Curriculum Vitae

5 April 2019

Jun Inoue

Date of Birth:	December 19th, 1973, Tokyo
Nationality:	Japanese citizen
Address:	National Institute of Genetics, Yata 1111, Mishima, Shizuoka 411-8540, JAPAN
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Web:	http://fish-evol.org/index_eng.html

Current position

2019–	Scientist – National Institute of Genetics

Grants

2018–2021	Grant-in-Aid for Scientific Research (C). “Estimation of phylogenetic position of species with accelerated evolutionary rate: a case study on urochordate Larvaceans”
2015–2019	Grant-in-Aid for Scientific Research (C). “Development of integrated orthology identification pipeline for comparative analysis of vertebrate genomes”
2012–2016	Grant-in-Aid for Young Scientists (B). “Towards the phylogenomics of actinopterygians: development of the phylogeny-based pipeline for the identification of orthologs”
2005–2007	Japan Society for the Promotion of Science, Grant-in-Aid for JSPS Fellows for Research Abroad. “Development of the novel molecular evolutionary model for the phylogenetic analysis among major vertebrate lineages”
2003–2005	Japan Society for the Promotion of Science, Grant-in-Aid for JSPS Fellows. “Phylogenetic analysis of basal actinopterygian fishes based on the whole mitochondrial genome sequences”

Position held

2013–2019	Staff Scientist –Okinawa Institute of Science and Technology Graduate University (OIST)
2010–2013	Researcher – Atmosphere and Ocean Research Institute, University of Tokyo
2008–2010	Postdoctoral Fellow – University College London

2007–2008	Postdoctoral Fellow - Florida State University
2005–2007	JSPS (Japan Society for the Promotion of Science) Postdoctoral Fellow for Research Abroad. Florida State University
2002–2005	Postdoctoral Fellow - Japan Society for the Promotion of Science. Ocean Research Institute, University of Tokyo
2001–2002	Postdoctoral Fellow - Ocean Research Institute, University of Tokyo

Educational background

2001	Ph.D., University of Tokyo, Japan [April 1st, 1998 – March 15th, 2001]
1998	M.Sc., University of Tokyo, Japan [April 1st, 1996 – March 30th, 1998]
1996	B. Sc., Waseda University, Japan [April 1st, 1992 – March 29th, 1996]

List of publications (Peer reviewed only)

40. **Inoue J.**, Nakashima K., Satoh, N. 2019. ORTHOSCOPE analysis reveals the presence of the cellulose synthase gene in all tunicate genomes but not in other animal genomes. *Genes.* **10:** 294. *Times Cited: –.*
39. Shiraishi A., Okuda T., Miyasaka N., Osugi T., Okuno Y., **Inoue J.**, and Satake H.. 2019. Repertoires of G protein-coupled receptors for *Ciona*-specific neuropeptides. *Proceedings of the National Academy of Sciences of the United States of America. in press. Times Cited: –.*
38. **Inoue, J.**, Satoh, N. 2019. ORTHOSCOPE: an automatic web tool for phylogenetically inferring bilaterian orthogroups with user-selected taxa. *Molecular Biology and Evolution*. **36:** 621–631. *Times Cited:* 0.
37. Kim, O.T.P., Nguyen, P.T., Shoguchi, E., Hisata, K., Vo T.T.B., **Inoue J.**, et al. 2018. A draft genome of the striped catfish, *Pangasianodon hypophthalmus*, for comparative analysis of genes relevant to development and a resource for aquaculture improvement. *BMC Genomics* **19:** 733. *Times Cited: 0.*
36. **Inoue, J.**, Satoh, N. 2018. Deuterostome genomics: Lineage-specific protein expansions that enabled chordate muscle evolution. *Molecular Biology and Evolution*. **35**:914–924. *Times Cited: 1.*
35. **Inoue, J.**, Yasuoka, Y., Takahashi, H., Satoh N. 2017. The chordate ancestor possessed a single copy of the *Brachyury* gene for notochord acquisition. *Zoological Letters*. **3:** 4. *Times Cited: 3.*
34. **Inoue, J.**, Sato, Y., Sinclair, R., Tsukamoto, K., Nishida, M. 2015. Rapid genome reshaping by multiple-gene loss after whole-genome duplication in teleost fish suggested by mathematical modeling. *Proceedings of the National Academy of Sciences of the United States of America* **112**: 14918–14923. *Times Cited: 34.*
33. Miya, M., Friedman, M, Satoh, T.P., Takeshima, H., Sado, T., Iwasaki, W., Yamanoue, Y., Nakatani, M., Mabuchi, K., **Inoue, J.G.**, Poulsen, J.Y., Fukunaga, T., Sato, Y., Nishida, M. 2013. Evolutionary origin of the Scombridae (tunas and mackerels): members of a

paleogene adaptive radiation with 14 other pelagic fish families. *Plos One* **8**:e73535. *Times Cited: 61*.

