

Keio SFC Academic Society: Grants for RESEARCH PROJECTS
Grant for Research presentation at academic conference (A)

Conference Report on Intelligent Systems for Molecular Biology (ISMB)

Kaoru Ogino

Keio University, Faculty of Environment and Information Studies, Third Year Undergraduate

Conference Overview:

Conference Name: Intelligent Systems for Molecular Biology (ISMB)

Date: July 12, 2024 – July 17, 2024

Venue: Palais des Congrès de Montréal, Montréal, QC, Canada

Format of Organization: Hybrid (Both in-person and online)

Research Title: Unveiling the Genomic Insight into the Exceptional Visual System of a Jumping spider, *Carrhotus xanthogramma*

Presentation Format: In-person Poster Presentation

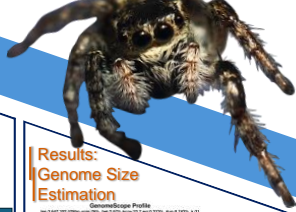
Conference Report:

I have participated in the conference, Intelligent Systems for Molecular Biology (ISMB) that was held in Montreal, Canada and had the precious opportunity to present my research through a poster presentation. This conference is held once every year by the International Society for Computational Biology (ISCB) and recognized as one of the largest bioinformatics and computational biology conference in the world that gathers various researchers to discuss and showcase developments and innovations made in various fields. It was held both in-person and online attendance bringing 1,900 participants from different countries and background, making it a priceless opportunity that enabled many learning experiences.

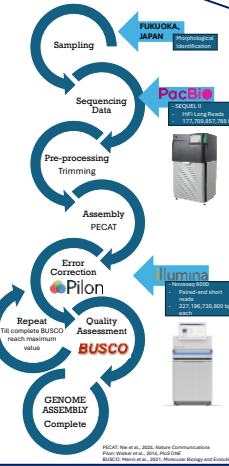
This was my first conference and an international one, as well as being the very few undergraduate participants, which made this experience invaluable. Being able to present my research on the genome assembly of the jumping spider, *Carrhotus xanthogramma* and the species identification of an unknown Japanese fruitfly, *Torinido-shoujoubae*, through COI DNA barcoding was rewarding. There were many opportunities to communicate with various researchers, professors and PhD students about my work and was able to receive insightful feedbacks which has given me directions for the future of my research. Especially since the conference accommodates experienced scientists from various fields within the larger entity of biology, I was able to broaden my understanding on the research that I undertook and provided me with potential ideas and techniques to apply to my studies.

The conference was not only about presenting my research but also learning and networking. I attended numerous talks and discussions that covered a wide range of topics in bioinformatics such as the use of language models in predictions of proteins or the development of algorithms for genomic analysis. These sessions were highly informative and allowed me to have an exposure to new ideas and the latest advancements and challenges in a wide ranging field. The attendance in ISMB 2024 was a pivotal experience in my academic journey with the exposure to the global scientific community, feedbacks on my research and the learning and networking opportunities have significantly contributed to my growth as a researcher. I am deeply grateful for this granted opportunity and look forward on applying what I have gained through this conference to further advance my research for a fruitful outcome.

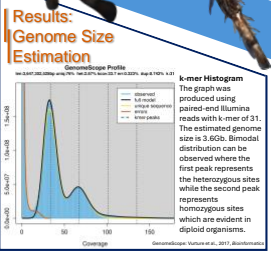
Poster:



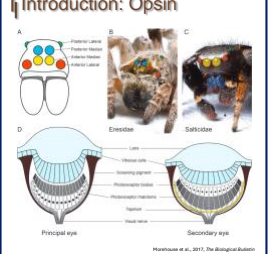
Methods



Results: Genome Size Estimation



Introduction: Opsin



Abstract

Jumping spiders (Araneae: Salticidae) exhibit exceptional visual acuity, unique courtship displays and hunting strategies, which diverge from the typical web-building tactics of other spiders. This visual system is supported by four pairs of eyes, specializing in prey identification and motion detection. This research aims to elucidate genetic underpinning of the visual system, physical attributes and silk production of jumping spiders, through both behavioral and molecular genomic approach, while conducting a comparative study with other spiders. Establishment of reliable breeding protocols is necessary for maintaining replicability and for generating controlled populations for genetic and behavioral analysis. As part of this effort, we identified a previously unknown *Drosophila* sp. feed, *Torinido-shoujoubae* in Japanese, as *Drosophila hydei* through COI DNA barcoding. This enables the maintenance of spiders' natural diet and behavior in captivity, thereby providing more authentic context for studying hunting strategies. Genome sequencing of *Carrhotus xanthogramma*, a jumping spider, was conducted through the use of two techniques: short paired-end reads by Illumina NovaSeq 6000 and long reads by PacBio Sequel II. However, the preliminary results of hybrid genome assembly using HASLR and MaSuRCA presented significantly low quality in BUSCO coverage, indicating challenges in obtaining a complete and accurate genome. The future direction of our research will focus on resolving assembly issues and analyzing the genetic basis of the jumping spider's visual system and silk production. By comparing these genes with those of other spiders, we aim to shed light on the evolutionary adaptations that have enabled the remarkable capabilities of jumping spiders.

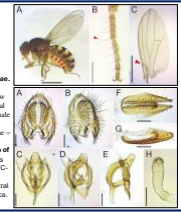
Future Work

- Further Assembly**
 - Polishing and Refinement: further rounds of error correction using Pilon
 - Alternative Assembly Tools: compare assembly tools to assess the efficacy
- Gene Prediction and Annotation**
 - Predict coding regions and annotate genes
 - BLAST analysis to assign functional information to predicted genes
- Functional Genomics**
 - Identification of Opsin Genes: insights to photoreceptive capabilities and visual adaptations
 - Spiridin Gene Characterization: analyze spiridin genes against their roles such as uses in dragline and burrow construction
- Comparative Genomics**
 - Genomic Comparison with Other Spiders: identify conserved and divergent regions
 - Phylogenetic Analysis: elucidate evolutionary relationships between *C. xanthogramma* and other spider species

Results: Assembly Statistics

Description	Statistics
Input Lengths (Coverage)	
Long reads	177,709,857,788 bp (-50x)
Paired-end (Forward)	227,196,730,800 bp (-65x)
Paired-end (Reverse)	227,196,730,800 bp (-65x)
Genome size	
Expected	3.2-3.6Gb
After Assembly with PECAT	4.3Gb
Complete BUSCOs	51.7%
Length	4,391,551,459
Number of Scaffolds	51247
NS0	120KB
GC Content (%)	30.81%

Results: Taxonomic Diagnosis



Species identification of livefood flightless fly (*Torinido-shoujoubae*) by using DNA barcoding

Unveiling the Genomic Insight into the Exceptional Visual System of Jumping spider, *Carrhotus xanthogramma*

Kaori Ogino^{1,2}, Koh Nakagawa¹, Nobuaki Kono^{1,2,3}

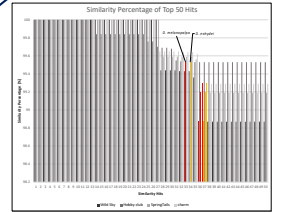
Institute for Advanced Biosciences, Keio University

1. Institute for Advanced Biosciences, Keio University

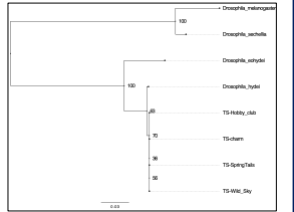
2. Faculty of Environment and Information Studies, Keio University

3. Graduate School of Media and Governance, Keio University

Results: BLAST Analysis



Results: Phylogenetic Tree



Acknowledgements

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Grants

