

JAMES RENNIE BEQUEST

REPORT ON EXPEDITION / PROJECT / CONFERENCE

**Expedition/Project/
Conference Title:** CSHL Biology of Genomes 2023 Meeting

Travel Dates: 7th – 16th May 2023

Location: Cold Spring Harbor Laboratory, New York

Group member(s): Anima Sutradhar

Aims:

- 1) Present my research at the top genomics conference and improve my science communication skills.
- 2) Gain knowledge of the field of genomics: latest trends, cutting-edge techniques and a sense of where the field is heading.
- 3) Network with other early career researchers and experts, building a strong community around me and gaining confidence as a scientist.

Photography consent form attached: Yes
(please refer to your award letter) No

OUTCOME (a minimum of 500 words):-

This May I had the privilege of attending the 36th annual meeting on Biology of Genomes at Cold Spring Harbor Laboratory (CSHL), New York. This is a renowned conference that gathers the top researchers and experts in the field of genomics. This report aims to provide a reflection of my experience at the conference, discuss how my goals were achieved and highlight key impressions left on me and their impact on my development as a scientist.

Conference overview:

The conference had a diverse range of sessions showcasing the entire breadth and depth of this rapidly advancing field, covering population genetics, microbiomes, epigenetics, evolutionary genomics, developmental and single-cell studies, as well as the latest computational approaches for larger-scale studies. Throughout these sessions, I learned about current popular methods in genomics research such as GWAS, perturb-seq and scRNA-seq. Meaning current genomics research is shifting away from an “averaged” view of phenotypic outcomes, towards more high-resolution data that aims to capture sequence, expression and cellular heterogeneity. This made me understand the limitations of my own research in codon usage based on bulk RNA-sequencing data, but also opened my eyes to future avenues to explore. It was also interesting to learn of the many consortia now existing, showing the growing collaborative nature of the genomics field.

My favourite talks:

Along with trending methods, I also learned of trending genomics topics. Some of my personal favourites included: **Telomere-to-telomere** (T2T) research, whereby the T2T consortium are

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now working to close sequencing gaps to finally provide more complete and accurate sequences of chromosomes. I further learned about how researchers were using T2T results in the development of **pan-genomes**. For example, rather than representing a species by a single reference genome (as traditionally done), researchers can combine multiple genome assemblies to create a “pan-genome” that more accurately captures the landscape of genetic variability within a species. I also realised, that by incorporating nearly 7,000 transcriptomes to account for genetic variation in my own work, I had created a sort of “pan-genome” for *E. coli*! However, one of the topics that really fascinated me is how genomics is being used to uncover our **ancient human origins and evolution**, especially the latest genomic findings of our more archaic hominin groups such as the Denisovans and Neanderthals.

We also had an ethics panel and discussion on scientists’ roles and responsibilities in combatting the **misuse of genomics research**. With the field’s past and CSHL’s history in being the base of the Eugenics Record Office, this panel was important in raising awareness of the current intentional and unintentional misuse and misinterpretation of genomics research. This field is especially susceptible to miscommunication given the complexity of data and technical jargon. Here, the panel raised awareness on how genomics is currently being used to justify the actions and beliefs of white supremacists, as well as in more subtle ways such as affecting policies around education, immigration and judicial sentencing. This panel acted as a starting point on the topic and I appreciated the methods presented for thinking about and communicating these issues to colleagues and the media. Altogether, I learned how powerful and precise genomics as a tool has become for very diverse applications as well as its potential for serious misuse if the field does not take a more active approach in science communication and outreach.

Poster presentation experience:

I presented my poster titled, “Transcriptome-wide meta-analysis of codon usage in *Escherichia coli*”. The most challenging (but ultimately most rewarding) part of the poster presentation was answering questions and seeing how those not in the field of codon usage understood my work. I initially thought that with genomics being a specialised field, that it would be a lot easier to communicate my work, even with the different sub-fields. Unfortunately I was very wrong about this. It turns out each of these different sub-fields carry with them their own language and technical jargon, and it was a very humbling experience to communicate my work from the perspective of a geneticist, a biostatistician, an RNA biologist, a synthetic biologist, a computer scientist (the list goes on).

However, I am happy to say my poster was well-attended, with researchers offering ideas to try (particularly on the experimental validation aspect of my project). Several researchers were also keen to stay in touch to follow my research progress, and with an interest to read my upcoming pre-print! One piece of advice I got from a very kind final-year PhD student was to have an elevator pitch when presenting my work, and to not be afraid of showing off the work I have done. This will be something I do going forwards, in conferences as well as during other events where I get to discuss my research. In future, I will also avoid putting too much text in my poster and be more selective of the figures. Overall, engaging with a range of genomics researchers and having them interrogate my work from multiple angles gave me confidence I am going in the right direction in terms of my research and its validation.

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Networking opportunities:

In this conference I got to connect with many researchers. Being at CSHL – a research institution that played a central role in the development of molecular biology – created a very unique environment and atmosphere. This, along with the conference being campus-based and surrounded by beautiful nature, contributed to a strong sense of community, making it very easy to meet with other researchers and exchange ideas. It was nice to connect with peers (majority US-based) and see the similarities and differences of our PhD experiences and learn about available career options. I also plucked up the courage to speak with some PIs my supervisor recommended, and learned I had no reason to be intimidated. This experience has given me the confidence to approach researchers and has also laid the foundation for a supportive professional network.

Concluding remarks:

I am very grateful to the James Rennie Bequest for contributing towards the cost of attending this conference, giving me the opportunity to meet wonderful researchers, establish connections with them and showcase my work at such a prestigious meeting. Overall, CSHL has left a lasting impression on me. Most importantly the conference gave me the confidence I needed, to see that I am developing into a capable and independent scientist who can put myself out there. The inspiring energy, enthusiasm and acceptance I felt here will not be forgotten and is something I aim to carry with me throughout my research.