32. dos Reis, M., **Inoue, J.**, Hasegawa, M., Asher, R.J., Donoghue, P.C.J. Yang, Z. 2012. Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. *Proceedings of the Royal Soceity B* **279**, 3491–3500. *Times Cited: 219*.
31. Aschliman, N.C., Nishida, M., Miya, M., **Inoue, J.G.**, Rosana, K.M., Naylor, G.J.P. 2011. Body plan convergence in the evolution of skates and rays (Chondrichthyes: Batoidea). *Molecular Phylogenetics and Evolution* **63**, 28–42. *Times Cited: 64*.
30. Parham, J.F., Donoghue, P.C.J., Bell, C.J., Calway, T.D., Head, J.J., Holroyd, P.A., **Inoue, J.G.**, Irmis, R.B., Joyce, W.G., Ksepka, D.T., Patané, J.S.L., Smith, N.D., Tarver, J.E., van Tuinen, M., Yang, Z., Angielczyk, K.D., Greenwood, J., Hipsley, C.A., Jacobs, L., Makovicky, P.J., Müller, J., Smith, K.T., Theodor, J.M., Warnock, R.C.M., Benton, M.J. 2012. Best practices for justifying fossil calibrations. *Systematic Biology* **61**, 346–359. *Times Cited: 258.*
29. Saitoh, K., Sado, T., Doosey, M.H., Bart, Jr., H.L., **Inoue, J.G.**, Nishida, M., Mayden, R.L., Miya, M. 2010. Evidence from mitochondrial genomics supports the lower Mesozoic of South Asia as the time and place of basal divergence of cypriniform fishes (Actinopterygii: Ostariophysi). *Zoological Journal of the Linnean Society* **161**, 633–662. *Times Cited: 65.*
28. **Inoue, J.G.**, Miya, M., Lam, K., Tay, B.-H., Danks, J.A., Bell, J., Walker, T.I., Venkatesh, B. 2010c. Evolutionary origin and phylogeny of the modern holocephalans (Chondrichthyes: Chimaeriformes): a mitogenomic perspective. *Molecular Biology and Evolution* **27**, 2576–2586. *Times Cited: 88.*
27. **Inoue, J.G.**, Miya, M., Miller, M.J., Sado, T., Hanel, R., Hatooka, K., Aoyama, J., Minegishi, M., Nishida, M., Tsukamoto, K. 2010b. Deep-ocean origin of the freshwater eels. *Biology Letters* **6**, 363–366. *Times Cited: 80.*
26. **Inoue, J.**, Donoghue, P.C.J., Yang Z. 2010a. The impact of the representation of fossil calibration on Bayesian estimation of species divergence times. *Systematic Biology* **60**, 74–89. *Times Cited: 142.*
25. Minegishi, Y., Aoyama, J., **Inoue, J.G.**, Azanza, R.V., Tsukamoto, K. 2009. Inter-specific and subspecific genetic divergences of freshwater eels, genus *Anguilla* including a recently described species, *A. luzonensis*, based on whole mitochondrial genome sequences. *Coastal Marine Science* **33**, 64–77. *Times Cited: 6*.*
24. Setiamarga, D.H., Miya, M., **Inoue, J.G.**, Ishiguro, N.B., Mabuchi, K., Nishida, M. 2009. Divergence time of the two regional medaka populations in Japan as a new time scale for comparative genomics of vertebrates. *Biology Letters* **5**, 812–816. *Times Cited: 53.*
23. **Inoue, J.G.**, Kumazawa, Y., Miya, M., Nishida, M. 2009. The historical biogeography of the freshwater knifefishes using mitogenomic approaches: A Mesozoic origin of the Asian notopterids (Actinopterygii: Osteoglossomorpha). *Molecular Phylogenetics and Evolution* **51**, 486–499. *Times Cited: 36.*
22. Setiamarga, D.H., Miya, M., Yamanoue, Y., Mabuchi, K., Satoh, T.P., **Inoue, J.G.**, Nishida, M. 2008. Interrelationships of Atherinomorpha (medakas, flyingfishes, killifishes, silversides, and their relatives): The first evidence based on whole mitogenome sequences. *Molecular Phylogenetics and Evolution* **49**, 598–605. *Times Cited: 67.*
21. Ma, T., Aoyama, J., Miller, M.J., Minegishi, Y., **Inoue, J.G.**, Tsukamoto, K. 2008.

