

FY2020 Annual Report (April 2020-March 2021)

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. Daria Gavriouchkina, postdoctoral researcher
- Dr. Chikatoshi Sugimoto, postdoctoral researcher
- Dr. Yuko Hasegawa, technician
- Mr. Jeff Jolly, technician
- Ms. Lin Zhang, technician
- Dr. Ferdinand Marletaz, visiting researcher
- Ms. Chika Azama, research unit administrator
- Ms. Kiyoko Yamada, research unit administrator

2. Collaborations

2.1 Theme: Origins and diversity of mandarin citrus

- Type of collaboration: Collaboration
- Researchers
 - Prof. Fred Gmitter (University of Florida, USA)
 - Dr. Albert Wu (DOE Joint Genome Institute, USA)
 - Dr. Hideyasu Kinjyo (Okinawa)
 - Dr. Fumimasa Musebe (Okinawa Prefectural Agricultural Research Center)
 - Prof. Manuel Talon (Instituto Valenciano de Investigaciones Agrarias, Spain)

2.2 Theme: The evolution of metazoan genomes

- Type of collaboration: Collaboration
- Researchers
 - Prof. Jeramiah Smith (U. Kentucky, USA)
 - Prof. Oleg Simakov (University of Vienna, Austria)
 - Prof. Richard E. Green (University of California, Santa Cruz, USA)
 - Prof. Chris Lowe (Hopkins Marine Station, Stanford University, USA)

2.3 Theme: Evolution and diversity of cephalopods

- Type of collaboration: Collaboration
- Researchers
 - Prof. Oleg Simakov (University of Vienna, Austria)
 - Dr. Carrie Albertin (Marine Biological Laboratory, Woods Hole)
 - Prof. Cliff Ragsdale (University of Chicago, USA)
 - Dr. Joshua Rosenthal (Marine Biological Laboratory, Woods Hole)
 - Prof. Gustavo Sanchez-Silva (Hiroshima University, Japan)

3. Activities and Findings

3.1 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, in part due to their propensity for hybridization and asexual reproduction by nucellar embryony (a form of apomixis). We have used genomic, phylogenetic and biogeographic analyses of diverse citrus germplasms to identify primary citrus species and their role in producing admixed or hybrid taxa. Our early studies established a new evolutionary framework for the genus *Citrus*, and we have extended this synthesis to include Japanese and Ryukyuan citrus. In addition to providing insights into the genealogy of well-known cultivars, we find an extensive network of relatedness that illuminates the population genetics of diverse Okinawan accessions and their relationship to mainland Japanese and Asian citrus. These studies also illuminate the origin and spread of an apomixis gene that allows hybrids with desirable traits to be stably propagated.

3.2 The evolution of metazoan genomes

We have developed new methods for analyzing the evolution of genomes at the level of their chromosomal organization and are using these methods to explore the evolution of animals. Our analysis conclusively answers several puzzles about early vertebrate evolution. We provide definitive 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 (“2R_{lv}”) that not found in lampreys, and (3) the jawed-vertebrate specific duplication occurred via allotetraploidy, a process that occurs via hybridization of distinct progenitors. We are applying these approaches to other animals including hydra, hemichordates, and hagfishes.

3.3 Evolution and diversity of cephalopods

Our unit previously led the genome sequencing of the Octopus genome, contributed to the study of the *E. scolopes* (Hawaiian bobtail squid) genome, and characterized the local bobtail squid around Okinawa. We are currently working on several new cephalopod genomes, including reference quality genomes for the longfin inshore squid famous for its giant axon and for a Japanese bobtail squid that is an emerging model system for cephalopod biology. Remarkably, we find that karyotypes are broadly stable among cephalopods but rearranged relative to other molluscs, and find distinct regimes of RNA editing based on in depth analysis of transcriptomes. Genome skimming of diverse bobtail squid illuminates the phylogeny and biogeography of this diverse group but whose an emerging model system. Bobtail squid are emerging models for host-microbe-interactions, behavior, and development, yet their species diversity and distribution remain poorly characterized. Ongoing studies include characterization of life history and culture conditions of Japanese bobtail squid, behavioral adaptation to light and texture, and the structure and organization of the central nervous system.

