



mabik
NATIONAL MARINE BIODIVERSITY INSTITUTE OF KOREA



2021
2030
United Nations Decade
of Ocean Science
for Sustainable Development



WORKSHOP REPORT

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Abbreviations

CCZ	Clarion-Clipperton Zone
eDNA	environmental DNA
EMBRC	European Marine Biological Resource Centre
EMO BON	European Marine Omics Biodiversity Observation Network
FAIR	findable, accessible, interoperable and reusable
GOOS	Global Ocean Observing System
Ifremer	Institut français de recherche pour l'exploitation de la mer
IOC-UNESCO	Intergovernmental Oceanographic Commission of the United Nations Educational, Scientific and Cultural Organization
ISA	International Seabed Authority
LTC	Legal and Technical Commission
MABIK	National Marine Biodiversity Institute, the Republic of Korea
MBON	Marine Biodiversity Observation Network
MOMAF	Ministry of Oceans and Fisheries, the Republic of Korea
OBIS	Ocean Biodiversity Information System
OEMMR	Office of Environmental Management and Mineral Resources
PCR	Polymerase Chain Reaction
UNCLOS	United Nations Convention on the Law of the Sea
USP	Universidade Federal de São Paulo
VME	vulnerable marine ecosystems

Introduction

1. The mandate of the International Seabed Authority (ISA), on behalf of the State Parties to the United Nations Convention on the Law of the Sea (UNCLOS), is to regulate and control activities in the international seabed area (the Area) for the benefit of humankind as a whole. ISA is also mandated to take necessary measures to ensure effective protection of the marine environment from potentially harmful effects that may arise from seabed activities (UNCLOS, Article 145).

2. ISA is also mandated to promote and encourage marine scientific research in the Area and coordinate and disseminate the results of such research and analysis when available (UNCLOS, Article 143). The importance of this obligation is highlighted in the Strategic Plan of ISA for 2019-2023 (ISBA/24/A/10, annex, para. 29), particularly strategic direction 4 (“Promote and encourage marine scientific research in the Area”), which is being implemented through the High-level Action Plan for 2019-2023 (ISBA/25/A/15).

3. To support fulfilling these mandates, the ISA Assembly in 2020 adopted the Action Plan of the [ISA] in support of the United Nations Decade of Ocean Science for Sustainable Development (ISBA/26/A/17). One of the six strategic research priorities identified in the Action Plan is focused on standardizing and innovating methodologies for deep-sea biodiversity assessment, including taxonomic identification and description, in the Area.

4. In this context and continuing the work of the ISA Secretariat to facilitate the integration of taxonomic knowledge into ISA’s efforts for the protection of the marine environment in the Area, two workshops have been convened in collaboration with the Ministry of Oceans and Fisheries of the Republic of Korea (MOMAF) and the National Marine Biodiversity Institute of Korea (MABIK). In the first of these workshops, held in September 2020,¹ several priority actions were identified for developing a collaborative platform to advance deep-sea taxonomic knowledge in the Area. The second workshop, held in October 2021,² identified key elements for a standardized model of image data exchange, archiving and sharing to support biodiversity assessment and monitoring.

5. Along with the increased use of deep-sea imagery as a powerful noninvasive methodology for investigating the deep-sea environment, significant advances are being made towards the use of environmental DNA (eDNA) as another non-destructive, cost-effective and easily replicable methodology for studying deep-sea biodiversity. Nonetheless, the utility and scientific value of the information generated by these approaches remains to be unfolded. This is due to the lack of consistency across surveys and the absence of comprehensive genetic reference catalogues, which are critical in identifying organisms and matching the genetic sequences. A standardized and comprehensive compilation of genetic data emerging from exploration activities and other scientific research projects in the Area will significantly contribute to enhancing species identification and description. An enhanced taxonomic knowledge base will further enable the application of innovative methodologies and improve broad-scale biodiversity assessments.

6. Building on the results of the abovementioned workshop on deep-sea taxonomic standardization, the ISA Secretariat, in collaboration with MOMAF and MABIK, convened a workshop,

¹ ISA. 2020. Workshop on Deep Sea Taxonomic Standardization: Strategic Approaches for Collaboration. Available at: <https://www.isa.org.jm/events/workshop-on-deep-sea-taxonomic-standardization-strategic-approaches-for-collaboration>.

