

The eDNA Society International Meeting 2023

Moving from knowledge into practice

Program



17 ^{WED} ▶ 19 ^{FRI} May 2023

Excursions 20 ^{SAT} ▶ 21 ^{SUN} May 2023

— Venue —

Piazza Omi, Otsu, Japan

— Chair —

Prof. Dr. Toshifumi Minamoto
Kobe University



Meeting schedule (UTC+9)

Day-1 May 17th (Wed)

- 14:00 - 15:00 Opening Ceremony
ANEMONE: Japan's eDNA-based biodiversity monitoring network
Michio Kondoh, Ph.D., Prof. (Tohoku University, Japan)
- 15:30 - 17:30 Plenary Session 1
From innovation to practice: Using eDNA to support evidence-based management
Hiroki Yamanaka, Ph.D., Associate Prof. (Ryukoku University, Japan)
- 18:00 - 19:30 Banquet
-

Day-2 May 18th (Thu)

- 09:00 - 11:00 Plenary Session 2
Understanding biodiversity hotspots using eDNA
Hitoshi Araki, Ph.D., Prof. (Hokkaido University, Japan)
Tadashi Kajita, Ph.D., Prof. (University of Ryukyus, Japan)
- 11:00 - 12:30 Corporate Workshop 1
Illumina K.K.
- 13:00 - 14:15 Oral Presentation
- 14:30 - 17:00 Poster Presentation (14:30 - 16:30 Core Time)
- 17:15 - 18:30 Oral Presentation
-

Day-3 May 19th (Fri)

- 09:00 - 11:00 Plenary Session 3
Environmental DNA moving from knowledge into practice
Hideyuki Doi, Ph.D., Prof. (Kyoto University, Japan)
- 11:00 - 12:30 Corporate Workshop 2
Go!Foton, Inc. and Pacific Consultants Co., LTD.
- 13:00 - 15:45 Oral Presentation
- 16:00 - 17:00 Closing Ceremony
Is eDNA good enough? Implications for science and society
Mehrdad Hajibabaei, Ph.D., Associate Prof. (University of Guelph, Canada)



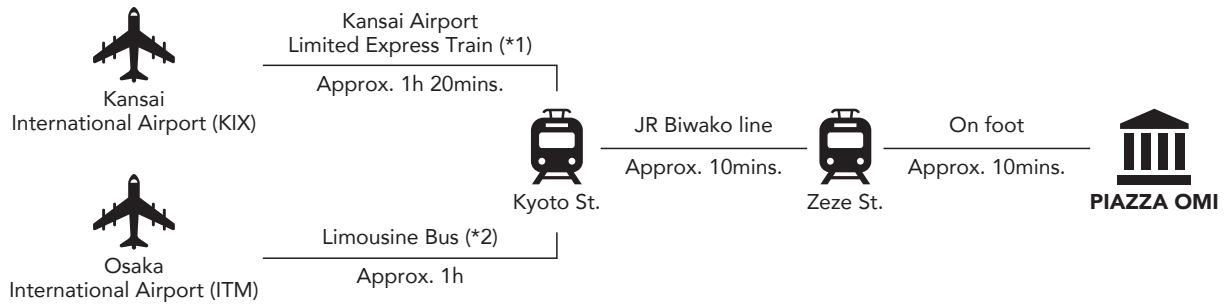
It is a great honor for us to host the first international conference of the eDNA Society. “The eDNA Society International Meeting 2023” will be held at Otsu City, Shiga Prefecture, on the shores of Lake Biwa, the largest and oldest lake in Japan. Lake Biwa is home to many endemic organisms and is the birthplace of eDNA studies in Japan, and research has been conducted on a wide range of organisms, from microbes to higher animals, present in the lake.

eDNA research began in Japan around 2009, and targeted Lake Biwa and its surrounding areas. In 2018, the eDNA Society was established with the participation of many members. Apart from Japan, eDNA research is extensively being conducted in Europe, North America, Oceania, and several other regions. The first eDNA study on a macroorganism was published 15 years ago in 2008. Presently, eDNA studies are transforming from a mere discipline of natural science into an important research tool for conserving global biodiversity. Under the theme of "Moving from knowledge into practice," the purpose of this conference is to provide a forum for discussing the practical applications of the knowledge we have gathered over the years. Biodiversity loss is occurring simultaneously throughout the planet. Therefore, it is important for eDNA researchers from around the world to gather together and discuss common issues such as accurate monitoring of biological distributions over large areas, establishment of protected areas based on the identification of breeding grounds, and, of course, to share the excitement of the science.

Otsu City, the host city, is adjacent to Kyoto, the ancient capital of Japan. Participants will thus be able to experience not only the rich natural environment of Lake Biwa, but also the history and culture of Japan. We look forward to welcoming you to Japan.

The chair of The eDNA Society International Meeting 2023
Toshifumi Minamoto, Ph.D., Prof.

Map & Direction (Piazza Omi)



Notes:

*1 <https://www.kansai-airport.or.jp/en/access/train>

*2 <https://www.okkbus.co.jp/en/route/itm/>

- Your hotel may be in walking distance of the station, but if not (e.g., Prince Hotel, Biwako Hotel), the easiest will be to take a cab.

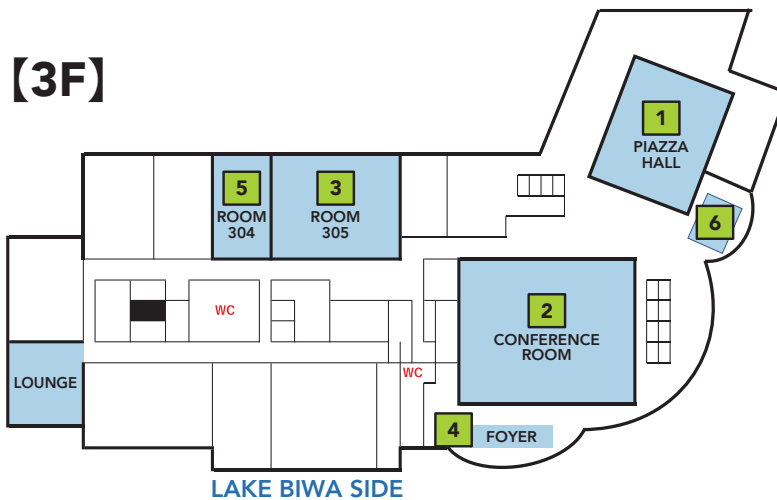
-MK taxi +81(0)77-526-4141

-Yasaka taxi +81(0)77-522-6767

- If you are going to the Lake Biwa Otsu Prince Hotel, you may be in time for the free shuttle from Otsu Station (JR Biwako line).

https://www.princehotels.com/otsu/wp-content/uploads/sites/21/2022/11/EN_shuttle-bus_20221121_english-4.pdf

Floor Map



- | | |
|--|--|
| <p>1 PIAZZA HALL</p> <p>Opening (17th)
Plenary Sessions (17th, 18th, 19th)
Closing (19th)</p> | <p>4 FOYER</p> <p>Corporate Exhibition (17th, 18th, 19th)</p> |
| <p>2 CONFERENCE ROOM</p> <p>Banquet (17th)
Poster Presentation (18th, 19th)</p> | <p>5 ROOM 304</p> <p>Cloak (17th, 18th, 19th)</p> |
| <p>3 ROOM 305</p> <p>Oral Presentation (18th, 19th)
Corporate Seminar (18th, 19th)</p> | <p>6 RECEPTION</p> <p>Registration (17th, 18th, 19th)</p> |

Precautions

- Smoking is only permitted in the designated smoking area.
- Permission from the presenter is required for photography, recording, audio recording, and taking pictures of both oral presentations and posters during the presentation.
- Since the contents of the presentations (oral, posters) contain much unpublished data, please refrain from publishing them outside of this conference without the presenter's consent.

Reception

- Registration for the meeting will commence at 12:30 PM on May 17th in front of Piazza Hall on the third floor.
- Please pick up your name tag and give it to the receptionist so they can scan the QR code.

Cloakroom (Luggage storage)

- Room 304 is to be utilized as the cloakroom. For further information, please inquire with the cloakroom staff in Room 304.

Internet connection (Wi-Fi)

- We will provide free Wi-Fi access at the conference venue. However, we cannot guarantee a stable and constant connection for all participants. If you require a stable and high-speed connection, we recommend that you bring your own mobile Wi-Fi device, to ensure uninterrupted and reliable internet access.

Accommodation

- Please make your own arrangements for accommodation during the meeting. Due to the shortage of hotels caused by the increase in the number of tourists, it may be difficult to make reservations, so we recommend that you make reservations for accommodation, including in Kyoto, as soon as possible.

Traffic Information

- Venue: Piazza Omi 1-1-20, Nionohama, Otsu, Shiga 520-0801
- There are a few parking lots nearby, but we recommend using public transportation as they may be full and parking may not be available. Please refer to the map and direction.

