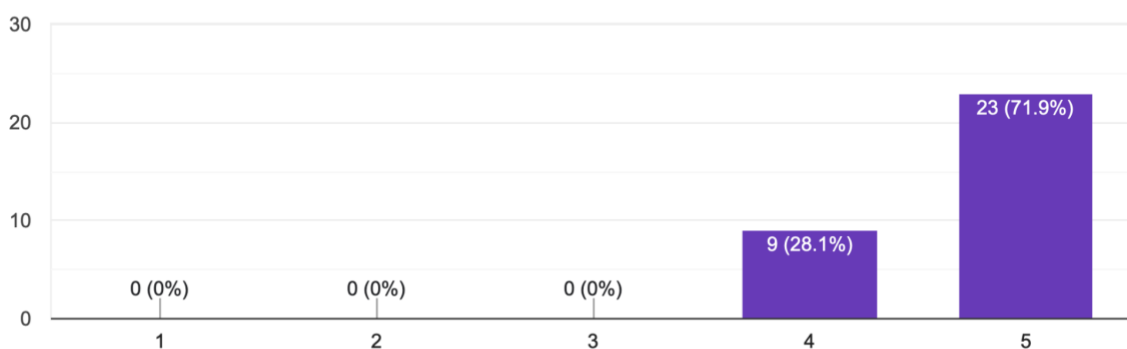
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34 responses



How would you rate the overall quality of the talks?

32 responses



Other points arising from the feedback process:

- All sessions were highly ranked, with 'selection and evolution' and 'pangenomes and tools' most popular.
- Lightning talks were popular, but the main piece of feedback for improvement we received was that over half of the respondents would have **also** liked a poster session to present work in more detail.

- The schedule format was consistently praised, with the session start time and lengths being very popular. The long lunch breaks were also noted as a good chance to meet and talk with other participants.
- All responses thought the balance of ECR to senior researcher talks was ideal, we also received in person feedback appreciating the support of ECRs at the meeting.
- Most (70%) responses thought the meeting was the right length, the others would have added a session or an extra day – though funding would likely have made this difficult.
- The format of the standing dinner was praised, although some responses noted more food options would have helped.
- A number of people commented that they would have liked more structured networking.
- Two people commented that more local (Japan, other Asia) or LMIC speakers could have been included. We endeavoured to cover geographies and had four speakers and 12 lightning talks from these regions, and added a reduced local rate which increased registrations from Japan substantially from previous satellite meetings. Stronger local engagement with these areas is a possible area for future improvement.
- Other possible points noted improvement included: providing more meals and coffee; internet for participants at the venue; adding a short social event on the first day.