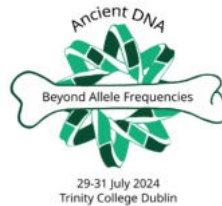


Event: SMBE Satellite Meeting on Ancient DNA: Beyond Allele Frequencies. Smurfit Institute of Genetics, Trinity College Dublin (TCD), Dublin, Ireland. 29th-31st July 2024

Organisers: Emily M. Breslin, TCD; Marco Rosario Capodiferro, TCD; Kevin G. Daly, University College Dublin (UCD); Anahit Hovhannisyan, TCD; Valeria Mattiangeli, TCD; Victoria E. Mullin, TCD; Linda Ongaro, TCD

Website: <https://www.tcd.ie/Genetics/events/ancient-dna-2024/>

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Meeting Overview

On 29th-31st July 2024, we welcomed 86 attendees (registered: 46 in-person, 37 online and 3 plenary speakers) to the SMBE Satellite Meeting on Ancient DNA: Beyond Allele Frequencies at Trinity College Dublin. Registered attendees represented researchers in 23 countries from 3 continents. The aim of the meeting was to bring together ancient DNA researchers working on large-scale ancient population datasets, high-coverage genomes and low coverage-optimised imputation algorithms. These datasets allow for a new phase of ancient genomic analysis, stepping beyond conventional allele-sharing approaches and utilising haplotype methods to allow for a fine-scaled understanding of ancient relationships and demographic reconstruction. We designed the meeting to be friendly to Early Career Researchers, and aimed to promote the exchange of knowledge and best practices for those working on a range of species. To facilitate this and to take stock of the field, we included both talks, a roundtable discussion and a panel discussion. In addition to the meeting organisers, we had volunteers from the ancient DNA groups in Trinity College including Prof Dan Bradley, Dr. Emilia Huerta-Sánchez and Dr. Shigeki Nakagome. A goal of this meeting is to write a review paper, with organisers and willing attendees, on the themes presented at this meeting. We are yet to start this process, but intend to in the coming months.



Plenary Speakers



We had three plenary speakers at the SMBE Satellite Meeting on Ancient DNA. Our plenary speakers represented different themes of ancient DNA research: kinship, ancestral recombination maps, and archaic admixture.

Our first plenary speaker was Dr. Lara Cassidy, who is an Assistant Professor in the School of Microbiology and Genetics, Trinity College Dublin. Lara delivered a talk on haplotype-based methods and their application in achieving fine-scale resolution, using an example focused on the demography of Ireland and Britain.

Our second plenary speaker was Dr. Leo Speidel, a Sir Henry Wellcome fellow at UCL, who shared insight into his novel methods about ancestry reconstruction using joint genealogies with ancient and modern genomes. Our last plenary speaker was Dr. Benjamin Peter, Group Leader Evolutionary Genetics MPI Leipzig, who delivered a talk on archaic human ancestry through time. All the speakers had 35 minutes for their presentation followed by 10 minutes for questions from the audience, which sparked active discussions.



Talk Sessions

The talk sessions were held in the lecture theatre at the Moyne Institute of Preventive Medicine, located on the TCD campus. This lecture theatre was the perfect size for our audience and was equipped with an audio/video system that allowed us to stream the talks live. Talks were recorded and, with the permission of the speaker, will be shared with SMBE for the benefit of the wider scientific community by the end of this year.

During the three days, there were five talk sessions organised by topic: two sessions on human genetics, one on animal genetics, one methodological session, and one open session. In total, there were twenty-eight talks, comprising twenty long talks (12 minutes + 3 minutes for questions) and eight short talks (5 minutes + 2 minutes for questions). This format allowed more attendees to present their work; more than 50% of the attendees presented their work with an oral presentation, including 14 postgraduate students and eight

post-doctoral researchers. Additionally, we prioritised diversifying our presenters to ensure a balanced representation of gender, career stage, and geographic background.

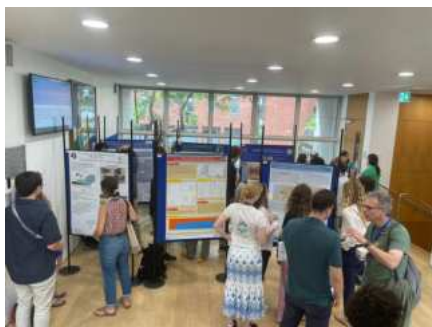
The talks were very well received and many questions were asked from the audience. We have attached the abstract book and programme to this report.



Finally, we presented two awards for presentations: one for the best postdoc talk (Stephen Gaughran, in the photo) and one for the best PhD student talk (Théo Cavinato). Each award came with a prize of €100. The judges of the awards were chosen among the PIs that attended the conference and the plenary speakers.

Poster Session

We organised two poster sessions, one on the morning of the 30th and another on the morning of the 31st. In total, twenty posters were presented, ten each day. However, all the posters remained on display, allowing attendees to view them during breaks as well. We



chose to hold the poster sessions in the atrium of the Smurfit Institute, where we also had our coffee breaks and lunches. We offered the poster presenters the opportunity to present their posters with a flash talk (2 minutes, with no slides); seven people agreed and presented before the first poster session.