Lunch

- There are some restaurants near the venue. Please refer to the following URL and map for more information.
<https://www.google.com/maps/d/edit?mid=16jy7ugaAH2fPENyJR4p08eG-OI2niw&usp=sharing>

- 1 Meeting Venue (Piazza Omi)
- 2 Anchov (Pasta)
- 3 Hashing Diner (Cafe)
- 4 Chanpon (Ramen)
- 5 Katsumugi (Port Cutlet)
- 6 WEST-EAST(Ethnic Cafe)
- 7 Jukusei-yakiniku Ichiban
- 8 Moriosumika(Japanese)
- 9 Chocola (Cafe)
- 10 Nagisa Warms (Vegan food)
- 11 Holly's Café(Cafe)
- 12 Friend Mart (Supermarket)
- 13 Yoshinoya Otsu Zeze
- 14 The Meshiya (Japanese dish)
- 15 Bikkuri Donkey (Hamburg)
- 16 Chojiro (Sushi)
- 17 Ion Town (Supermarket)
- 18 Kura Sushi (Sushi)
- 19 Convenience Store



May 17th (Wed) 14:00 - 15:00 (Venue: Piazza Hall)

ANEMONE: Japan's eDNA-based biodiversity monitoring network

Michio Kondoh, Ph.D., Prof. (Tohoku University, Japan)



ANEMONE (All Nippon eDNA Monitoring Network) is a nationwide biodiversity monitoring network in Japan that uses eDNA metabarcoding. The first eDNA monitoring was initiated by academic scientists in 2015 at Maizuru Bay, Kyoto, and since then, >5,000 surveys have been conducted at >1,000 sites, identifying a total of 1,000 fish taxonomical groups. The current objective of the network is to monitor fish biodiversity in aquatic ecosystems, including coastal and pelagic oceans, rivers, and lakes. There are currently 77 fixed monitoring stations supported by research sites of universities, national research institutes, and local governments, and their survey frequencies vary from weekly to seasonal. Since 2020, hundreds of local citizens have also started contributing to eDNA-based surveys, and the number of citizen partners is increasing year by year. The procedure for eDNA metabarcoding, including water collection, filtration, DNA extraction, and molecular analysis and sequencing, is conducted under a common methodology that follows a standardized protocol provided by The eDNA Society (<https://ednasociety.org/en/manuals/>). Claident, a high-throughput analysis pipeline for metabarcoding data, translates sequence data into taxonomic occurrence, and the data are made available to the public in a dedicated database, ANEMONE DB (<https://db.anemone.bio>), maintained at Tohoku University. In June 2022, a consortium of academia, government, and private sectors was established to study how eDNA monitoring data can provide solutions to a wide range of nature-related social issues.

May 17th (Wed) 15:30 - 17:30 (Venue: Piazza Hall)

From innovation to practice: Using eDNA to support evidence-based management

Hiroki Yamanaka, Ph.D., Associate Prof. (Ryukoku University, Japan)

The data obtained through environmental DNA (eDNA) analysis is increasing globally year by year. However, to actually utilize the data for biodiversity conservation and fisheries resource management, it is essential to build robust and reliable observation systems, including the establishment and maintenance of long-term monitoring networks and robust programs. In addition, legal and policy frameworks must be updated to allow the inclusion of eDNA-based data to support management of natural systems. At this symposium, researchers who have been involved in this series of steps will give an overview of past and current practices, with examples of current challenges, possible solutions, and a focus on the incorporation of eDNA into long term management. We will review and invite discussion on all stages of the eDNA workflow from sampling through policy and management.



Hiroki Yamanaka



Elizabeth Andruszkiewicz Allan



Adam Sepulveda



Alison Watts



Ryan Kelly

- 15:30 - 15:35 **Introduction**
Hiroki Yamanaka, Ph.D., Associate Prof. (Ryukoku University, Japan)
- 15:35 - 15:58 **The Evolution of eDNA Sampling: From Bottles to Robots**
Elizabeth Andruszkiewicz Allan, Ph.D., Chief Scientist (The eDNA Collaborative, USA)
- 15:58 - 16:21 **Transitioning eDNA biomonitoring from research to operational use for invasive species early detection**
Adam Sepulveda, Ph.D., Research Zoologist (United States Geological Survey, USA)
- 16:21 - 16:44 **Establishing Long Term Monitoring Programs to Support Actionable Science and Conservation**
Alison Watts, Ph.D., Research Faculty (University of New Hampshire, USA)
- 16:44 - 17:07 **Moving eDNA Methods from Knowledge into Action**
Ryan Kelly, Ph.D., Associate Prof. (University of Washington, USA)
- 17:07 - 17:30 **Discussion**

May 18th (Thu) 09:00 - 11:00 (Venue: Piazza Hall)

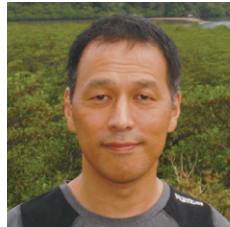
Understanding biodiversity hotspots using eDNA

Hitoshi Araki, Ph.D., Prof. (Hokkaido University, Japan),
Tadashi Kajita, Ph.D., Prof. (University of Ryukyus, Japan)

Biodiversity hotspots are important platforms for a wide variety of ecosystem services. However, our knowledge of these hotspots and their maintenance is limited due to shortages in budget, workforce, and other factors. In this symposium, we discuss how to evaluate biodiversity hotspots using eDNA. The topics include organisms in mangrove forests, coral reefs, and open oceans. They illustrate the power of eDNA for biodiversity monitoring and its potential for obtaining a more profound understanding of ecosystems.



Hitoshi Araki



Tadashi Kajita



Christoph Deeg



James Davis Reimer



Sophie von der Heyden

- 09:00 - 09:15 **Monitoring aquatic ecosystems in Hokkaido as a salmonid diversity hotspot in Japan**
Hitoshi Araki, Ph.D., Prof. (Hokkaido University, Japan)
- 09:15 - 09:45 **Environmental DNA surveys of Pacific salmon ecosystems from natal rivers to the open ocean**
Christoph Deeg, Ph.D. (University of British Columbia, Canada)
- 09:45 - 10:15 **Using eDNA to understand the diversity of and anthropogenic impacts on coral reefs in southern Japan**
James Davis Reimer, Ph.D., Prof. (University of Ryukyus, Japan)
- 10:15 - 10:45 **Applications of eDNA metabarcoding for baseline biodiversity surveys in southern African marine and freshwater ecosystems**
Sophie von der Heyden, Ph.D., Prof. (Stellenbosch University, South Africa)
- 10:45 - 11:00 **Understanding global mangrove biodiversity by eDNA metabarcoding**
Tadashi Kajita, Ph.D., Prof. (University of Ryukyus, Japan; Universiti Malaysia Sabah, Malaysia)

May 19th (Fri) 09:00 - 11:00 (Venue: Piazza Hall)

Environmental DNA moving from knowledge into practice

Hideyuki Doi, Ph.D., Prof. (Kyoto University, Japan)

Environmental DNA (eDNA) methods for biological monitoring have become increasingly popular over the past decade. Currently, there is an urgent need to develop survey methods and indicators to assist in understanding the status of ecosystems. eDNA survey methods, which enable broad-area and high-frequency surveys, can significantly contribute to developing these indicators. In this session, we will introduce the latest eDNA surveys and examples of their social implementation and discuss the potential limitations of such implementation and measures to resolve them.



Hideyuki Doi



Florian Leese



Kristy Deiner



Keigo Nakamura

- 09:00 - 09:10 **Environmental DNA moving from knowledge into practice: Introduction**
Hideyuki Doi, Ph.D., Prof. (Kyoto University, Japan)
- 09:10 - 09:50 **Advancing biodiversity monitoring with environmental DNA: From method innovation to nationwide implementation across terrestrial and aquatic ecosystems**
Florian Leese, Ph.D., Prof. (Duisburg-Essen University, Germany)
- 09:50 - 10:30 **Coordinating a global biodiversity monitoring system with eDNA and the blockchain**
Kristy Deiner, Ph.D., Assistant Prof. (ETH Zurich, Switzerland)
- 10:30 - 11:00 **Social implementation of environmental DNA and its barriers in Japan**
Keigo Nakamura, Ph.D., Chief Researcher (Riverfront Research Center, Japan)

May 18th (Thu)

Session A (Venue: Piazza Hall)

- OA-1 **"Making eDNA biodiversity records FAIR (Findable, Accessible, Interoperable and Reusable)"**
13:00 - 13:15 Oliver Berry (CSIRO Environomics Future Science Platform), Simon Jarman (The University of Western Australia), Andrew Bissett (CSIRO, Environment), Michael Hope (The Atlas of Living Australia), Corinna Paeper (The Atlas of Living Australia), Cindy Bessey (CSIRO, Environment), Michael Schwartz (US National Genomics Center for Wildlife and Fish Conservation), Josh Hale (Jacobs, Australia), Michael Bunce (Department of Conservation, Te Papa Atawhai)
- OA-2 **"Comparison of NCBI gene registration rates for South Korea aquatic organisms for eDNA research"**
13:15 - 13:30 Ji-Hoon Kim, Won-Seok Kim, Chang Woo Ji (Chonnam National University), Dong Soo Kong (Kyonggi University), Ihn-Sil Kwak (Chonnam National University)
- OA-3 **"An authoritative DNA reference library for Australia's species"**
13:30 - 13:45 Jenny Giles (CSIRO Environomics Future Science Platform), Andreas Zwick, Stephen Bent (CSIRO National Collections and Marine Infrastructure), Troy Denyer (CSIRO Information Management and Technology), Anna Kearns, James Nicholls, Jesse Wallace (CSIRO National Collections and Marine Infrastructure), Mark Wallace (CSIRO Environomics Future Science Platform/CSIRO National Collections and Marine Infrastructure), Claire Yang (CSIRO National Collections and Marine Infrastructure), Olly Berry (CSIRO Environomics Future Science Platform)
- OA-4 **"MitoFish and MiFish Pipeline: recent updates for facilitating environmental DNA research"**
13:45 - 14:00 Tao Zhu (The University of Tokyo), Yukuto Sato (The University of the Ryukyus), Tetsuya Sado, Masaki Miya (Natural History Museum and Institute, Chiba), Wataru Iwasaki (The University of Tokyo)
- OA-5 **"MitoSearch: Construction of fish species composition database with environmental DNA using public data"**
14:00 - 14:15 Kazutoshi Yoshitake, Takumi Ito, Guanting Liu, Hideaki Mizobata, Shigeharu Kinoshita, Shuichi Asakawa (The University of Tokyo)
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Session B (Venue: Room 305)