Evidence of genetic differentiation in the genus *Uroconger* (Congridae) in the Indo-Pacific. *Aquatic Biology* **2**, 29–35. *Times Cited: 6.*

20. Kawahara, R., Miya, M. Mabuchi, K., Lavoué, S., **Inoue, J.G.**, Satoh, T.P., Kawaguchi, A., Nishida, M. 2008. Interrelationships of the 11 gasterosteiform families (sticklebacks, pipefishes, and their relatives): a new perspective based on whole mitogenome sequences from 75 higher teleosts. *Molecular Phylogenetics and Evolution* **47** 224–236. *Times Cited: 81.*
19. Ma, T., Miller, M.J., Aoyama, J., Minagawa, M., **Inoue, J.G.**, Watanabe, S., Tsukamoto, K. 2008. Genetic identification of two types of *Ariosoma* leptocephali. *Coastal Marine Science* **32**, 48–53. *Times Cited: 5.*
18. Yamanoue, Y., Miya, M., **Inoue, J.G.**, Matsuura, K., Nishida, M. 2006. The mitochondrial genome of spotted green pufferfish *Tetraodon nigroviridis* (Teleostei: Tetraodontiformes) and divergence time estimation among model organisms in fishes. *Gene and Genetic Systems* **81**, 29–39. *Times Cited: 97.*
17. Lavoué, S., Miya, M., **Inoue, J.G.**, Saitoh, K., Ishiguro, N.B., Nishida, M. 2005. Molecular systematics of the gonorynchiform fishes (Teleostei) based on whole mitogenome sequences: Implications for higher-level relationships within the Otocephala. *Molecular Phylogenetics and Evolution* **37**, 165–177. *Times Cited: 80.*
16. Ishiguro, N.B., Miya, M., **Inoue J.G.**, Nishida, M. 2005. *Sundasalanx* (Sundasalangidae) is a progenetic clupeiform, not a closely-related group of salangids (Osmeriformes): Mitogenomic evidence. *Journal of Fish Biology* **67**, 561–569. *Times Cited: 19.*
15. **Inoue, J.G.**, Miya, M., Venkatesh, B., Nishida, M. 2005. The mitochondrial genome of Indonesian coelacanth *Latimeria menadoensis* (Sarcopterygii: Coelacanthiformes) and divergence time estimation between the two coelacanths. *Gene* **349**, 227–235. *Times Cited: 86.*
14. Minegishi, Y., Aoyama, J., **Inoue, J.G.**, Miya, M., Nishida, M., Tsukamoto, K. 2005. Molecular phylogeny and evolution of the freshwater eels genus *Anguilla* based on the whole mitochondrial genome sequences. *Molecular Phylogenetics and Evolutio*n **34**, 134–146. *Times Cited: 105.*
13. Miyai, T., Aoyama, J., Sasai, S., **Inoue, J.G.**, Miller, M.J., Tsukamoto, K. 2004. Ecological aspects of the downstream migration of introduced European eels in the Uono River, Japan. *Environmental Biology of Fishes* **71**, 105–114. *Times Cited: 17.*
12. **Inoue, J.G.,** Miya, M., Tsukamoto, K., Nishida, M. 2004. Mitogenomic evidence for the monophyly of elopomorph fishes (Teleostei) and the evolutionary origin of the leptocephalus larva. *Molecular Phylogenetics and Evolution* **32**, 274–286. *Times Cited: 77.*
11. **Inoue, J.G.,** Miya, M., Tsukamoto, K., Nishida, M. 2003. Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels. *Molecular Biology and Evolution* **20**, 1917–1924. *Times Cited: 81.*
10. Saitoh, K., Miya, M., **Inoue, J.G.,** Ishiguro, N.B., Nishida, M. 2003. Mitochondrial genomics of ostariophysan fishes: perspectives on phylogeny and biogeography. *Journal of Molecular Evolution* 56**,** 464–472. *Times Cited: 130.*
9. Miya, M., Takeshima, H., Endo, H., Ishiguro, N.B., **Inoue, J.G.,** et al. 2003. Major patterns of higher teleostean phylogenies: a new perspective based on 100 complete mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution* **26**, 121–138. *Times Cited: 544.*
8. **Inoue, J.G.,** Miya, M., Tsukamoto, K., Nishida, M. 2003. Basal actinopterygian

