OIST SEMINAR

Date: Monday, November 27, 2017
Time: 10:30 – 11:30
Venue: Seminar Room C700, Lab 3, Level C
Speaker: **Wataru Iwasaki**
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(Department of Biological Sciences, Department of Bioinformatics and Systems Biology, Department of Computational Biology and Medical Sciences, and Atmosphere and Ocean Research Institute)

Title: How do small organisms spread and evolve across environmental barriers?

Abstract:

Technological innovations in the life science domain have enabled us to obtain and analyze massive amount of data that can unveil the underlying principles of biological systems and their evolutionary histories. While massive genomic data provide an overview of the history of genome evolution, other omic data illustrate how genomic sequences perform their functions. Furthermore, bioimaging data provide ways to quantitatively characterize phenotypes and behavior of organisms. Last but not least, environmental DNA data illustrate complex ecosystems. Under this context, we are conducting various researches at the interface between the life and information sciences, which will be briefly introduced in this seminar.

Specifically, I will explain our "generalist-driven evolution hypothesis" based on our meta-analysis of microbial community sequencing datasets, which supports a model of microbial evolution in which generalists play key roles in introducing new species and maintaining taxonomic diversity. Microbes form fundamental bases of every Earth ecosystem. As their key survival strategies, some microbes adapt to broad ranges of environments, while others specialize to certain habitats. While ecological roles and properties of such "generalists" and "specialists" had been examined in individual ecosystems, general principles that govern their distribution patterns and evolutionary processes have not been characterized. Here, we thoroughly identified microbial generalists and specialists across 61 environments via meta-analysis of community sequencing data sets and reconstructed their evolutionary histories across diverse microbial groups. This revealed that generalist lineages possess 19-fold higher speciation rates and significant persistence advantage over specialists. Yet, we also detected three-fold more frequent generalist-to-specialist transformations than the reverse transformations.

References:

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Sriswasdi, Takashima, Manabe, Ohkuma, Sugita, and Iwasaki. Global deceleration of gene evolution following recent genome hybridizations in fungi. *Genome Research*, **26**, 1081-1090. (2016)

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Miya, Sato, Fukunaga, Sado, Poulsen, Sato, Minamoto, Yamamoto, Yamanaka, Araki, Kondoh, and Iwasaki. MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. *Royal Society Open Science*, **2**, 150088. (2015)