- OB-1 **"Revealing the potential for environmental DNA (eDNA) to detect species interactions in two economically important plants: *Carica papaya* and *Ananas comosus*"**
13:00 - 13:15 Pritam Banerjee (National Chung Cheng University), Kathryn A. Stewart (Leiden University), Gobinda Dey, Raju Kumar Sharma (National Chung Cheng University), Jyoti Prakash Maity (KIIT Deemed to be University), Michael W.Y. Chan, ChienYen Chen (National Chung Cheng University)
- OB-2 **"Using airborne eDNA techniques to track invasive species in high-quality hemlock forests"**
13:15 - 13:30 Charlyn Partridge, Megan Sanders, Katherine Geller (Annis Water Resources Institute, Grand Valley State University), Alexandra Locher (Grand Valley State University), Keely Dunham, Renee Tardani (Annis Water Resources Institute, Grand Valley State University)

- OB-3 **"Comparison of fish fauna evaluated using aqueous eDNA, sedimentary eDNA, and catch surveys in Tokyo Bay, central Japan"**
 13:30 - 13:45 Mengyao Zhu (Ocean Policy Research Institute of the Sasakawa Peace Foundation), Mari Kuroki, Tatsushi Kobayashi, Takashi Yamakawa (The University of Tokyo), Tetsuya Sado (Natural History Museum and Institute, Chiba), Keita Kodama, Toshihiro Horiguchi (National Institute for Environmental Studies), Masaki Miya (Natural History Museum and Institute, Chiba)
- OB-4 **"Metabarcoding of modern aquatic and terrestrial vegetation composition from lacustrine sediment in Yakutia, Eastern Siberia"**
 13:45 - 14:00 Izabella Baisheva (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research/University of Potsdam/North-Eastern Federal University/Hokkaido University), Kathleen R. Stoof-Leichsenring (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research), Ramesh Glückler (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research/University of Potsdam/Hokkaido University), Amelie Stieg, Iris Eder (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research), Aital Egorov (North-Eastern Federal University), Evgenii S. Zakharov (NorthEastern Federal University/Siberian Branch of Russian Academy of Sciences), Lena A. Ushnitskaya, Paraskovya V. Davydova (NorthEastern Federal University), Boris K. Biskaborn (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research), Luidmila A. Pestryakova, Sardana N. Levina, Ruslan M. Gorodnichev (NorthEastern Federal University), Birgit Heim (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research), Jorge García Molinos (Arctic Research Center, Hokkaido University), Ulrike Herzsuh (Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research/University of Potsdam)
- OB-5 **"Estimation of paleoenvironment in Lake Shinji through aquatic plant eDNA and CNS analyses using brackish lake sediment cores"**
 14:00 - 14:15 Satoshi Yamagishi (Shimane University), Koji Seto, Yasuhide Nakamura, Teruhiko Takahara (Estuary Research Center, Shimane University)

Session C (Venue: Piazza Hall)

- OC-1 **"Hypoxia-associated seasonal variations of zooplankton community in Jinhae Bay, South Korea: A case study through environmental DNA metabarcoding"**
 17:15 - 17:30 Chang-Bum Jeong, Heesang Shin, In-Cheol Yeo, Kyu-Young Shim, Kyu-Hyung Kim (Incheon National University)
- OC-2 **"Oyashio-specific zooplankton survey by eDNA in coastal Sanriku of the Northeast Japan"**
 17:30 - 17:45 Marty Kwok Shing Wong (Atmosphere and Ocean Research Institute, the University of Tokyo), Yuki Minegishi, Mako Nakao (The University of Tokyo), Yuichiro Nishibe (Atmosphere and Ocean Research Institute, The University of Tokyo), Aiko Tachibana (Tokyo University of Marine Science and Technology), Yoo-Jun Kim, Susumu Hyodo (Atmosphere and Ocean Research Institute, The University of Tokyo)
- OC-3 **"Metagenomics and metabarcoding experimental choices and their impact on microbial community characterization in freshwater recirculating aquaculture systems"**
 17:45 - 18:00 Jessica Rieder (University of Bern), Adamandia Kapopoulou, Claudia Bank (University of Bern/Swiss Institute of Bioinformatics), Irene Adrian-Kalchhauser (University of Bern)
- OC-4 **"Assessment of benthic invertebrate diversity in streams of the Han River using eDNA metabarcoding"**
 18:00 - 18:15 Yong Jun Kim, Chang Woo Ji (Chonnam National University), Dong Soo Kong (Kyonggi University), Ihn-Sil Kwak (Chonnam National University)
- OC-5 **"What is happening during rainfall? Transition in aquatic/terrestrial invertebrate ratio detected by eDNA"**
 18:15 - 18:30 Noriko Uchida (Tohoku University)

Session D (Venue: Room 305)

- OD-1 **"Environmental DNA and RNA detection using Cas13"**
17:15 - 17:30 Jiwei Yang, Shoma Matsushita, Fei Xia, Susumu Yoshizawa, Wataru Iwasaki (The University of Tokyo)
- OD-2 **"Application of DNA methylation analysis to eDNA studies"**
17:30 - 17:45 Itsuki Hirayama, Luhan Wu, Toshifumi Minamoto (Kobe University)
- OD-3 **"Study on the ayu spawning sites using environmental DNA analysis in the Naka River"**
17:45 - 18:00 Kensuke Sugimoto, Yoichi Kawaguchi, Takahiro Sato (Tokushima University), Kyosuke Minami, Shingo Aoki, Koichiro Mizushima, Munehiro Oota (Civil Engineering and Ecotechnology Consultants company limited)
- OD-4 **"The distribution and dispersal of invasive black basses in Japan revealed by eDNA haplotyping"**
18:00 - 18:15 Kei Wakimura (Osaka Ohtani University), Shin-ichiro Matsuzaki (National Institute for Environmental Studies), Hitoshi Araki (Hokkaido University), Satoshi Kitano (Nagano Environmental Conservation Research Institute), Yoshiaki Tsuda (University of Tsukuba), Jun-ichi Tsuboi (Japan Fisheries Research and Education Agency), Tetsu Yatsuyanagi (Hokkaido University), Tomohiro Kando (University of Tsukuba), Kimiko Uchii (Osaka Ohtani University)
- OD-5 **"Preserving an Endangered Freshwater Mussel Species through Species-Specific Environmental DNA Markers"**
18:15 - 18:30 Hiroki Hata (Ehime University)

May 19th (Fri)

Session E (Venue: Piazza Hall)

- OE-1 **"Fish biodiversity across environmental gradient: a comparative approach of eDNA and underwater visual census (UVC)"**
 13:00 - 13:15 Arthur Chung (The University of Hong Kong), Stan Shea (The ADM Capital Foundation Ltd./BLOOM Association, Hong Kong), Celia Schunter (The University of Hong Kong)
- OE-2 **"Investigation of the effect of Artificial Light at Night (ALAN) on wild fish community ~manipulative field experiment and species composition analysis using eDNA methods~"**
 13:15-13:30 Aisha Oyabu, Luhan Wu, Takehiro Matsumoto, Natsumi Kihara (Kobe University), Hiroki Yamanaka (Ryukoku University), Toshifumi Minamoto (Kobe University)
- OE-3 **"Morphological, DNA barcode and eDNA metabarcoding monitoring of fish in east coastal of North Sumatera and Aceh, Indonesia"**
 13:30 - 13:45 Mohammad Basyuni, Arida Susilowati, Ahmad Baiquni Rangkuti, Desrita Desrita, Ipanna Enggar Susetya, Siti Halimah Larekeng, Hidayah Abidiah (Center of Excellence for Mangrove, Universitas Sumatera Utara), Koko Tampubolon (Universitas Sumatera Utara), Yukinobu Isowa, Tadashi Kajita (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus)
- OE-4 **"Using eDNA metabarcoding to establish targets for freshwater fish composition following river restoration"**
 13:45 - 14:00 Gen Ito (Ryukoku University), Hiroshi Yamauchi, Miwa Shigeyoshi, Kousuke Ashino, Chie Yonashiro (Chuo Fukken Consultants), Maki Asami, Yuko Goto (Center for Biodiversity Science, Ryukoku University), Jeffrey J. Duda (U.S. Geological Survey), Hiroki Yamanaka (Ryukoku University/Center for Biodiversity Science, Ryukoku University)
- OE-5 **"Evaluation of fish taxonomic and functional diversity in riverine systems using quantitative environmental DNA metabarcoding"**
 14:00 - 14:15 Seiji Miyazono, Michihito Takiyama, Hideaki Miyahira, Ryohei Nakao, Yoshihisa Akamatsu (Yamaguchi University)
- OE-6 **"Environmental DNA Monitoring for Marine Protected Areas Designation in Tsushima Island, JAPAN"**
 14:30 - 14:45 Satoquo Seino, Yukihiko Kuratani, Yoko Unoki, Mitsuhiro Aizu-Hirano, Hidefumi Hatashima (Kyushu University)
- OE-7 **"Fish eDNA survey on Taiwanese waters and marine protected areas"**
 14:45 - 15:00 Wei-Jen Chen (National Taiwan University)
- OE-8 **"Large scale eDNA database revealing latitudinal diversity gradients with seasonal variations"**
 15:00 - 15:15 Minoru Kasada, Naoto Shinohara, Riku Fukasawa, Akifumi Tanabe, Michio Kondoh (Tohoku University)
- OE-9 **"Spatiotemporal dynamics of eDNA monitoring in Hong Kong marine environments"**
 15:15 - 15:30 Mathew Seymour (The University of Hong Kong)
- OE-10 **"Spatio-temporal dynamics of fish communities along the coastal region of Boso Peninsula, central Japan: preliminary results from eDNA metabarcoding based on biweekly sampling for two years"**
 15:30 - 15:45 Ryo Gotoh, Tetsuya Sado, Takehiko Fukuchi, Masaki Miya (Natural History Museum and Institute, Chiba)

Session F (Venue: Room 305)