² ISA. 2021. Workshop on Enhancing Image-based Biodiversity Assessments to Advance Deep-Sea Taxonomy. Available at: <https://www.isa.org.jm/events/workshop-enhancing-image-based-biodiversity-assessments-oct2021>.

Enhancing genetic approaches to advance deep-sea taxonomy. The workshop aimed at identifying key elements and technical means necessary for the effective sharing and use of genetic data, including through a collaborative platform in the context of ISA, to enhance deep-sea species identification and quantification and increase capacity and literacy in deep-sea taxonomy.

7. The workshop was conducted in two separate sessions: an in-person technical session from 23-24 November 2022 and a hybrid in-person/online session on 25 November 2022. The technical session focused on topics related to i) challenges and opportunities for enhancing data interoperability between the ISA DeepData database and international genetic databases (e.g. BOLD, Ocean Biodiversity Information System [OBIS], etc.), ii) best available protocols for quality assurance and control, as well as practical approaches for standardizing methods for eDNA surveys in benthic and pelagic habitats and iii) use of genetic data in environmental baseline and monitoring studies. The hybrid session focused on i) providing updates on the outcomes of the technical session, ii) discussing the effective use of genetic information for deep-sea biodiversity assessment and monitoring in support of sustainable ocean governance and iii) exploring potential ways and means to enhance collaboration among members and stakeholders of ISA, including the scientific community, contractors and decision makers to build deep-sea research capacity and literacy with a focus on genetic technologies, methodologies and tools and their adequate application at a larger scale.

8. The workshop outcomes provided the ISA Secretariat with key elements to work towards enhancing scientific knowledge and assessment of deep-sea biodiversity in the Area. This included recommendations on improving data interoperability between the ISA DeepData database and international genetic databases and identifying means to provide optimized and standardized methods for deep-sea genetic research. The workshop also provided opportunities for members, contractors and other relevant stakeholders of ISA to explore opportunities to collaborate in DNA-based research, increasing the awareness of associated methodologies and promoting capacity-building efforts in the field of deep-sea taxonomy.

9. Part I of the workshop (technical session) was attended by 17 invited experts. A total of 46 participants attended Part II of the workshop (hybrid in-person/online session). The full list of workshop participants is provided in Annex I of this report.

10. The ISA Secretariat issued an information note for participants containing logistics details to facilitate their participation, including information on how to join the online workshop and navigate different functions of the online meeting platform. The workshop was conducted in English.

11. The workshop commenced at 08:00 (Seocheon, Republic of Korea, GMT+9) on Wednesday, 23 November 2022.

Part I: Technical session (23-25 November 2022)

12. The ISA Secretariat moderated the workshop.

Item 1. Opening of the workshop

13. Mr. José Dallo Moros, the Director of the ISA Office of Environmental Management and Mineral Resources (OEMMR), delivered his opening remarks. He first expressed his appreciation to the President of MABIK, Mr. Wan-hyun Choi, for his support in organizing the workshop. He also expressed gratitude to all speakers and participants contributing to the workshop. Mr. Dallo highlighted that the deep-sea community celebrated 40 years since UNCLOS was adopted in 2022. He stressed that the workshop was a milestone in implementing the mandate given to ISA by UNCLOS as an activity to support the protection of the marine environment. Mr. Dallo also emphasized that the event corresponded with ISA's unique role to promote and encourage marine scientific research in the Area and coordinate and disseminate the results of such research. He then underlined that the workshop is the third edition of the deep-sea taxonomic standardization workshop series, developed in collaboration with the MOMAF and MABIK since 2020. Lastly, he introduced the main topics to be discussed during the workshop: enhancing data interoperability between the ISA DeepData database and other international genetic databases, discussing practical approaches to standardizing methods for eDNA surveys in benthic and pelagic habitats and identifying better use of the genetic data in environmental baseline and monitoring studies. He concluded by reiterating the commitment of ISA to expanding and deepening our scientific knowledge of the deep seabed and building the capacities to protect the marine environment and sustainably manage the ocean and its vast resources for the benefit of all humankind.

