

FY2014 Annual Report (April 2014-March 2015)

Molecular Genetics Unit

Professor Daniel Rokhsar (Adjunct; Visiting)

1. Staff

- Dr. Oleg Shimakov, Researcher
- Dr. Eric Edsinger, Researcher
- Ms. Kiyomi Iha, Research administrator

2. Collaborations

2.1 Theme: The genome of the octopus and cephalopod novelty

- Type of collaboration: Collaboration
- Researchers
 - Prof. Clifton Ragsdale (University of Chicago, USA)
 - Carrie Albertin (University of Chicago, USA)
 - Z. Yan Wang (University of Chicago, USA)
 - Judit Pungor (University of Chicago, USA)
 - Therese Mitros (University of California, Berkeley, USA)
 - Dr. Sydney Brenner (OIST and A*STAR, Singapore)

2.2 Theme: Decoding hemichordate genomes and deuterostome origins

- Type of collaboration: Collaboration
- Researchers
 - Prof. Noriyuki Satoh, OIST and team
 - Prof. John Gerhart (University of California at Berkeley, USA)
 - Dr. Takeshi Kawashima (University of Tsukuba, Japan)
 - Prof. Chris Lowe (Stanford University, USA) and team
 - Prof. Marc W. Kirschner (Harvard Medical School, USA) and team
 - Prof. Jr-Kai Yu (Academia Sinica, Taiwan) and team
 - Prof. Kim C. Worley (Baylor College of Medicine, USA) and team

2.3 Theme: Mechanisms of Hydra head regeneration

- Type of collaboration: Collaboration
- Researchers
 - Prof. Thomas Holstein (University of Heidelberg, Germany) and team

3. Activities and Findings

Our Unit is generally interested in the genetic underpinnings of the origin and diversification of animals. We use genomics and experimental methods to infer and analyze evolutionary changes throughout metazoan phylogeny. Of special interest in the past year has been the analysis of the octopus genome in search of features that enable the remarkable complexity of cephalopods

relative to other molluscs, and the analysis of hemichordate genomes in the context of deuterostome evolution and the origin of vertebrate characters.

3.1 Analysis of the genome of *Octopus bimaculoides*

Coleoid cephalopods (octopus, squid, and cuttlefish) are active, resourceful predators with a rich behavioral repertoire. They have the largest nervous systems among the invertebrates, and present other striking morphological innovations including camera-like eyes, prehensile arms, embryogenesis, and the most sophisticated adaptive coloration system among all animals. To investigate the molecular bases of cephalopod brain and body innovations we are sequencing the genome of the California two-spot octopus, *Octopus bimaculoides*, an emerging model cephalopod. In collaboration with the Ragsdale group at the University of Chicago, we are also analyzing transcriptomes from multiple tissues and organs of octopus, including the nervous system, skin, and other organs. The genomes of cephalopods are substantially larger than those of other molluscan relatives, and we are seeking the genomic bases of cephalopod complexity through the analysis of gene families expressed during development and in the neuronal tissues; gene families unique to octopus or cephalopods; and the activity of transposons that may have contributed to large-scale genomic rearrangements. We have found no evidence for hypothesized whole genome duplications in the octopus lineage, and the core developmental and neuronal gene repertoire of the octopus appears to be broadly similar to that found across invertebrate bilaterians, with certain exceptions that are the subject of ongoing study. This work is continuing in FY2015.

3.2 Hemichordate genomes and deuterostome origins

Hemichordates, or acorn worms, are marine invertebrates with a filter-feeding lifestyle, enabled by pharyngeal gill pores. These animals are members of the deuterostome superphylum, a group that includes chordates (vertebrates and ascidians, and amphioxus) and echinoderms (sea stars and urchins) that diversified over 500 million years ago. As part of an international consortium of researchers in Okinawa, California, and Texas we have been analyzing the genomes of the direct developing acorn worm *Saccoglossus kowalevskii* and the indirect developing *Ptychodera flava*. Comparing these genomes to those of other animals we can identify over 8,000 shared gene families that were already present in the last common bilaterian ancestor, and can begin to pinpoint genes that originated in their modern form in the lineage leading to deuterostomes, and from the deuterostome ancestor to vertebrates. Strikingly, we have found evidence that hemichordate genomes share many short- and long-range linkages with other animals, implying that these gene linkages were also present in the deuterostome ancestor. We suggest that some of these linkages are preserved to maintain ancient gene regulatory networks. The paper will be published in FY2015.

3.3 The link between genomic innovation and regeneration

The cnidarian freshwater polyp *Hydra* sp. exhibits a regeneration capacity unparalleled in the animal kingdom. Decapitated animals can regrow a new head, and a complete animal can even be produced from dissociated cells. Together with the Holstein laboratory, Dr. Simakov guided bioinformatics studies of head regeneration in *Hydra* polyps, using an integrative transcriptomic/proteomic/phosphoproteomic approach. Diverse signaling pathways are activated during the regeneration response, and novel genes unique to *Hydra* are also turned on. A paper describing these analyses will be published in FY2015.