- OF-1 **"Strengthening large-scale biodiversity observation with advances in environmental genomics"**
 13:00 - 13:15 Nicole Fahner, Avery McCarthy, Beverly McClenaghan, Greg Singer, Mehrdad Hajibabaei (Centre for Environmental Genomics Applications, eDNAtec)
- OF-2 **"Multiplex approach to ameliorate primer bias in MiFish eDNA metabarcoding: a case study of Ayu, *Plecoglossus altivelis*"**
 13:15 - 13:30 Daisuke Isobe (Ryukoku University), Yusuke Koseki (Otsuma Women's University), Hirohiko Takeshima (Fukui Prefectural University), Hiroki Yamanaka (Ryukoku University)
- OF-3 **"Primed and ready: Nanopore metabarcoding can now recover highly accurate consensus barcodes that are almost always indel free"**
 13:30 - 13:45 Jia Jin Marc Chang (National University of Singapore), Yin Cheong Aden Ip (National University of Singapore/Animal & Veterinary Service, National Parks Board), Wan Lin Neo, Maxine Mowe, Zeehan Jaafar (National University of Singapore), Danwei Huang (National University of Singapore/Lee Kong Chian Natural History Museum, National University of Singapore/Centre for Nature-based Climate Solutions, National University of Singapore/Tropical Marine Science Institute, National University of Singapore)
- OF-4 **"Environmental DNA study in Insects using the ""MtInsects-16S"", a newly developed primer for mtDNA 16S region: Achieving highly sensitive detection"**
 13:45 - 14:00 Masaki Takenaka (Shinshu University), Yuta Hasebe (Kanagawa Environmental Research Center), Koki Yano (National Institute for Basic Biology), Koji Tojo (Shinshu University)
- OF-5 **"Developing lab standard procedures and guidelines to improve uptake of eDNA methods by resource managers: An overview of two national programs (READI-Net and iTrackDNA)"**
 14:00 - 14:15 Katy Klymus, Margaret Hunter (U.S. Geological Survey, Wetland and Aquatic Research Center), Caren Helbing (University of Victoria), Valerie Langlois (Institut National de la Recherche Scientifique), Jacob Imbrey (University of Victoria), Julie Couillard (Institut National de la Recherche Scientifique), Adam Sepulveda (U.S. Geological Survey, Northern Rocky Mountain Science Center)
- OF-6 **"Putting eDNA science into practice: lessons learned from implementation in citizen science and business"**
 14:30 - 14:45 Michael Traugott (University of Innsbruck), Daniela Sint (Applied Animal Ecology Research Unit, Department of Zoology, University of Innsbruck, Austria/Sinsoma GmbH, Austria), Corinna Wallinger (University of Innsbruck)
- OF-7 **"Targeting states of eDNA impacts the biodiversity captured and can improve interpretations of eDNA data"**
 14:45 - 15:00 Anish Ajay Kirtane, Kristy Deiner (ETH Zurich)
- OF-8 **"Challenges of monitoring poorly characterized marine and freshwater habitats in Sub-Saharan Africa: an eDNA prospect"**
 15:00 - 15:15 Quentin Mauvisseau (Natural History Museum, University of Oslo)
- OF-9 **"Detection of herbivore fish using environmental DNA: implication for controlling herbivore fish populations toward macroalgal bed restoration"**
 15:15 - 15:30 Masaaki Sato, Tatsuru Kadota, Tsutomu Noda (Japan Fisheries Research and Education Agency), Masami Hamaguchi (Fukui Prefectural University), Kengo Suzuki (Japan Fisheries Research and Education Agency)

May 18th (Thu)

14:30 - 17:00 (14:30 - 16:30 Core time)

(Venue: Conference Room)

Community structure/Population dynamics

- P-01 **"Temperature sensitivity of the interspecific interaction strength of coastal marine fish communities"**
Masayuki Ushio (Department of Ocean Science, The Hong Kong University of Science and Technology), Tetsuya Sado, Takehiko Fukuchi (Natural History Museum and Institute, Chiba), Sachia Sasano (Fisheries Technology Institute, Japan Fisheries Research and Education Agency/Maizuru Fisheries Research Station, Kyoto University), Reiji Masuda (Maizuru Fisheries Research Station, Kyoto University), Yutaka Osada (Graduate School of Life Sciences, Tohoku University), Masaki Miya (Natural History Museum and Institute, Chiba)
- P-02 **"Regional-scale effects of deer-induced forest degradation on river ecosystem dynamics"**
Hikaru Nakagawa (Aqua Restoration Research Center, Public Works Research Institute), Daisuke Fujiki (Institute of Natural and Environment Science, University of Hyogo/Wildlife Management Research Center, Hyogo), Hiroo Numata (Wildlife Management Research Center, Hyogo), Luhan Wu (Graduate School of Human Development and Environment, Kobe University), Terutaka Mori (Aqua Restoration Research Center, Public Works Research Institute), Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)
- P-03 **"Integrating bacterial DNA metabarcoding, EcoPlate metabolic profiling, and sparse regression modeling to predict ecosystem function sensitivity to biodiversity loss"**
Wan-Hsuan Cheng (Taiwan International Graduate Program -Earth System Science Program, Academia Sinica/Taiwan International Graduate Program -Earth System Science Program, National Central University/Center for Biodiversity Science, Ryukoku University), Takeshi Miki (Center for Biodiversity Science, Ryukoku University), Chih-hao Hsieh (Institute of Oceanography, National Taiwan University/Research Center for Environmental Changes, Academia Sinica/National Center for Theoretical Sciences, Mathematics Division/Institute of Ecology and Evolutionary Biology, Department of Life Science, National Taiwan University), Chun-Wei Chang (Institute of Fisheries Science, National Taiwan University/National Center for Theoretical Sciences, Mathematics Division), Fu-H-Kwo Shiah (Research Center for Environmental Changes, Academia Sinica)
- P-04 **"Characteristics of assemblages and species richness of *Sebastes* rockfishes along the coasts of northern Japan"**
Tetsu Yatsuyanagi, Takashi Kanbe (Hokkaido University), Hiroki Mizumoto (Hokkaido University/Japan Fisheries Research and Education Agency), Shouko Inoue, Hitoshi Araki (Hokkaido University)
- P-05 **"The effect of climate fluctuation on microbial biodiversity in soil and rice paddy field ecosystem"**
Takuya Kageyama (Center for Ecological Research, Kyoto University), Kenta Suzuki (RIKEN BioResource Research Center), Hirokazu Toju (Center for Ecological Research, Kyoto University)
- P-06 **"Elucidating the Relationship Between Environmental Conditions and Alternative Stable States in a Actual Microbial Community Using Quantitative DNA Metabarcoding"**
Genta Shima, Hiroaki Fujita, Hrikazu Toju (Center for Ecological Research, Kyoto University)
- P-07 **"Factors Affecting Variation in Seed Bacterial Communities of Wild Tree, *Mallotus japonicus*"**
Marin Komojiri (Center for Ecological Research, Kyoto University), Masayuki Ushio (The Hong Kong University of Science and Technology), Kazuya Takeda (The University of Tokyo), Shoko Sakai (Center for Ecological Research, Kyoto University)

- P-08 **"Integrated community analysis using mass DNA metabarcoding revealed close relationships among plant root-associated fungi"**
Mikihito Noguchi, Hirokazu Toju (Center for Ecological Research, Kyoto University)
- LBP-09 **"Characterization of floral bacteria by their context-dependency and host specificity"**
Kazuya Takeda (The Botanical Garden, Graduate School of Science, The University of Tokyo/Center for Ecological Research, Kyoto University), Shoko Sakai (Center for Ecological Research, Kyoto University)

Methodology

- P-10 **"Water drunk by raccoons: how long can their DNA be detected?"**
Chinatsu Kozakai (National Agriculture and Food Research Organization), Hiroyoshi Koyama (Saitama Agricultural Technology Research Center), Hirotaka Matsumura (Chiba Prefecture), Ryusuke Fujimoto, Hiroyuki Shibaie (National Agriculture and Food Research Organization)
- P-11 **"The environmental RNA of fishes, algae, and arthropods is an effective indicator of ecological survey and water quality assessment in rivers"**
Kaede Miyata, Yasuaki Inoue, Yuto Amano, Tohru Nishioka (R&D Safety Science Research, Kao Corporation), Tomohisa Nagaike, Takamitsu Kawaguchi (Bioindicator Co., Ltd.), Osamu Morita, Hiroshi Honda, Masayuki Yamane (R&D Safety Science Research, Kao Corporation)
- P-12 **"Assessing environmental nucleic acid pollution in freshwater bodies by domestic wastewater toward simulation of the distribution of nucleic acid causing false positives"**
Yasuaki Inoue, Kaede Miyata, Masayuki Yamane, Hiroshi Honda (R&D Safety Science Research, Kao Corporation)
- P-13 **"Development and Evaluation of microfluidic filtration extraction method (Biryu-Chip method)"**
Takashi Fukuzawa (GoFoton/Biryu Planning), Naofumi Nishizawa, Hisao Nagata, Hiromi Shirakura (GoFoton), Hideyuki Doi (Kyoto University)
- P-14 **"Environmental DNA metabarcoding of benthic invertebrates in riverine environments: a model-based assessment of species detectability for optimized study design"**
Keiichi Fukaya (National Institute for Environmental Studies), Yuta Hasebe (Kanagawa Environmental Research Center)
- P-15 **"Detection of Southeast Asian liver fluke by multi-region PCR assay"**
Riko Matsuo (Graduate School of Human Development and Environment, Kobe University), Megumi Sato (Graduate School of Health Sciences, Niigata University), Mercello Sato (Niigata University of Pharmacy and Medicinal and Life Sciences), Poom Adisakwattana, Orawan Phuphisut, Tippayarat Yoonuan (Department of Helminthology, Faculty of Tropical Medicine, Mahidol University), Yanin Limpanont, Yupa Chusongsang, Paporn Poodeepiyasawat (Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University), Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)
- P-16 **"Zooplankton sedimentary DNA as an effective tool for tracking past population dynamics"**
Narumi Tsugeki (Faculty of Law, Matsuyama University), Kai Nakane (Center for Marine Environmental Studies, Ehime University), Hideyuki Doi (Graduate School of Informatics, Kyoto University), Kazuaki Tadokoro (Shiogama Field Station, Fisheries Resource Institute), Michinobu Kuwae (Center for Marine Environmental Studies, Ehime University)
- P-17 **"Environmental mRNA-seq of *Xenopus laevis* and *Gasterosteus aculeatus*"**
Fei Xia, Jiwei Yang, Yuanyu Wang (Graduate School of Frontier Sciences, The University of Tokyo), Yihan Ma (Faculty of Environment and Information Studies, Keio University), Susumu Yoshizawa (Graduate School of Frontier Sciences, The University of Tokyo), Hiroki Kuroda (Graduate School of Media and Governance, Keio University), Asano Ishikawa, Wataru Iwasaki (Graduate School of Frontier Sciences, The University of Tokyo)