relationships: a mitogenomic perspective on the phylogeny of the “ancient fish.” *Molecular Phylogenetics and Evolution* **26**, 110–120. *Times Cited: 219.*

7. Aoyama, J., Ishikawa S., Otake, T., Mochioka, N., Suzuki, Y., Watanabe, S., Shionoda, A., **Inoue, J.G.,** et al. 2001. Molecular approach to species identification of eggs with respect to determination of the spawning site of the Japanese eel *Anguilla japonica*. *Fisheries Science* **67**, 761–763. *Times Cited: 17.*
6. **Inoue, J.G.,** Miya, M. 2001. Phylogeny of the basal teleosts, with special reference to the Elopomorpha. *Japanese Journal Ichthyology* **48**, 75–91 (in Japanese with English abstract). *Times Cited: 8*.*
5. **Inoue, J.G.,** Miya, M., Tsukamoto, K., Nishida, M. 2001d. A mitogenomic perspective on the basal teleostean phylogeny: resolving higher-level relationships with longer DNA sequences. *Molecular Phylogenetics and Evolution* **20**, 275–285. *Times Cited: 137.*
4. **Inoue, J.G.,** Miya M., Tsukamoto, K., Nishida, M. 2001c. Complete mitochondrial DNA sequence of *Conger myriaster* (Teleostei: Anguilliformes): novel gene order for vertebrate mitochondrial genomes and the phylogenetic implications for anguilliform families. *Journal of Molecular Evolution* **52**, 311–320. *Times Cited: 70.*
3. **Inoue, J.G.,** Miya, M., Tsukamoto, K., Nishida, M. 2001b. Complete mitochondrial DNA sequence of the Japanese anchovy *Engraulis japonicus*. *Fisheries Science* **67**, 828–835. *Times Cited: 53.*
2. **Inoue, J.G.,** Miya, M., Aoyama, J., Ishikawa, S., Tsukamoto, K., Nishida, M. 2001a. Complete mitochondrial DNA sequence of the Japanese eel *Anguilla japonica*. *Fisheries Science* **67**, 118–125. *Times Cited: 55.*
1. **Inoue, J.G.,** Miya M., Tsukamoto, K., Nishida, M. 2000. Complete mitochondrial DNA sequence of the Japanese sardine *Sardinops melanostictus*. *Fisheries Science* **66**, 924–932. *Times Cited: 134.*

Prize from an academic society

2016 Encouragement Prize, Society of Evolutionary Studies, Japan
“Phylogenetic and genome evolution of fish”
http://sesj.kenkyuukai.jp/special/?id=22072

2014 Open Science Award, Database Center for Life Science, Web category
(http://www.geocities.jp/ancientfishtree), http://2014.openscienceaward.org

2011 Award for Education and Enlightenment, Society of Evolutionary Studies, Japan
“Educational broadcasting of phylogenetic analysis via homepage (http://www.geocities.jp/ancientfishtree)”
http://sesj.kenkyuukai.jp/special/?id=3468

2006 Encouragement Prize, The Ichthyological Society of Japan
“The estimation of phylogenetic relationships and divergence times among basal actinopterygians based on the whole mitochondrial genome sequences”
http://www.fish-isj.jp/iin/award/2006_senkou.html

List of publications-2 (Book chapters)

井上 潤．2018．古代魚の系統進化．魚類学の百科事典．日本魚類学会 編．丸善出版．

井上 潤．2018．下位真骨類の系統進化．魚類学の百科事典．日本魚類学会 編．丸善出版．
井上 潤．2009．古代魚の進化を探る．海洋生命系のダイナミクス 1 ：海洋の生命史．西田睦編．第 6 章．(pp. 102–121)．東海大学出版会．
井上 潤，宮正樹．2001．ウナギ属 *Anguilla* の進化的起源．海洋と生物. 133: 153–159.