14. Dr. Wan-hyun Choi, the President of MABIK, also delivered his opening remarks. He first expressed his gratitude to the Secretary-General of ISA, Mr. Michael W. Lodge, for the partnership on advancing marine scientific research. He also appreciated the ISA Secretariat for organizing the workshop and all speakers and participants for joining the workshop. Dr. Choi emphasized the importance for MABIK to host a deep-sea taxonomy workshop in Seocheon with experts worldwide. He mentioned that the workshop was part of ISA's deep-sea taxonomic standardization workshop series. He highlighted that this edition focused on identifying key elements and technical means necessary for effectively sharing and using genetic data. He stressed that eDNA approaches are non-destructive, cost-effective and replicable but require standardization and comprehensive genetic reference catalogues for deep-sea research. Mr. Choi stated to be pleased to host a workshop that aimed to provide elements to overcome these challenges, identify collaborative opportunities and build research capacity. He concluded by reiterating MABIK's continued support for the work of ISA and wishing the participants a fruitful discussion.

Item 2. Workshop background, scope and expected outputs

15. Under this item, participants had before them the draft background document, which provided information on the topics to be discussed during the workshop.

16. Dr. Luciana Genio, ISA Secretariat, presented on background, scope and expected outputs of the workshop.

17. Participants were invited to ask questions and exchange insights, views and suggestions on the workshop scope and outputs in response to the presentation.
18. Summary of the above presentation is provided in Annex II of this report.

Item 3. Using genetic information to advance deep-sea taxonomy and biodiversity assessment in the Area

19. Under this item, Thomas Dahlgren, University of Gothenburg, Sweden, delivered a theme presentation on using genetic information for deep-sea taxonomy and biodiversity assessment in the Area.
20. Participants were invited to exchange insights and views in response to the presentation above.
21. Summary of the above presentation is provided in Annex II of this report.

Item 4. Technological advances and methodological challenges in large-scale genetic surveys to assess deep-sea biodiversity

22. Under this item, a panel discussion was organized with the following experts, who delivered brief presentations on technological advances and methodological challenges for deep-sea genetic surveys, with a focus on large-scale projects:
 - a) Nicolas Pade, European Marine Biological Resource Centre (EMBRC-ERIC), France, *The European Marine Omics Biodiversity Observation Network (EMO BON)*
 - b) Xue-Wei Xu, Second Institute of Oceanography, Ministry of Natural Resources, China, *Molecular Techniques for Assessment of Deep-Sea Microbial Communities*
 - c) Franck Lejzerowicz, University of Oslo, Norway, *Mining eDNA and RNA: taxonomy and benchmark needs to understand and preserve deep-sea benthic life*
23. Summaries of the above presentations are provided in Annex II of this report.
24. Participants were invited to ask questions and exchange insights and views in response to the ideas, examples and experiences presented by the panellists.
25. This was followed by a discussion moderated by Franck Lejzerowicz, University of Oslo, Norway, focusing on methodological standardization in deep-sea genetic research.
26. The following points, inter alia, were highlighted during the discussion:
 - **Standardizing sampling, labelling and metadata collection.** During this discussion, participants highlighted the importance of efficient labelling and suggested defining a unique code system to standardize biological samples and specimens. The databases should be linked to the unique codes. Sample metadata should be informative to future generations; the projects should pre-define the set of information to be stored, i.e. a minimal list of metadata. Participants stressed that standard sets of metadata had been previously established for different purposes, including the minimum information about any (x) sequence (MixS) created by the Genomic Standards Consortium and the Darwin Core for Environmental Metadata. Such definitions are essential for integrating large-scale data and for data interoperability.

- **Protocols and guidelines.** Participants discussed the need to define sample collection, processing and preservation protocols. They discussed how to define the amount of sample collection to ensure data interoperability. e.g. the volume of water to be filtered across different depths and regions may change because of changes in biomass. Parameters such as oxygen level and chlorophyll content can be used to define the water volume to be filtered. The choice of preservation solution, which may differ for morphological and molecular taxonomic approaches, was also discussed. It was emphasized that contractors are interested in step-by-step protocols for sample collection and processing and staff training for different standard methods. EMO BON handbook was identified as an initial reference. This handbook attempts to provide accessible and inclusive protocols.
- **eDNA surveys.** The participants highlighted the challenges in eDNA surveys, including limited laboratory infrastructure and bioinformatic capacity, mainly in developing countries. Issues with contamination, the need for curated reference libraries, ancient DNA (DNA from dead organisms) and the presence of sinking pelagic DNA in sediment samples were also identified as major challenges in eDNA surveys.
- **Baseline studies versus environmental monitoring.** Participants highlighted that baseline and monitoring studies may have different sampling requirements. Baseline studies require in-depth research with a larger sampling to comprise the natural variability of a region and to identify the indicators and representative species for long-term monitoring. Participants also discussed the importance of collecting representative specimens for biobanks during baseline studies and having the respective barcode information. Participants suggested that eDNA could be a valuable tool linking baseline and monitoring data.
- **Centralization of management.** Participants stressed that ISA could facilitate the generation and access to knowledge by having a platform to register samples and encouraging information-sharing and cooperation.