- P-18 **"Differences in concordance ratios between environmental DNA metabarcoding and capture surveys among fish species"**
 Kazuki Kanno, Ryusuke Shinohara, Souta Nakajima, Keiko Muraoka (Watershed Restoration Team, Water Environment Research Group, Public Works Research Institute), Masashi Kanaya (River Environment Division, Water and Disaster Management Bureau, Ministry of Land, Infrastructure, Transport and Tourism), Kazutaka Sakiya (Watershed Restoration Team, Water Environment Research Group, Public Works Research Institute)
- P-19 **"Evaluation of the efficacy of sponges as a passive environmental DNA sampler"**
 Ryohei Nakao, Manami Inaba, Seiji Miyazono (Graduate School of Science and Technology for Innovation, Yamaguchi University), Minoru Saito (Japan International Research Center for Agricultural Sciences/Graduate School of Science and Technology for Innovation, Yamaguchi University), Keita Maruyama, Yoshihisa Akamatsu (Graduate School of Science and Technology for Innovation, Yamaguchi University)
- P-20 **"Use of environmental DNA for seasonal monitoring of invasive aquatic plant *Egeria densa* in a riverine system"**
 Hideaki Miyahira, Seiji Miyazono, Yoshihisa Akamatsu (Yamaguchi University)
- P-21 **"The eDNA analysis using rainwater to understand forest canopy biota"**
 Takumaru Miwa (University of Hyogo), Hideyuki Doi (Kyoto University), Naoya Miyashita (Himeji City Science Museum)
- P-22 **"Development of species-specific qPCR assays for detecting raccoon (*Procyon lotor*) eDNA from field water"**
 Hiroyoshi Koyama (Saitama Agricultural Technology Research Center), Chinatsu Kozakai (National Agriculture and Food Research Organization), Hirotaaka Matsumura (Chiba Prefecture), Hiroyuki Shibaie (National Agriculture and Food Research Organization)
- P-23 **"Environmental DNA Surveillance of Biocontamination in a Drinking Water Treatment Plant"**
 Kyu-Young Shim, Heesang Shin, In-Cheol Yeo (Department of Marine Science, College of Natural Sciences, Incheon National University), Kyu Ri Kim (Hoseo Toxicology Research Center, Hoseo University), In-Sil Kwak (Department of Ocean Integrated Science, Chonnam National University), Chang-Bum Jeong (Department of Marine Science, College of Natural Sciences, Incheon National University)
- P-24 **"Validation of metabarcoding using eDNA to detect bivalves of Unionidae"**
 Natsuko Kondo, Kazuya Nishida, Hiroshi Ito, Makoto Yoshida, Kohji Mabuchi (National Institute for Environmental Studies)
- P-25 **"Photocontrolled one-pot RPA-CRISPR-Cas12a assay for Detection of *Bahaba taipingensis* from Environmental DNA"**
 Junjie Wang, Jinxian Wu, Jiabo Chen (School of Life Science, South China Normal University), Xiao Chen (South China Agriculture University), Jun Zhao, Xiaoming Zhou (School of Life Science, South China Normal University)
- P-26 **"Detection of eDNA from unionid bivalve *Nodularia nipponensis* using multi-copy nuclear DNA marker"**
 Kotaro Sugawara (Lake Biwa Museum), Sota Sugawara, Kunihiro Okano, Miho Watanabe, Naoyuki Miyata (Akita Prefectural University)
- P-27 **"Design of an Agricultural Environment Genetic Metabarcoding Database (DB) Platform"**
 Keonhee Kim (Konkuk University), Junghwan Park (PJ Factory Ltd.)
- P-28 **"Attached DNA on tree leaves as a source for eDNA metabarcoding analysis on terrestrial vertebrates"**
 Soutarou Miyake, Koki Kinoshita, Takashi Fujimori, Hiroki Yamanaka (Ryukoku University)

- P-29 **"Targeted PCR is more effective to detect Eurasian otters (*Lutra lutra*) than metabarcoding- A case study of f Yeoido Ecological Park, Seoul, Korea"**
 Yujin Kang (Interdisciplinary Program in Landscape Architecture, Seoul National University), Jeoungeun Jeon, Youngkeun Song (Department of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University)
- P-30 **"Comparison of environmental DNA analysis and traditional method (capture survey): For efficient fish surveys"**
 Takaya Hirohara, Masatoshi Hayashi, Tomoki Nakamichi, Takahiko Okamura, Takanori Nishikawa, Masahiro Ono (KANSO TECHNOS CO., LTD.)
- P-31 **"Application of eDNA in lake ecosystem assessment: use of eDNA metabarcoding on the development of zooplankton index for health assessment"**
 Yerim Choi (Department of Environmental Science and Engineering, Kyung Hee University), Chang Woo Ji (Fisheries Science Institute, Chonnam National University), Hye-Ji Oh, Geun-Hyeok Hong, Hyunjoon Kim, Jong Min Oh (Department of Environmental Science and Engineering, Kyung Hee University), Ihn-Sil Kwak (Department of Ocean Integrated Science, Chonnam National University/Fisheries Science Institute, Chonnam National University), Young-Seuk Park (Department of Biology, Kyung Hee University), Kwang-Hyeon Chang (Department of Environmental Science and Engineering, Kyung Hee University)
- P-32 **"Development and availability of a local DNA database for DNA meta-barcoding of aquatic insects"**
 Sakiko Yaegashi, Aoi Hamamoto, Yuto Sasaki (University of Yamanashi), Yuta Hasebe (Kanagawa Environmental Research Center)
- P-33 **"A feasibility study of automated underwater sampling devices to analyze environmental and microbial DNA"**
 Shuji Goto (Atmosphere and Ocean Research Institute, The University of Tokyo), Tatsuhiro Fukuba (Institute for Marine-Earth Exploration and Engineering, Japan Agency for Marine-Earth Science and Technology/Institute of Industrial Science, The University of Tokyo), Marty Kwok-Shing Wong, Yuki Minegishi, Susumu Hyodo, Yoko Makabe-Kobayashi, Yota Sugai, Koji Hamasaki (Atmosphere and Ocean Research Institute, The University of Tokyo)
- P-34 **"Detection of the Japanese sea nettle *Chrysaora pacifica* through RPA-CRISPR-Cas12a environmental DNA assay and its field validation in Jinhae Bay, South Korea"**
 Kyuhyeong Kim, Usha Jyoti Maji, Kyu-Young Shim, In-Cheol Yeo, Su-Eon Song, Chang-Bum Jeong (Department of Marine Science, College of Nature Science, Incheon National University)
- P-35 **"Investigating a method for detecting environmental DNA from rare wildlife species by a mobile PCR platform"**
 Toshiya Suzuki, Kazuki Toida, Naoya Ishiguro (Josai University)
- P-36 **"Improving environmental DNA sampling in rice paddies"**
 Satoshi Yamamoto, Naoki Katayama, Junsuke Yamasako, Kenji Ito, Hiroaki Ikeda, Yuki Baba (National Agriculture and Food Research Organization)
- P-37 **"Maximizing the potential of eDNA samples: using whole genome amplification technologies to expand the possibilities of downstream analyses"**
 Kimiko Uchii, Kana Taguchi (Faculty of Pharmacy, Osaka Ohtani University), Tomoaki Ichijo (Faculty of Health and Nutrition, Osaka Shoin Women's University), Masao Nasu (Graduate School of Pharmaceutical Sciences, Osaka Ohtani University)
- P-38 **"Optimization of sampling methods for detection of fish environmental DNA in the open ocean"**
 Akihide Kasai, Makoto Ozaki, Tatsuya Kawakami, Hiromichi Ueno (Faculty of fisheries sciences, Hokkaido University)

