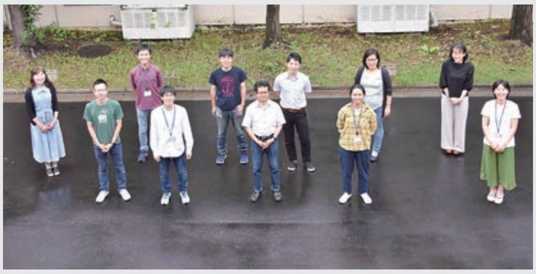
Laboratory of Evolutionary Genomics

Professor:
SHIGENOBU, Shuji

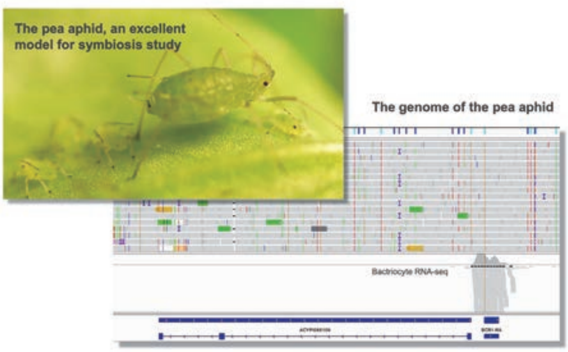
Assistant Professor:	*HUANGH, Jia-Hsin*
Specially Appointed Assistant Professor:	
	YODA, Shinichi
Postdoctoral Fellow:	*KOBAYASHI, Yuuki*
	CHUNG, Chen-yo
JSPS Postdoctoral Fellow:	*NOZAKI, Tomonari*
	MATSUDA, Naoki
SOKENDAI Graduate Student:	*YORIMOTO, Shunta*
	TAN, Kathrine
Visiting Graduate Student :	*TONG, Xin*
Technical Assistant:	*SUZUKI, Miyuzu*
	WEN, Hsin-I
	IKEDA, Mika
Admin Support Staff:	*ICHIKAWA, Mariko*



Symbiogenomics

"Nothing, it seems, exists except as part of a network of interactions." (Gilbert & Epel, 2008)

Every creature on Earth exists among a network of various biological interactions. For example, many multicellular organisms, including humans, harbor symbiotic bacteria in their bodies. Some of them provide their hosts with essential nutrients deficient in the host's diet and others digest foods that are indigestible by the host alone. Despite numerous examples of symbioses and its intriguing outcomes, the genetic and molecular basis underlying these interactions remains elusive. The goal of our group is to establish a new interdisciplinary science known as "Symbiogenomics", where we aim to understand the network of biological interactions at the molecular and genetic level. To this end, we take advantage of state-of-the-art genomics, such as next-generation sequencing technologies and CRISPR-Cas9 genome editing.



Visual overview of this lab's work.

Genomic revelations of a mutualism: the pea aphid and its obligate bacterial symbiont

Aphid species bear intracellular symbiotic bacteria in the cytoplasm of bacteriocytes, which are specialized cells for harboring said bacteria. This mutualism is so obligate that neither can reproduce independently. The genome sequence of the pea aphid, *Acyrthosiphon pisum*, in consort with that of bacterial symbiont *Buchnera aphidicola* illustrates the remarkable interdependency between these two organisms (IAGC, PLOS Biol. 2010; Shigenobu *et al*., Nature. 2000). The genetic capacities of the pea aphid and the symbiont for amino acid biosynthesis are complementary. Genome analysis revealed that the pea aphid has undergone characteristic gene losses and duplications. The IMB antibacterial immune pathway is missing several critical genes, which might account for the evolutionary success of aphids in obtaining beneficial symbionts. Lineage-specific gene duplications have occurred in genes over a broad range of functional categories, which include signaling pathways, miRNA machinery, chromatin modification and mitosis. The importance of these duplications for symbiosis remains to be determined. We found several instances of lateral gene transfer from bacteria to the pea aphid genome. Some of them are highly expressed in bacteriocytes.