4. Publications

4.1 Journals

1. Martín-Durán JM, Vellutini BC, **Marlétaz F**, Cetrangolo V, Cvetesic N, Thiel D, Henriët S, Grau-Bové X, Carrillo-Baltodano AM, Gu W, Kerbl A, Marquez Y, Bekkouche N, Chourrout D, Gómez-Skarmeta JL, Irimia M, Lenhard B, Worsaae K, Hejnol A (2020). "Conservative route to genome compaction in a miniature annelid." *Nature Ecology Evolution*. doi: 10.1038/s41559-020-01327-6. PMID: 33199869.
2. Mitros, T., Session, A.M., James, B.T., Wu, G.A., Belaffif, M.B., Clark, L.V., Shu, S., Dong, H., Barling, A., Holmes, J.R., Mattick, J.E., Bredeson, J.V., Liu, S., Farrar, K., Głowacka, K., Jeżowski, S., Barry, K., Chae, W.B., Juvik, J.A., Gifford, J., Oladeinde, A., Yamada, T., Grimwood, J., Putnam, N.H., De Vega, J., Barth, S., Klaas, M., Hodgkinson, T., Li, L., Jin, X., Peng, J., Yu, C.Y., Heo, K., Yoo, J.H., Ghimire, B.K., Donnison, I.S., Schmutz, J., Hudson, M.E., Sacks, E.J., Moose, S.P., Swaminathan, K., **Rokhsar, D.S.** 2020. "Genome biology of the paleotetraploid perennial biomass crop *Miscanthus*." *Nature Communications* 11(1):5442. doi: 10.1038/s41467-020-18923-6.
3. Peijnenburg KTCA, Janssen AW, Wall-Palmer D, Goetze E, Maas AE, Todd JA, **Marlétaz F** (2020). "The origin and diversification of pteropods precede past perturbations in the Earth's carbon cycle." *Proc National Academy Sciences USA*. 117(41):25609-25617. doi: 10.1073/pnas.1920918117. PMID: 32973093.
4. Mudd, A.B., Bredeson, J.V., Baum, R., Hockemeyer, D., **Rokhsar, D.S.** 2020. "Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution." *Communications Biology* 3(1):480. doi: 10.1038/s42003-020-1096-9.
5. **Simakov, O.***, **Marlétaz, F.***, Yue, J.X., O'Connell, B., Jenkins, J., Brandt, A., Calef, R., Tung, C.H., Huang, T.K., Schmutz, J. and Satoh, N., Yu, J.-K., Putnam, N.H., Green, R.E. & **Rokhsar, D.S.**, 2020. "Deeply conserved synteny resolves early events in vertebrate evolution." *Nature Ecology and Evolution*, 4:820–830. doi: 10.1038/s41559-020-1156-z.
6. Almudi, I., Vizueta, J., Wyatt, C.D.R., de Mendoza, A., **Marlétaz, F.**, Firbas, P.N., Feuda, R., Masiero, G., Medina, P., Alcaina-Caro, A., Cruz, F., Gómez-Garrido, J., Gut, M., Alioto, T.S., Vargas-Chavez, C., Davie, K., Misof, B., González, J., Aerts, S., Lister, R., Paps, J., Rozas, J., Sánchez-Gracia, A., Irimia, M., Maeso, I., Casares, F. 2020. "Genomic adaptations to aquatic

and aerial life in mayflies and the origin of insect wings." *Nature Communications* 11(1):2631. doi: 10.1038/s41467-020-16284-8.

4.2 Books and other one-time publications

1. Minemizu, R., Ikeda, N., **Sugimoto C** (as the editorial supervisor) (2020). "'How different between octopus and squid?' picture book about comparing animals." Poplar Publishing, 32 pages.

4.3 Oral and Poster Presentations

1. Sugimoto, C., Rokhsar, D. S. *Evaluation of spatial cognitive and communicative ability of bobtail squids with LED light stimuli*, Japanese Society of Fisheries Science, online meeting, Japan, March 29 (2021)

5. Intellectual Property Rights and Other Specific Achievements

Nothing to report

6. Meetings and Events

Nothing to report

7. Other

Nothing to report