- P-39 **"Development and practice application of Asian Black Bear (*Ursus thibetanus japonicus*) monitoring methods using airborne eDNA"**
 Kazushi Masuda (Graduate School of Innovation and Practice for Smart Society, Hiroshima University), Mikio Nishihara, Fumika Ito (Graduate School of Integrated Sciences for Life, Hiroshima University), Jun Hatase, Ayako Noda (Hiroshima City Asa Zoological Park), Hiroshi Yasue (Tsukuba Gene Technology Laboratories Inc.), Masahide Nishibori (Graduate School of Innovation and Practice for Smart Society, Hiroshima University/Graduate School of Integrated Sciences for Life, Hiroshima University)
- P-40 **"Understanding the ecology of eRNA toward the improvement of eRNA analysis"**
 Toshiaki Jo (Ryukoku University)
- LBP-41 **"Modeling and simulation of environmental DNA dynamics"**
 Tatsuya Saito, Hideyuki Doi (Graduate School of Informatics, Kyoto University)
- LBP-42 **"Development of a highly sensitive eDNA detection method"**
 Ryo Iwamoto, Tomohiro Kuroita (Shionogi & Co. Ltd./AdvanSentinel Inc.), Yuta Kunimasa, Yuna Yamamoto, Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)
- LBP-43 **"High-Resolution Insights into Microbiomes under Stress: The Promise of eDNA Approaches?"**
 Jinping Cheng (The Education University of Hong Kong)
- LBP-44 **"Challenges and progress in the application of eDNA metabarcoding as a biomonitoring tool for mangrove-associated fauna in the Philippines"**
 Venus Leopardas, Ruby Gonzales, Nonillon Aspe, Allyn Duvin Hinoguin (Mindanao State University at Naawan), Joel Hassan Tolentino, Joan Acaso (Philippine Genome Center, University of the Philippines Mindanao), Roger Dolorosa (College of Fisheries and Aquatic Sciences, Western Philippines University), Renan Bobiles (Coastal Resource Management Section, Bicol University - Tabaco Campus), Thesa Mendoza (Aklan State University - New Washington Campus)
- LBP-45 **"Applicability of environmental DNA metabarcoding for the hyporheic zone of a stream bed"**
 Izumi Katano (Faculty, Division of Natural Science, Nara Women's University), Aki Tanaka (KYOUSEI Science Center, Nara Women's University), Hideyuki Doi (Graduate School of Informatics, Kyoto University), Mami Iguchi (Department of Chemistry, Biology, and Environmental Science, Faculty of Science, Nara Women's University), Shohei Koike (School of Human Science and Environment, University of Hyogo)

Spatiotemporal variation

- P-46 **"Seasonal environmental DNA analyses of rivers in Fukuoka Prefecture"**
 Shusaku Hirakawa, Jun Nakajima (Fukuoka Institute of Health and Environmental Sciences)
- P-47 **"Fish population dynamics in Lake Akan associated with eutrophication reconstructed by sedimentary DNA"**
 Masayuki K. Sakata (Research Faculty of Agriculture, Hokkaido University/Graduate School of Human Development and Environment, Kobe University), Michinobu Kuwae (Center for Marine Environmental Studies, Ehime University), Hajime Ohtsuki (Graduate School of Life Sciences, Tohoku University), Isamu Wakana (Kushiro International Wetland Centre), Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University), Jotaro Urabe (Graduate School of Life Sciences, Tohoku University)
- P-48 **"Seasonal movement of Rainbow Trout detected by year-round water sampling"**
 Akio Imamura (Hokkaido University of Education), Masayuki K Sakata (Hokkaido University), Toshifumi Minamoto (Kobe University)

P-49 **"Intra-annual fauna variation in urban wetlands detected by eDNA metabarcoding and camera trapping"**
 Jiyeon Park (Department of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University), Yujin Kang, Seungwoo Han (Interdisciplinary Program in Landscape Architecture, Seoul National University), Jeongeun Jeon, Youngkeun Song (Department of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University)

P-50 **"Seasonal variation of fish fauna in Otsuchi Bay by environmental DNA metabarcoding analysis"**
 Mai Teruya (Iwate University), Yuki Minegishi (The University of Tokyo)

Diet

P-51 **"The combinational analyses of environmental and stomach content DNA may reveal piscivory of the Japanese Spiny Lobster (*Panulirus japonicus*)"**
 Shoju Shi, Reiji Masuda (Maizuru Fisheries Research Center, Kyoto University)

P-52 **"Seasonal- and Size- dependent foraging by the masu salmon (*Oncorhynchus masou*) revealed by DNA metabarcoding"**
 Yumiko Ishii, Jaeick Jo (National Institute for Environmental Studies), Tsutomu Kanasashi, Toshihiro Wada (Fukushima University), Natsuko Kondo, Nobuyoshi Nakajima (National Institute for Environmental Studies), Rie Saito (University of Georgia), Masanori Tamaoki, Seiji Hayashi (National Institute for Environmental Studies)

P-53 **"Application of DNA Metabarcoding for identifying the potential food of *Corbicula* (Asian Clam) in the lower part of the Seomjin and Nakdong River, Korea"**
 Yu-Ji Heo (Department of Environmental Education, Suncheon National University), Kang-Hui Kim, Hyunbin Jo (Department of Integrated Biological Science, Pusan National University), Hyun-Woo Kim (Department of Environmental Education, Suncheon National University)

P-54 **"Prey Species for Yellowjacket Wasps (*Vespa shidai*) Raised for Consumption by Ordinary Citizens in Central Japan and Wild Nests"**
 Tatsuya Saga (Graduate School of Human Development and Environment, Kobe University)

Distribution

P-55 **"Development of qPCR based eDNA detection assay to assess the distribution of a fish species in the Himalayan hill stream"**
 Rishikesh Krishan Laxmi, Varunendra Singh Rawat, Nitika Sharma, Neeta Sehgal (Department of Zoology, University of Delhi)

P-56 **"Differences in vertical distribution of two salmonid species: the impacts of warm water temperature and hypoxia in a stratified lake"**
 Kayoko Fukumori, Natsuko I. Kondo, Ayato Kohzu, Kenji Tsuchiya, Hiroshi Ito, Taku Kadoya (National Institute for Environmental Studies)

P-57 **"Distribution of finless porpoise (*Neophocaena asiaeorientalis*) in Osaka bay, Japan using eDNA analysis"**
 Nagisa Hashimoto (Graduate School of Human Development and Environment, Kobe University), Takashi Iwata (Graduate School of Maritime Sciences, Kobe University), Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)

P-58 **"Distribution analysis of the invasive diatom *Cymbella janischii* using environmental DNA from benthic diatoms in river systems"**
 Yoko Kato-Unoki (Kyushu University), Tamie Suzawa (Institute of River Biology Ltd), Tran Thu Trang (Kyushu University), Yoshitsugu Masuda, Jun-ichi Tsuboi (Japan Fisheries Research and Education Agency), Satoquo Seino (Kyushu University)

- P-59 **"Surveying the Habitat of *Blotched tabira* Bitterling and their Spawning Host Mussels Using Environmental DNA: A Novel Methodological Approach"**
Kazuyuki Ooi, Tomoyuki Jouuchi (Kyushu Environmental Evaluation Association)
- P-60 **"Unraveling the effects of cross river structures on the habitat of Japanese eel"**
Yuta Kunimasa, Natsumi Kihara, Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)
- P-61 **"Investigation of eDNA Quantitative Analysis Method for Understanding Fish Dynamics in Mountain Streams"**
Shiori Nagahora, Masateru Nishiyama (Department of Food, Life and Environmental Sciences, Faculty of Agriculture, Yamagata University), Takahiro Sato (Fukken Gijyutsu Consultants Co., Ltd), Kazuya Watanabe (Department of Food, Life and Environmental Sciences, Faculty of Agriculture Yamagata University)
- P-62 **"Comparative phylogeography by environmental DNA analysis: investigating the relationship between phylogeographic patterns and ecological traits in *Rhinogobius* species"**
Satsuki Tsuji, Shota Kunimatsu, Katsutoshi Watanabe (Kyoto University)
- P-63 **"Characterization of the distribution of the flagship species, *Gobiobotia nakdongensis*, within the stream basin where the dam was constructed: application of species-specific markers and targeted qPCR methods"**
Hye-Ji Oh (Department of Applied Environmental Science, Kyung Hee University), Keun-Sik Kim (Research Center for Endangered Species, National Institute of Ecology), Keun-Yong Kim (AquaGenTech Co., Ltd), Jeongwoo Yoo (Research Center for Endangered Species, National Institute of Ecology), Kyu-Jin Kim, Min-Ho Jang (Department of Biology Education, Kongju National University), Jeong-Hui Kim (EcoResearch incorporated), Doo-Hee Won (Doohee Institute of Ecological Research, Korea Ecosystem Service Inc.), Ju-Duk Yoon (Research Center for Endangered Species, National Institute of Ecology), Kwang-Hyeon Chang (Department of Applied Environmental Science, Kyung Hee University)
- P-64 **"Species distribution of Korean raccoon dog in urban wetland using eDNA and conventional survey"**
Seungwoo Han (Interdisciplinary Program in Landscape Architecture, Seoul National University), Jeongeun Jeon (Dept. of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University), Yujin Kang (Interdisciplinary Program in Landscape Architecture, Seoul National University), Youngkeun Song (Dept. of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University/Transdisciplinary Program in Smart City Global Convergence, Seoul National University)
- P-65 **"Distribution estimation of *Cervus nippon taionaus* using environmental DNA (eDNA)"**
Suyeon Won, Yujin Kang, Suengwoo Han, Jeongeun Jeon, Jiwoon Park (Seoul National University), Shinjae Rhim (Chung Ang University), Youngkeun Song (Seoul National University)
- P-66 **"Use of quantitative environmental DNA metabarcoding for grasping the habitat of threatened fish species in the first class rivers of the Chugoku District"**
Michihito Takiyama, Seiji Miyazono, Hideaki Miyahira, Ryohei Nakao, Takumi Hanaoka, Yoshihisa Akamatsu (Yamaguchi University)
- P-67 **"Efficient assessment of cryptic invasions using environmental DNA: the case of the minnow *Pseudorasbora parva* in Japan"**
Atsushi Kogayu, Satsuki Tsuji, Katsutoshi Watanabe (Department of Biology, Graduate School of Science, Kyoto University)