Invited talks and conference presentations

Invited talks

Inoue J. Phylogenetic evolution and genome evolution of chordates, JT Biohistory Research Hall (October, 2018).

Inoue J., Sato, Y., Sinclair, R., Nishida, M. Genome reshaping and explosive radiation of teleosts. NGS field meeting (May, 2017).

Inoue J., Sato, Y., Sinclair, R., Nishida, M. Selection of gene markers for teleost phylogenetics considering the whole genome duplication and the species tree (March, 2016).

Inoue J. Origin and evolution of the freshwater eel, Nihon University, Kanagawa, Japan (December, 2015).

Inoue J., Sato, Y., Sinclair, R., Nishida, M. Rapid genome reshaping by multiple-gene loss after whole-genome duplication in teleost fish suggested by mathematical modeling. Introduction to the analysis of molecular evolution in the genomic era, Fudan University, Shanghai, China (November, 2015).

Inoue. J., Selecting molecular markers from transcriptome data for fish phylogenetics. Fudan University, Shanghai, China. (March 2014).

Inoue. J., The estimation of phylogenetic relationships and divergence times among basal actinopterygians based on the whole mitochondrial genome sequences. University of Tsukuba, Tsukuba, Japan. (November 2010).

Inoue. J.G., Deep-ocean origin of the freshwater eels. University of Tokyo, Kashiwa, Japan. (November 2010).

Inoue. J.G., The divergence time estimation of the basal actinopterygians based on the whole mitochondrial genome sequences. University of Konstanz, Konstanz, Germany. (July, 2010).

Inoue. J.G., The phylogenetic relationships and divergence time of the basal actinopterygians based on the whole mitochondrial genome sequences. Natural History Museum, London, UK. (November 2009).

Inoue J.G., The estimation of phylogenetic relationships and divergence times among basal actinopterygians based on the whole mitochondrial genome sequences. Award lecture in the Ichthyological Society of Japan, Shizuoka, Japan (October, 2006).

Conference presentations (International only)

Inoue, J., Satoh, N. A Genomic survey of muscle structural proteins that enabled the rise of chordates. Society for Molecular Biology and Evolution Conference 2016. Gold Coast, Australia (July, 2016).

Inoue J., Sato, Y., Sinclair, R., Nishida, M. Selecting molecular markers from transcriptome data for fish phylogenetics. Workshop on Methods for Biodiversity Research, Shanghai (March, 2014).

Inoue, J.G., Donoghue, P.C.J., Yang, Z. The impact of the representation of fossil calibration on Bayesian estimation of species divergence times. Evolution 2009, Moscow (June, 2009).

Miya, M., **Inoue, J.G.**, Mabuchi, K., Nishida, M. Patterns of diversification in modern ray-finned fishes: a mitogenomic overview. Christchurch (June, 2007).

Inoue, J.G., M. Miya, B. Venkatesh, and M. Nishida. Mitochondrial phylogenomics of fishes: estimation of divergence times among basal ray-finned fish lineages. Phylogenomics conference, Montreal (March, 2006).

Inoue, J.G., M. Miya, B. Venkatesh, and M. Nishida. The mitochondrial genome of Indonesian coelacanth Latimeria menadoensis (Sarcopterygii: Coelacanthiformes) and divergence time estimation between the two coelacanths. ASIH Annual Meetings, Tampa (July, 2005).

Lavoue S., Miya, M., **Inoue J.G.**, Saitoh, K., Ishiguro, N. B., Nishida, M. Molecular phylogeny of the Clupeiformes (Teleostei) inferred from whole mitogenome sequences. ASIH Annual Meetings, Tampa (July, 2005).

Inoue, J.G., M. Miya, B. Venkatesh, and M. Nishida. The mitochondrial genome of Indonesian coelacanth Latimeria menadoensis (Sarcopterygii: Coelacanthiformes) and divergence time estimation between the two coelacanths. Seventh Indo-Pacific Fish Conference, Taipei (May, 2004).