We recently discovered a novel class of genes in the pea aphid genome that encode small cysteine-rich proteins with secretion signals that are expressed exclusively in the bacteriocytes of the pea aphid, and named these bacteriocyte-specific cysteine-rich proteins (BCR) (Shigenobu & Stern, Proc. R. Soc. B 2013). The BCR mRNAs are first expressed at a developmental time point coinciding with the incorporation of symbionts strictly in the cells that contribute to the bacteriocyte, and this bacteriocyte-specific expression is maintained throughout the aphid's life. Furthermore, some BCRs showed antibiotic activity (Uchi *et al*., Microbes. Environ. 2019). These results suggest that BCRs act within bacteriocytes to mediate the symbiosis with bacterial symbionts, which is reminiscent of the cysteine-rich secreted proteins of leguminous plants that also regulate endosymbionts. Employment of small cysteine-rich peptides may be a common tactic of host eukaryotes to manipulate bacterial symbionts.

Figure 1. Pea aphids and the bacterial symbiont, *Buchnera*. Adult aphids (Left). A developing viviparous embryo which symbionts are infecting (Right). Scale bar = 20 um.

Publication List

〔**Original papers**〕

- Bessho-Uehara, M., Yamamoto, N., Shigenobu, S., Mori, H., Kuwata, K., and Oba, Y. (2020). Kleptoprotein bioluminescence: *Parapriacanthus* fish obtain luciferase from ostracod prey. Sci. Adv. 6, eaax4942. DOI: 10.1126/sciadv.aax4942
- Fukutomi, Y., Kondo, S., Toyoda, A., Shigenobu, S., and Koshikawa, S. (2021). Transcriptome analysis reveals wingless regulates neural development and signaling genes in the region of wing pigmentation of a polka-dotted fruit fly. FEBS J. *288*, 99–110. DOI: 10.1111/febs.15338
- Tominaga, T., Yamaguchi, K., Shigenobu, S., Yamato, M., and Kaminaka, H. (2020). The effects of gibberellin on the expression of symbiosis-related genes in Paris-type arbuscular mycorrhizal symbiosis in *Eustoma grandiflorum*. Plant Signal. & Behav. *15*. DOI: 10.1080/15592324.2020.1784544
- Mondal, S.I., Akter, A., Koga, R., Hosokawa, T., Dayi, M., Murase, K., Tanaka, R., Shigenobu, S., Fukatsu, T., and Kikuchi, T. (2020). Reduced genome of the gut symbiotic bacterium "*Candidatus* Benitsuchiphilus tojoi" provides insight into its possible roles in ecology and adaptation of the host insect. Front. Microbiol. *11*. DOI: 10.3389/fmicb.2020.00840
- Li, Y., Omori, A., Flores, R.L., Satterfield, S., Nguyen, C., Ota, T., Tsurugaya, T., Ikuta, T., Ikeo, K., Kikuchi, M., *et al*. (2020). Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. Commun. Biol. *3*. DOI: 10.1038/s42003-020-1091-1
- Vu, T.-D., Lwasaki, Y., Shigenobu, S., Maruko Akiko and Oshima, K., Lioka, E., Huang, C.-L., Abe T., Tamaki, S., Lin, Y.-W., Chen, C.-K., Lu Mei-Yeh and Hojo, M., *et al*. (2020). Behavioral and brain-transcriptomic synchronization between the two opponents of a fighting pair of the fish *Betta splendens*. PLoS Genet. *16*. DOI: 10.1371/journal.pgen.1008831
- Cui, S., Kubota, T., Nishiyama, T., Ishida, J.K., Shigenobu, S., Shibata, T.F., Toyoda, A., Hasebe, M., Shirasu, K., and Yoshida, S. (2020). Ethylene signaling mediates host invasion by parasitic plants. Sci. Adv. *6*. DOI: 10.1126/sciadv.abc2385