

FY2019 Annual Report (April 2019-March 2020)

Molecular Genetics Unit

Professor Daniel Rokhsar (Adjunct; Visiting)

Abstract

Genomic perspective on the evolution of plants and animals

The comparative study of genomes provides a window into the origin and evolution of plant and animal diversity. Contemporary genomes evolved by descent with modification from earlier sequences, accumulating both neutral and adaptive mutations, with varying genomic impact ranging from small changes in sequence to radical changes in chromosome number and gene content. We apply the general comparative principle: features that are shared by two or more genomes were either present in their common ancestor, or evolved convergently.

This principle allows us, for example, to infer the gene content and even genome structure of early vertebrate by comparing genomes of appropriately chosen living species, and to discern macro-evolutionary trends. Similarly, analysis of genetic variation within individual species or between closely related populations sheds light on the evolutionary mechanisms underlying the origin and diversification of new species. The dynamic nature of genomes, including the waxing and waning of transposable elements that generate complex repetitive patterns, also provide opportunities for inferring past events that shaped the diversity of life.

1. Staff

- Dr. Ferdinand Marletaz, postdoctoral researcher
- Dr. Daria Gavriouchkina, postdoctoral researcher
- Dr. Chikatoshi Sugimoto, postdoctoral researcher
- Dr. Yuko Hasegawa, technician
- Mr. Jeff Jolly, technician
- Ms. Chika Azama, Research Administrator

2. Collaborations

2.1 Theme: Origins of Japanese Citrus

- Type of collaboration: Collaboration
- Researchers
 - Prof. Fred Gmitter (University of Florida, USA)
 - Dr. Albert Wu (DOE Joint Genome Institute, USA)
 - Prof. Manuel Talon (Instituto Valenciano de Investigaciones Agrarias, Spain)

2.2 Theme: Amphioxus genome and the evolution of vertebrate chromosomes

- Type of collaboration: Collaboration
- Researchers
 - Prof. Oleg Simakov (University of Vienna, Austria)

- Prof. Richard E. Green (University of California, Santa Cruz, USA)
- Prof. Nori Satoh (OIST)

2.3 Theme: Evolution and diversity of cephalopods

- Type of collaboration: Collaboration
- Researchers
 - Prof. Amanda Reid (Australian Museum Research Institute)
 - Prof. Spencer Nyholm (University of Connecticut, USA)
 - Prof. Margaret McFall-Ngai (University of Connecticut, USA)
 - Prof. Oleg Simakov (University of Vienna, Austria)

3. Activities and Findings

3.1 Amphioxus genome and the evolution of vertebrate chromosomes

We have assembled the chromosome of the Florida lancelet, *Branchiostoma floridae*, and developed new methods for comparing the chromosomal organization of this species with the organization of other invertebrates and vertebrates. This analysis conclusively answers several puzzles about early vertebrate evolution. We provide conclusive proof that (1) all vertebrates (including jawless lampreys and the jawed fishes and land-dwelling vertebrates) share one common whole genome duplication (“1R”), (2) jawed vertebrates share a second whole genome duplication (“2Rjv”) that not found in lampreys, and (3) the jawed-vertebrate specific duplication occurred via allotetraploidy, a process that occurs via hybridization of distinct progenitors. Dr. Marletaz in our unit also led a functional study of the European amphioxus, shedding light on the origins of vertebrate gene regulation.

3.2 Evolution and diversity of citrus

The species diversity of the genus *Citrus*, which includes some of the most widely cultivated fruit crops worldwide, is poorly understood. Using genomic, phylogenetic and biogeographic analyses of 60 accessions representing diverse citrus germplasms, we describe ten natural citrus species. Further identification and analyses of hybrids and admixed genomes provides insights into the genealogy of major commercial cultivars of citrus. Among mandarins and sweet orange, we find an extensive network of relatedness that illuminates the domestication of these groups. Widespread pummelo admixture among these mandarins and its correlation with fruit size and acidity suggests a plausible role of pummelo introgression in the selection of palatable mandarins. We propose that citrus diversified during the late Miocene epoch through a rapid southeast Asian radiation that correlates with a marked weakening of the monsoons. A second radiation enabled by migration across the Wallace line gave rise to the Australian limes in the early Pliocene epoch. This work provides a new evolutionary framework for the genus *Citrus*, which we are extending to include Japanese and Ryukyuan citrus.

3.3 Evolution and diversity of cephalopods

Our unit previously led the genome sequencing of the Octopus genome, and is engaged in the sequencing and analysis of several additional cephalopod genomes, including bobtail squid from Japan and the Ryukyu Islands. Bobtail squid are emerging models for host-microbe-interactions, behavior, and development, yet their species diversity and distribution remain poorly

characterized. We undertook a comprehensive analysis of the local Ryukyuan bobtail squid in the broader context of bobtail phylogeny. Our morphological and genomic analysis revealed the existence of at least one new species of bobtail, which we formally described and named *Euprymna brenneri* in honor of Sydney Brenner, the founding president of OIST. We also showed that the previous definition of the genus *Euprymna* needed modification. Ongoing studies include culturing and morphological, genomic, and behavioral analysis of local and mainland Japanese bobtail squid. As part of this project, we contributed to the sequencing of the Hawaiian bobtail squid *Euprymna scolopes*, published in 2019.

4. Publications

4.1 Journals

1. Gustavo Sanchez, **Jeffrey Jolly**, Amanda Reid, **Chikatoshi Sugimoto**, **Chika Azama**, **Ferdinand Marlétaz**, Oleg Simakov, **Daniel S. Rokhsar**, “New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis” *Communications Biology*. (2019) 2:465 | doi: <https://doi.org/10.1038/s42003-019-0661-6>

4.2 Books and other one-time publications

1. Frederick G Gmitter, Jr, G. Albert Wu, Daniel S. Rokhsar, Manuel Talon (2020). “The Citrus Genome”. Chapter 1 in “The Genus Citrus,” edited by M. Talon, M. Caruso, FG Gmitter Jr. (Elsevier). Doi: <https://doi.org/10.1016/B978-0-12-812163-4.00001-2>.
2. Manuel Talon, G Albert Wu, Frederick G. Gmitter Jr, Daniel S Rokhsar. “The Origin of Citrus”. Chapter 2 in “The Genus Citrus”, edited by M. Talon, M. Caruso, FG Gmitter Jr. (Elsevier). Doi: <http://doi.org/10.1016/B978-0-12-812613-4.00002-4>

4.3 Oral and Poster Presentations

Nothing to report

5. Intellectual Property Rights and Other Specific Achievements

Nothing to report

6. Meetings and Events

6.1 Seminar: Deconstructing DNA methylation: provocative insights from non-model species

- Date: November 6, 2019
- Venue: OIST Campus Lab3
- Speaker: Dr. Alex de Mendoza (The University of Western Australia)

7. Other

Nothing to report