Inoue, J.G., M. Miya, K. Tsukamoto, and M. Nishida. Basal actinopterygian relationships: a mitogenomic perspective on the phylogeny of the "ancient fish." Society of Integrative and Comparative Biology Annual Meeting, Sheraton Centre Toronto (January, 2003).

Inoue, J.G., Novel gene order for vertebrate mitochondrial genomes and the phylogenetic implications for anguilliform families. International Symposium Advances in Eel Biology. University of Tokyo (September, 2001).

Inoue, J.G., M. Miya, K. Tsukamoto, and M. Nishida. Mitogenomic analysis of elopomorph relationships and origin of leptocephalus larva. International Commemorative Symposium 70th Anniversary of Japanese Society of Fisheries Science, Pacifico Yokohama (October, 2001).

Inoue, J.G., M. Miya, K. Tsukamoto, and M. Nishida. Gene rearrangements in the mitochondrial genomes of the order Anguilliformes (Teleostei: Elopomorpha): phylogenetic implication for the interfamilial relationships. International Symposium on Diversity of Fishes, National Science Museum, Tokyo (February, 2000).

Peer review activities

BMC Biology, BMC Evolutionary Biology, Gene, Genes and Genetic Systems, Genome Biology and Evolution, Fisheries Science, Journal of Molecular Evolution, Ichthyological Research, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, JEZ Part B: Molecular and Developmental Evolution, Systematic Biology, Zoological Science, etc.

Scientific or technical skills

Web tool development (https://www.orthoscope.jp).
Molecular phylogenetic analysis.
Data mining of molecular data.
Programming using language Perl, Python, and R.
Field sampling.
Laboratory work of DNA data decoding.

Participation in professional organization

2007–	Society for Molecular Biology and Evolution (USA)
2005–	American Society Ichthyologists and Herpetologists (USA)
2001–	Molecular Biology Society of Japan (Japan)
2000–	Society of Evolutionary Studies, Japan (Japan)
1999–	Ichthyological Society of Japan (Japan)
1997–	Japan Society of Fisheries Science (Japan)

Presented lectures

2016–	Bayesian estimation of divergence time. 3 hours lecture *in* Workshop on "Analysis of Genome diversity (https://genomeanalysis.wordpress.com/3rd_workshop/)". Hokkaido University, Hokkaido, Japan.
2013–2015	Bayesian estimation of divergence time. 3 hours lecture *in* Summer School on "Computational Biology Based on Tree of Life: Methods and Applications". Fudan University, Shanghai, China.
2010–	Bayesian estimation of divergence time. 1.5 hours lecture *in* Workshop "Theory and practice in molecular phylogenetics (http://sto.affrc.go.jp/event/workshop/176ws)". Agriculture, Forestry and Fisheries Research Information Technology Center, Ministry of Agriculture, Forestry and Fisheries of Japan, Tsukuba, Japan

Selected media appearance

2010	January	Several Japanese new papers reported my freshwater eel study (Inoue et al. 2010).
2007	October	Japanese new paper, Asahi-shinbun, reported my study about the ancient fish phylogenetics (Inoue et al. 2005).
2005	May	National Geographic reported my study of coelacanths (Inoue et al. 2005).

2003	June	Japanese new paper, Sankei-shinbun, reported my study of ancient fish phylogenetics (Inoue et al. 2003).

Major field experiences

2012	July	KH12-2 cruise of the R/V Hakuho Maru
2011	July	KH11-6 cruise of the R/V Hakuho Maru
2011	June	KH11-4 cruise of the R/V Hakuho Maru
2005	March	Yonaguni, Ishigaki, and Okinawa Island (Japan)
2004	November	Ogasawara Islands (Japan)
2004	July	Yonaguni Island (Japan)
2002	August	KY02-08 cruise of the R/V Kaiyou
2002	May	KT02-03 cruise of the R/V Tansei Maru
2001	August	YK01-08 cruise of the R/V Yokosuka
2000	January	KH00-1 cruise of the R/V Hakuho Maru
1999	July	KT99-10 cruise of the R/V Tansei Maru
1999	May	KT99-6 cruise of the R/V Tansei Maru
1998	June	KH98-2 cruise of the R/V Hakuho Maru
1997	July	KT97-10 cruise of the R/V Tansei Maru
1996	November	KT96-19 cruise of the R/V Tansei Maru
1996	July	Hachijo Island (Japan)