Item 5. Promoting effective access and use of deep-sea genetic data and information

27. Under this item, a panel discussion was organized with the following experts, who delivered brief presentations on challenges and opportunities to promote effective access and use of deep-sea genetic data and information:

- a) Tristan Cordier, Norwegian Research Centre, Norway, *Integrating large metabarcodes data sets and references databases: probing the known and the unknown in the deep ocean*
- b) Magdalini Christodoulou, Senckenberg Museum, Germany, *Biodiversity of the Clarion-Clipperton Zone (CCZ) – from field sampling to data-sharing: an SGN perspective*
- c) Saara Suominen, OBIS Secretariat, Intergovernmental Oceanographic Commission of the United Nations Educational, Scientific and Cultural Organization (IOC-UNESCO), *OBIS and genetic data*
- d) Luciana Genio, ISA Secretariat, *DeepData database*

28. Summaries of the above presentations are provided in Annex II of this report.

29. Participants were invited to ask questions and exchange insights and views in response to the ideas, examples and experiences presented by the panellists.

30. This was followed by a discussion session moderated by Nicolas Pade, EMBRC, focusing on necessary steps for the standardization of genetic data and information, from field sampling to data-sharing.

31. Participants discussed the following topics, building on the ideas, examples and experiences provided by the panellists:

- Availability of genetic data from deep-sea eukaryotes in public databases
- Availability of genetic data from deep-sea prokaryotes in public databases (taxonomy and function)
- Interoperability of genetic data and information among databases.

32. The following points, inter alia, were highlighted during the discussion:

- **Training and capacity-building.** During this discussion, participants highlighted a need for training opportunities, including taxonomy, database systems, data analysis platforms, bioinformatics and FAIR (findable, accessible, interoperable and reusable) data principles. The importance of sustained training (sustained funding) and hands-on experiences was discussed, particularly for developing countries. Participants mentioned that many institutions already offer such courses; specific requests can be made to build tailored courses. A list of course providers, taxonomists and other experts could facilitate the implementation of training programmes and workshops. Participants suggested that ISA could centralize this information, linking people, needs and experts. Training at an individual level and promoting collaborations between government institutions, academics and industry could increase national capacity-building.
- **Genetic data sharing.** Participants also discussed possible collective efforts to use databases more efficiently and to increase data availability. In addition, they discussed how ISA could contribute to improving databases and filling the gaps. In this regard, participants highlighted that DeepData has the potential to play an important role in deep-sea data resources. (e.g. location of sample). Participants questioned whether metadata could be submitted immediately after the cruise, even if biological data are unavailable, encouraging collaboration for the region sampled. They also emphasized that the list of experts discussed in the previous session could be valuable in identifying expert taxonomists to contribute to expanding the database coverage. It was stressed that the major databases are interconnected and provide data interoperability. DeepData is also connected with the World Register of Marine Species and OBIS. Finally, it was discussed that a team of data curators would ensure data quality and consistency for DeepData.

Item 6. Use of genetic information for environmental management, including baseline studies, impact assessment and monitoring

33. Under this item, Gustavo Fonseca, Universidade Federal de São Paulo (USP), Brazil, delivered a theme presentation on the use of genetic information for environmental baseline studies and environmental monitoring, focusing on machine learning approaches.

34. Summary of the above presentation is provided in Annex II of this report.

35. Participants were invited to exchange insights and views in response to the presentation.

36. This was followed by a discussion moderated by Fabiana Paula, ISA consultant, focusing on using genetic data for setting baselines and monitoring deep-sea biodiversity.