At the end, we awarded two Best Poster Presentation prizes (Nicola Vogel and Megha Srigyan), each worth €100. The judges of the awards were senior researchers attendees, including the plenary speakers.

Breakout Sessions and Panel Discussion

In the breakout sessions attendees were split into groups of approximately eight people, based in their own discussion space. The plenary speakers, in addition to some PIs in attendance, led the discussions, focussing on different topics in the field of ancient DNA. These discussion leaders rotated between breakout groups at regular intervals, allowing each group to have discussions on different topics and areas of debate in the field, as well as allowing similar discussion points to be brought to multiple groups. Notes were taken by conference volunteers in each breakout group to aid in writing the follow-up review paper from the conference. Some of the questions posed by discussion leaders are listed below:



- Will the field of aDNA be transformed by ARGs?
- What ethical questions are we neglecting in aDNA? Should we be fostering research growth in countries lacking established aDNA groups?
- What is the most exciting aDNA paper of the last three years?
- Should (demographic) modelling be more frequently incorporated into aDNA studies?
- Should we be trying to better integrate aDNA from multiple species in the same (or linked) studies? Or different aDNA subfields, e.g. pathogens and humans, genomics and epigenomics?
- What is a neglected source of bias and error the aDNA is overlooking? For example, batch effects, differences between sequencing platforms
- What fields beyond genetics should aDNA studies be engaging with more? E.g. Conservation? Ecology? Other subfields of archaeology?
- What can the human aDNA field learn from the animal aDNA field?
- What is the next big direction for aDNA?
- What are the necessary steps for haplotype-based methods to be applied beyond human and domesticated research?
- Genome assembly projects such as the Vertebrate Genomes Project and Darwin Tree of Life are producing high-quality reference genomes for species across the globe. Where do we go from here? How do we make the best use of them?
- Choosing between shotgun sequencing and genome capture for ancient DNA analyses (or are there other alternatives?)
- Approaches to integrate pangenomes in aDNA research?
- How to merge different sequencing technologies in different analyses OR can we future-proof ancient DNA? How do we avoid getting trapped on specific platforms or protocols?
- What best practices should be applied to haplotypes methods?
- Application of ethnographic data in aDNA interpretation?



A panel discussion was held at the end of the last day of the conference. The panel consisted of the plenary speakers and an invited contributor (Federico Sánchez-Quinto) and was moderated by Prof Dan Bradley. A number of questions based on the discussion points from the breakout sessions and presentations

throughout the conference were posed, with some time allocated for open questions from the floor. This was an excellent opportunity to synthesise the ideas which had emerged from the conference and provided a space for discussion that included all attendees.

Logistics

We were greatly facilitated in the planning of the meeting by support staff in the School of Genetics and Microbiology, to which we remain grateful. Almost all attendees were housed on-campus, made possible due to reduced rates for university events. Several attendees required additional days of accommodation either before or after the meeting, which we facilitated. A number of attendees also brought their young families or partners with them to the meeting, which we facilitated by booking larger rooms or entire apartments. Prior to arrival, we supplied attendees with an "Information Package", highlighting travel logistics/options, the layout of the university, cafes/restaurants nearby, and also safety details (including the contact information of on-campus security, our designated Safety Officers, and gathering points in the event of a fire). Online streaming of the talks was via Zoom, questions by the online audience were asked via the chat function. We also had a Slack account set-up for all attendees to further discussions. The posters were placed online in the slack channel for all attendees to look at and ask questions.

Social Events



As the main aim of this event was to promote discussion and networking for researchers, we structured the meeting to provide time for this to take place, including four coffee breaks and two evening social events. The social events were followed by two trips to iconic Irish pubs. We tied the two poster sessions into coffee breaks to help promote discussion during these sessions. Additionally, we set up a Slack account for all attendees to enable discussion and a WhatsApp community for in-person attendees to help

communication during the conference.

Challenges

An issue we foresaw prior to the conference was last minute cancellations due to Covid and other emergency issues, and also the possibility of Covid outbreaks at the meeting. We planned our talk sessions to take place in a lecture hall with live-stream capability. This allowed one speaker to present *in absentia* and for a substantial number of online-only attendees to join us. We were fortunate to avoid any Covid outbreaks but had hand sanitiser, masks, and antigen tests available for attendees.

An additional challenge we saw was engagement between researchers focusing on animal and human ancient genomics as it is uncommon for single session aDNA conferences where this interaction occurs. However, the animal presentations were very well received by the entire audience, and one of the animal presentations was given an award for best presentation by a postdoc. We believe the meeting successfully bridged a perceived gap between those working in human and animal ancient genomics, which was one of our intended aims.

Twitter account

For dissemination and public engagement, we created a Twitter account, @SMBESat2024_TCD, where we actively tweeted updates, highlights and key moments from each day of the conference. By the end of the SMBE Satellite Meeting, we had reached 154 followers.