- P-68 **"Horizontal and vertical distribution of environmental DNA of jack mackerel *Trachurus japonicus* and Japanese anchovy *Engraulis japonicus* in Maizuru Bay, Kyoto Prefecture"**
 Hiroaki Murakami (Tohoku University), Keiichi Fukaya (National Institute for Environmental Studies), Satoshi Yamamoto (National Agriculture and Food Research Organization), Toshifumi Minamoto (Kobe University), Kenji Minami, Kazushi Miyashita (Hokkaido University), Taishin Kameoka (Japan International Research Center for Agricultural Sciences), Reiji Masuda, Yoh Yamashita (Kyoto University), Michio Kondoh (Tohoku University)
- LBP-69 **"An environmental DNA survey reveals orthotopic habitat of *Anguilla japonica* and *A. marmorata* in Nagasaki, Japan"**
 Yurika Ono, Katsuya Hirasaka (Graduate School of Fisheries Science and Environmental Studies, Nagasaki University), Taijun Myosho (Department of Environmental and Life Sciences, Faculty of Food and Nutritional Sciences, University of Shizuoka), Shingo Fujimoto (Tropical Biosphere Research Center, University of the Ryukyus), Mitsuharu Yagi (Graduate School of Fisheries Science and Environmental Studies, Nagasaki University)
- LBP-70 **"Detection of spatio-temporal change in herbivorous fish distribution around the coast of Japan using ANEMONE eDNA data"**
 Chris Bayne, Mahiko Abe (Japan Fisheries Research and Education Agency), Toshinori Baba (Yamaguchi Prefectural Fisheries Research Center), Hideki Hamaoka (Niigata Prefectural Fisheries and Marine Research Institute), Natsuki Hasegawa (Japan Fisheries Research and Education Agency), Hiroyo Igari (Kagoshima Prefectural Fisheries Technology and Development Center), Mitsuhiro Ishii (Chiba Prefectural Fisheries Research Center), Atsushi Ito (Japan Fisheries Research and Education Agency), Yusuke Marume (Miyazaki Prefectural Fisheries Research Institute), Toshihiro Nishioka (Kagawa Prefectural Fisheries Experiment Station), Masaaki Sato (Japan Fisheries Research and Education Agency), Shiyouchi Takenaka (Fisheries Research Center, Ehime Research Institute of Agriculture, Forestry and Fisheries), Yoshiyuki Tanaka (Hachinohe Institute of Technology), Hideaki Yamada (Japan Fisheries Research and Education Agency), Masayuki Yamamoto (Kagawa Prefectural Fisheries Experiment Station/Fukui Prefectural University), Kosuke Yatsuya (Japan Fisheries Research and Education Agency), Keiichiro Yoshimi (Fisheries Research Division Tokushima Agriculture, Forestry, and Fisheries Technology Support Center), Satoshi Nagai (Japan Fisheries Research and Education Agency), Masami Hamaguchi (Fukui Prefectural University), Masakazu Hori (Japan Fisheries Research and Education Agency/Tokyo University of Marine Science and Technology)

Diversity

- P-71 **"Comprehension of Species Compositions Using Environmental DNA Metabarcoding in Beppu Bay Sediment"**
 Chisato Numa (Graduate School of Information Sciences, University of Hyogo)
- P-72 **"Non-destructive monitoring of arthropod community on woody plant, *Quercus serrata*, using environmental DNA metabarcoding"**
 Kinuyo Yoneya (Kindai University/Center for Biodiversity Science, Ryukoku Univ.), Takeshi Miki (Center for Biodiversity Science, Ryukoku University), Akio Kashimura (Kindai University)
- P-73 **"Classification of abandoned rice paddy fields using environmental variables and eDNA metabarcoding of Amphibia"**
 Jeongeun Jeon (Dept. of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University), Yujin Kang, Seungwoo Han (Interdisciplinary Program in Landscape Architecture, Seoul National University), Jiyeon Park (Dept. of Landscape Architecture, Graduate School of Environmental Studies, Seoul National University), Youngkeun Song (Interdisciplinary Program in Landscape Architecture, Seoul National University/Transdisciplinary Program in Smart City Global Convergence, Seoul National University)

- P-74 **"Monitoring fish biodiversity using eDNA metabarcoding in a World Natural Heritage Island, Iriomote, Okinawa, Japan"**
Bernadeth Grace Pananganan, Yukinobu Isowa, Maria Daniela Artigas Ramirez (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus), Takashi Yamamoto (Tama University Hijirigaoka High & Junior High School), Masaki Miya (Natural History Museum and Institute, Chiba), Tadashi Kajita (Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Malaysia/Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus/United Graduate School of Agricultural Sciences, Kagoshima University)
- P-75 **"Environmental DNA metabarcoding for Measuring Fish Species Diversity in Pearl River Estuary surrounding Chinese Bahaba nature reserve ecosystems during the migration and non-migration period"**
Jinxian Wu, Jiabo Chen, Xiao Chen, Lei Zhou, Xuehui Wang, Jun Zhao, Junjie Wang
- P-76 **"eDNA metabarcoding of water stream flowing the Japanese garden in Kyoto"**
Kazutoshi Tsuda (Kyoto Institute of Technology/Yamaguchi Center for Arts and Media), Fumie Takahara (Yamaguchi Center for Arts and Media), Tomohiro Inoue (Kyoto Institute of Technology), Takayuki Ito (Yamaguchi Center for Arts and Media)
- P-77 **"Investigating intraspecific and species-level diversity in marine species using COI DNA metabarcoding: a case study of *Zostera* sp. community in the northern Sea of Japan?"**
Sergei Turanov (A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences)
- P-78 **"Environmental DNA as an assessment tool for wetland biodiversity in Heuksando, Korea"**
Gawoo Kim (Interdisciplinary Program of Landscape Architecture, Seoul National University)
- P-79 **"Investigation of the potential applicability of eDNA as an environmental education tool"**
Ryota Kitani, Mieko Kiyono, Masayuki Sato, Atushi Ushimaru, Toshifumi Minamoto (Graduate School of Human Development and Environment, Kobe University)
- LBP-80 **"Detection of the Fish Biodiversity in Mangrove Ecosystem in Nakara River at Iriomote Island, Japan using MiFish eDNA Metabarcoding"**
Severino G. Salmo III (Institute of Biology, College of Science, University of the Philippines Diliman), Yukinobu Isowa (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus), Takashi Yamamoto (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus/Faculty of Science, University of the Ryukyus /Tama University Hijirigaoka High & Junior High School), Tetsuya Sado (Department of Ecology and Environmental Sciences, Natural History Museum and Institute Chiba), Katsuya Ito (Faculty of Science, University of the Ryukyus), Mohammad Basyuni (Center of Excellence for Mangrove, Universitas Sumatera Utara), Shinya Imura, Keiichi Ishigaki (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus), Masaki Miya (Department of Ecology and Environmental Sciences, Natural History Museum and Institute Chiba), Tadashi Kajita (Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus/Graduate School Union of Agriculture, Kagoshima University/Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah)

Date: May 18th (Thu), 11:00 - 12:30 (Venue: Room 305)

Explanation: (Illumina K.K.)

15-minute company talk from Illumina is planned at the beginning of the workshop.

OceanOmics: Bolstering marine research and conservation with genomic technologies

Priscila Goncalves

Minderoo Foundation • Flourishing Oceans

The world's ocean is the largest, least understood and yet one of the most exploited realms on our planet. Although the ocean covers around 71% of Earth's surface and supports 90% of its biosphere, more than 80% of the ocean is unmapped, unexplored and unobserved. The OceanOmics program at the Minderoo Foundation set out to transform how we observe, measure and understand life in our ocean to ultimately accelerate ocean conservation and halt biodiversity loss. We believe that eDNA-based marine genomics can form the technological basis for innovations that can revolutionise how we collect biodiversity data across space and time. We are working with globally renowned scientists and industry partners to advance eDNA-based technologies for biodiversity monitoring in these vast and highly dynamic ocean environments. This involves optimisation and scaling of eDNA collection, processing, and characterisation, including the development of novel approaches for species detection and quantification. To enable ocean-scale eDNA-based biodiversity surveys, OceanOmics is committed to generating and openly publishing reference genomic resources for thousands of species of marine vertebrates, as well as developing the most comprehensive analytical tools for marine sequencing data based on standardised, reproducible processes and artificial intelligence. These evolving technologies have been deployed at sea from a unique marine genomics platform, which houses onboard high-throughput sequencing and bioinformatics resources. Over the last two years, this vessel has enabled multiple research expeditions across Australia, and represents a powerful asset for the establishment of biodiversity baselines and long-term biomonitoring programs. The development and application of such comprehensive genomic tools and resources will facilitate the rapid, accurate and large-scale generation of biodiversity data to support ocean management and conservation efforts.

Collaborative eDNA initiatives in Australia and New Zealand

Oliver Berry

CSIRO Environomics Future Science Platform

Southern eDNA Society

Environmental DNA research and application is rapidly evolving globally, including in Australia and New Zealand. As this Australasian eDNA community has grown and matured we have begun to address shared barriers to technical feasibility and adoption by government and industry. In this presentation I will introduce four initiatives that illustrate this collective approach and that have international analogues or relevance: 1) the establishment of the Southern eDNA Society - a society advocating for best practice and adoption of eDNA science in the region; 2) the first Australian and New Zealand eDNA conference held in February 2023; 3) The National Biodiversity DNA Library – a library of complete DNA reference sequences for all named Australian species; and 4) the Making eDNA FAIR project – data standards that enable eDNA data sharing. The objectives of my presentation are to create awareness of eDNA activities in Australia and New Zealand, seek feedback and contributions, and to encourage collaborations that will grow the cohesiveness and effectiveness of this remarkable and much needed technology around the world.

*Lunch box will be provided for those who pre-register.

Date: May 19th (Fri), 11:00 - 12:30 (Venue: Room 305)

Explanation: Naofumi Nishizawa (President, Go!Foton, Inc.)

Demonstration of mobile PCR operation

~Detects genes in about 30 minutes from water sampling~

Go!Foton, Inc. and Pacific Consultants Co., Ltd

Go!Foton and Pacific Consultants have been jointly developing applications for PicoGene, a portable PCR device for the environmental DNA field.

With conventional methods, water samples must be brought back to the laboratory for analysis, and it takes several days to a week before results are available. In contrast, by using a simple extraction and microfluidic chip, and a portable PCR device named PicoGene, DNA detection results can be obtained in about 30 minutes on site. It also allow the user to move on to the next place while PCR analysis is ongoing. This method is particularly effective for screening target species in tributaries and streams with high DNA concentrations.