3.4 Cephalopod culture at OIST

Dr. Edsinger has been active in screening the cephalopod diversity on Okinawa and assessing the feasibility of different squid and octopus species for laboratory culture, molecular biology experimentation, and high-throughput imaging. This led to the investigation of the pygmy tropical species of Okinawa and greater Indo-Pacific, including the pygmy squid *Idiosepius spp.* Genome and transcriptome sequencing of several species has been initiated. Advances in cephalopod husbandry and the development of resources for diverse models is described in (Vidal *et al.* 2014).

3.5 Analysis of other animal genomes

Members of our unit have also contributed to the analysis of other genomes published in FY2014, including cichlid fish (Brawand *et al.* 2014), coelacanth (Chalopin *et al.* 2014), and limpet (Mann and Edsinger, 2014).

4. Publications

4.1 Journals

1. Lauri A., Brunet T., Handberg-Thorsager M., Fischer A.H., **Simakov O.**, Steinmetz P.R., Tomer R., Keller P.J., Arendt D. (2014). "Development of the annelid axochord: insights into notochord evolution." *Science* 345(6202):1365-8.
2. Brawand D., Wagner C.E., Li Y.I., Malinsky M., Keller I., Fan S., **Simakov O.**, Ng A.Y., Lim Z.W., Bezault E., Turner-Maier J., Johnson J., Alcazar R., Noh H.J., Russell P., Aken B., Alföldi J., Amemiya C., Azzouzi N., Baroiller J.F., Barloy-Hubler F., Berlin A., Bloomquist R., Carleton K.L., Conte M.A., D'Cotta H., Eshel O., Gaffney L., Galibert F., Gante H.F., Gnerre S., Greuter L., Guyon R., Haddad N.S., Haerty W., Harris R.M., Hofmann H.A., Hourlier T., Hulata G., Jaffe D.B., Lara M., Lee A.P., MacCallum I., Mwaiko S., Nikaido M., Nishihara H., Ozouf-Costaz C., Penman D.J., Przybylski D., Rakotomanga M., Renn S.C., Ribeiro F.J., Ron M., Salzburger W., Sanchez-Pulido L., Santos M.E., Searle S., Sharpe T., Swofford R., Tan F.J., Williams L., Young S., Yin S., Okada N., Kocher T.D., Miska E.A., Lander E.S., Venkatesh B., Fernald R.D., Meyer A., Ponting C.P., Streelman J.T., Lindblad-Toh K., Seehausen O., Di Palma F. (2014). "The genomic substrate for adaptive radiation in African cichlid fish." *Nature* 513(7518):375-81.
3. Chalopin D., Fan S., **Simakov O.**, Meyer A., Scharl M., Volff J.N. (2014). "Evolutionary active transposable elements in the genome of the coelacanth." *J Exp Zool B Mol Dev Evol.* 322(6):322-33.
4. Mann K., **Edsinger E.** (2014). "The *Lottia gigantea* shell matrix proteome: re-analysis including MaxQuant iBAQ quantitation and phosphoproteome analysis." *Proteome Sci.* 12:28.
5. Vidal E.A., Villanueva R., Andrade J.P., Gleadall I.G., Iglesias J., Koueta N., Rosas C., Segawa S., Grasse B., Franco-Santos R.M., Albertin C.B., Caamal-Monsreal C., Chimal M.E., **Edsinger-Gonzales E.**, Gallardo P., Le Pabic C., Pascual C., Roumbedakis K., Wood J. (2014). "Cephalopod culture: current status of main biological models and research priorities." *Adv Mar Biol.* 2014;67:1-98.

4.2 Books and other one-time publications

Nothing to report

4.3 Oral and Poster Presentations

1. Edsinger, E. *Human vs. Octopus: Post-genomic research needs a cephalopod model*. Young Zoologists Meeting, Oki Islands Marine Station, Okinoshima, Japan (July 2014)
2. Edsinger, E. *The world's smallest cephalopod: pygmy squid as a cephalopod lab rat*. EMBO Lightsheet Microscopy Course, Dresden, Germany (August 2014)
3. Edsinger, E. *The world's smallest cephalopod: An Okinawan pygmy squid is being developed for laboratory research*. Kyuyo Senior High School, Naha, Okinawa, Japan (December 2014).
4. Rokhsar, D. *In Search of the Perfect Assembly*. Plant and Animal Genomes XXIII, San Diego, California, USA (January 2015).
5. Simakov O, *Genomic signature of Hydra regeneration*. MPI, Dresden (April 2014)
6. Simakov O, *Genomic signatures and stem cells in Hydra regeneration*. SFB meeting, Heidelberg, Germany (July 2014)
7. Simakov, O. *Transposable element evolution in animal genomes*. Heidelberg, Germany (July 2014).
8. Simakov, O. *Evolutionary dynamics of genome architecture across metazoans*. Academia Sinica, Taiwan (December 2014)
9. Simakov, O. *Dynamics of genome architecture evolution in cephalopods*. 2015 Genome10K Conference, Santa Cruz, California, USA (March 2015).

6. Intellectual Property Rights and Other Specific Achievements

Nothing to report

7. Meetings and Events

Nothing to report

8. Other

Nothing to report