The results of the development of the process and the simplified extraction method, which can be completed in about 30 minutes from water sampling to filtration, extraction, and PCR detection, have been summarized in a paper by Dr. Doi of Kyoto University.

The method using a microfiltration chip with a microfluidic channel, which was devised to further simplify filtration and extraction, is also summarized in the paper.

On-site environmental DNA detection of species using ultrarapid mobile PCR,

DOI: 10.1111/1755-0998.13448

Filtration and extraction using microfiltration channel for measuring environmental DNA,

DOI: 10.1111/1755-0998.13657

In this demonstration, we show all of process from filtration, extraction, and PCR detection using actual sample water. We plan to show you both the simple method and the microfluidic chip method, as well as have you try them out for yourself.

Go!Foton has acquired PicoGene PCR1100 business from Nippon Sheet Glass Co., Ltd. as of 2023/04/01.

Go!Foton expand PCR business with PicoGene from now on.

May 19th (Fri) 16:00 - 17:00 (Venue: Piazza Hall)

Is eDNA good enough? Implications for science and society

Mehrdad Hajibabaei, Ph.D., Associate Prof. (University of Guelph, Canada)



Our linkages to biodiversity impacts every aspect of our life and wellbeing. However, our ability to measure and study biodiversity has been limited because conventional methods are not scalable or feasible for many applications. The need for tools and approaches for biodiversity analysis is at an all-time high given that we are facing a “biodiversity crisis” triggered by climate change and other anthropogenic activities. Methods developed based on environmental DNA (eDNA) are clearly making significant contributions to biodiversity analysis in a wide range of settings backed by thousands of scientific papers in the last decade. However, these use cases are somewhat limited to academic, artisanal and proof-of-concept cases. Real-world, systematic and on-going use of eDNA tools in scientific initiatives or environmental assessment and monitoring programs has been somewhat limited. In the absence of an absolute and precise measure of biodiversity in most settings, users have difficulty verifying and validating data generated through eDNA studies as compared to traditional approaches. Coupled with a lack of standardized and interoperable protocols and an ever quickly evolving technologies, these issues have created barriers to widespread use of eDNA. While we need to address these concerns by directing resources and strategic planning, it is also important to focus on the eDNA’s core premise and ask if eDNA is good enough for the tasks at hand. I argue that eDNA tools, when properly applied, are currently one of the best available options for rapid and accurate biodiversity analysis at the scale we need to better understand and mitigate the biodiversity crisis. The recent COVID-19 pandemic has taught us that solutions which are “good enough” can be justified when the urgency of the task at hand requires rapid deployment of the best available tools.

A powerful tool for studying ecosystem biodiversity

NGS offers the ability to analyze complex environmental DNA samples



eDNA sequencing is a powerful method to analyze samples from different types of environments for various applications such as air and water quality monitoring, detection of rare and invasive species, diet analysis, and more, to ultimately monitor and protect our ecosystems.

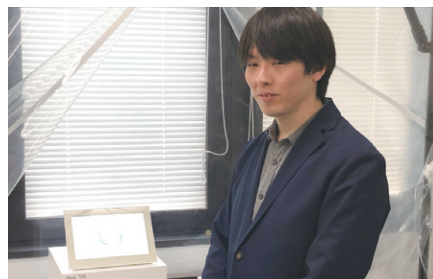
Visit Illumina's eDNA page to learn more about eDNA sequencing.
<https://sapac.illumina.com/destination/edna.html>



Videos



Customer Interviews



Literatures



The NextSeq™ 1000/2000 enhances the potential of eDNA sequencing by enabling higher throughput applications, as well as deeper and larger studies. With over 75 updates, the NextSeq system offers dry instrumentation, easier run setup, and fast second run analysis with DRAGEN™ software onboard.

Drop by Illumina booth to discover the possibilities for eDNA sequencing via NextSeq 2000.



ゴーフォトン、モバイルPCR装置 (*PicoGene*[®]、*PCR1100*) で、環境DNA分析法の社会実装を目指しています。

PicoGene[®]を用いて15分という短時間でPCR結果が得られるようになって、フィールドでPCR実験を行う場合「抽出」という大きなハードルがあります。

一般的な抽出は、工程が複雑でかつ各種装置が必要なこともあり、ラボにサンプルを持ち帰ってPCR実験を行うことがほとんどでした。

その問題を解決するため、ろ過・抽出を簡略化する方法を開発し、以下論文がMolecular Ecology Resourcesに掲載されました。

簡易抽出法、DOI: 10.1111/1755-0998.13448

微流チップによるろ過・抽出、DOI: 10.1111/1755-0998.13657



本学会では、ろ過～PCR検出を30分で完了できるプロセスのデモンストレーションを行います。皆様に*PicoGene*[®]を実際に触って頂けるように用意しておりますので、是非、ご参加下さい。

協賛セミナー:

モバイルPCR装置の操作デモンストレーション

～採水から約30分で遺伝子を検出します～

(パシフィックコンサルタンツ株式会社と共催)

日時: 5月19日(金)、11:00～(1時間半程度) @305会議室

製品ラインアップ:

①モバイルリアルタイムPCR装置、*PicoGene*[®] *PCR1100*、

*日本板硝子㈱から*PicoGene*[®]の事業譲渡を受け4月1日より弊社製品となりました。

- ・超高速(15分、50サイクル) ・持ち運び可能(バッテリー駆動可能)
- ・マルチプレックス対応(3種を同時に検出)

<https://pcr.gofoton.co.jp/index.html>

②PCR試薬(PCR1100に最適化、検体と混ぜるだけで使用可能)

食品検査用:

カンピロバクター(鶏肉検査)

環境調査用:

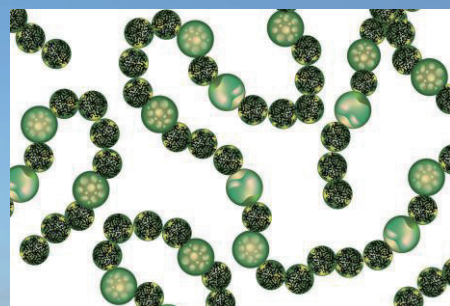
レジオネラ(温浴施設検査)、ジェオスミン/2-MIB(上水検査)、

鮎、マンソン住血吸虫、ウチダザリガニ、カミツキガメ、等

マルチプレックス:複数種を同時検出

- ・ニホンウナギ、ヨーロッパウナギ
- ・オオサンショウウオ、チュウゴクサンショウウオ
- ・オオクチバス、コクチバス、ブルーギル
- ・キタノメダカ、ミナミメダカ

これ以外にも各種検出試薬の開発を行っております。お気軽にお問い合わせ下さい。



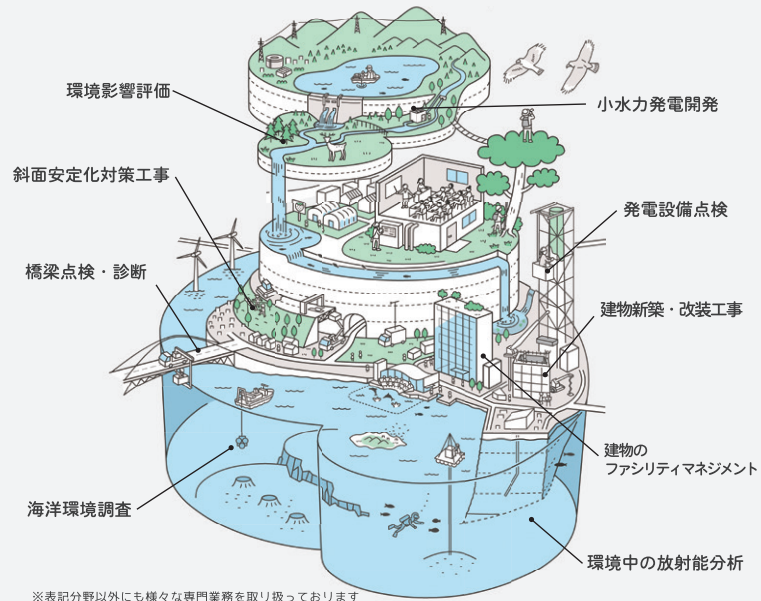
株式会社ゴーフォトン

〒300-2635 茨城県つくば市東光台5-4-2

TEL: 029-847-8686 / sales-tp@gofoton.com

地球・社会・暮らしの『緑の下エンジニアリング。』

わたしたちは、豊かな地域社会の実現とかけがえない地球環境の保全に向けてあらゆるフィールドで社会基盤を支えつづけます



※表記分野以外にも様々な専門業務を取り扱っております

環境 DNA 分析受託サービス

サンプリング計画から解析・精査まで
トータルでサポートいたします。

・魚類相等の網羅的解析(メタバーコーディング)
・種特異的プライマーを用いた在不在判定
etc.



「自然と共生」をテーマに豊富な経験と最新のテクノロジーを活かし
未来につながる優れた社会資本の整備
それが私たちの使命です。

 **株式会社 建設環境研究所**

〒170-0013 東京都豊島区東池袋2-23-2 TEL. 03-3988-1818 (代表)

URL: <https://www.kensetsukankyo.co.jp/>

 **KANSOテクノス**

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TEL 06-6263-7378 (環境部 営業グループ)
FAX 06-6263-7313 (環境部 営業グループ)



KANSOテクノスHP: <http://www.kanso.co.jp/>
環境DNA分析HP: <http://www.kanso.co.jp/environment/DNAAnalysis/index.html>

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The eDNA Society International Meeting 2023

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Yukiko Kobayashi (Secretariat, The eDNA Soc.)

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The eDNA Society International Meeting 2023 Program

Meeting May 17th – 19th

Excursions May 20th – 21st

Piazza Omi 1-1-20, Nionohama, Otsu, Shiga, 520-0801, JAPAN

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