37. Participants discussed the following topics, building on the theme presentations' ideas, examples and experiences

- Effectively designing DNA-based research for environmental baseline, impact/risk assessment and monitoring
- Identifying indicator species from DNA data for environmental impact/risk assessment and monitoring
- Using machine learning to describe biodiversity, monitor and predict community responses from DNA big data
- Integrating data to assess ecosystem functioning – interactions between different ecosystem components
- Lessons learned from other industries operating in shallow and deep waters to monitor potentially impacted benthic and pelagic communities.

38. The following points, inter alia, were highlighted during the discussion:

- ***Challenges to using eDNA for environmental assessment and monitoring.*** Participants highlighted the need to overcome the challenges discussed in the previous discussion sessions, including limitations of reference libraries and the presence of ancient DNA to achieve the full potential of eDNA approaches. During this discussion session, participants also mentioned that eDNA approaches are limited in providing quantitative data (abundance). In addition, eDNA approaches generate large data sets, which require advanced and complicated computer tools for analysis and interpretation, including bioinformatics, statistics and modelling. Capacity development is highly needed in these fields, mainly in developing countries.
- ***Recommendations for the use of eDNA in deep-sea biodiversity assessments.*** Participants suggested that, while setting standards in baseline studies, eDNA tools can be valuable if associated with traditional approaches to assessing fauna composition and abundance. Sampling efforts should be increased to comprise the natural variability of different environments. During monitoring, eDNA could be used to detect pattern changes and link with possible causes/drivers. Once the change is detected, additional sampling efforts and other tools should be applied. Association with computer tools, such as machine learning, can reveal patterns and allow for predictions.

Item 7. Summary and conclusion

39. The ISA Secretariat summarized the workshop results, including suggested approaches to promote coherent, collaborative and scientifically robust ways and means for enhancing genetic approaches to advance deep-sea taxonomy. Key points are summarized below, inter alia:

- a) Genetic approaches in deep-sea research, including DNA barcoding and eDNA-focused methodologies, contribute to advancing scientific knowledge in deep-sea biodiversity. However, this field still faces several challenges, mainly regarding methodology standardization and limited coverage of deep-sea species in public DNA libraries.
- b) Standardization of sampling protocols and collection of metadata were suggested as key steps in deep-sea genetic research, allowing for future comparative studies and data interoperability. In this regard, guidelines for sample processing and preservation are needed

(e.g. definition of a parameter to indicate the volume of water to be filtered and procedures for subsampling specimens for different study purposes, such as DNA and chemical studies). As an initial reference, the EMO BON handbook was suggested. Metadata standards, such as Darwin Core for environmental data and MixS for genomic data, can contribute to setting parameters in deep-sea genetic research. The importance of establishing an informative labelling system of samples using unique code systems was also highlighted. Defining minimum standard requirements can contribute to ensuring comparability across studies, and establishing more accessible and inclusive protocols can facilitate cooperation and large-scale observations.

- c) Collaborative efforts have great importance in advancing deep-sea research. In this context, cooperation could be encouraged by creating a platform to register samples across different institutions and potentially be available for other studies. eDNA research also provides means to facilitate cross-disciplinary cooperation, with studies comprising prokaryotes and eukaryotes, promoting the development of deep-sea ecology and conservation. Finally, collaborations could also facilitate the access of less equipped research groups to laboratory facilities, as DNA research requires appropriate structure.
- d) Low coverage of deep-sea species in public DNA libraries was identified as one of the main challenges for using genetic tools in deep-sea research. Other methodological challenges to be overcome for the successful utilization of eDNA tools include the definition and optimization of efficient Polymerase Chain Reaction (PCR) primers, means to differentiate benthic community DNA from sinking pelagic DNA and limited data on the quantitative capability of eDNA.
- e) Baseline studies and monitoring efforts may have different methodological requirements. While baseline studies demand multiple approaches, monitoring may initially use a narrow range of protocols to identify changes, which can trigger broader and deeper sampling and analysis. Machine learning approaches could play a role in connecting baseline and monitoring data.
- f) Capacity-building for developing countries should comprise hands-on and sustained training. Identifying the needs (e.g. FAIR/Open science principle, database and data management recommendation, taxonomy) and existing platforms providing such services is important. Training at an individual level and promoting collaborations between government institutions, academics and industry to increase national capacity-building.
- g) DeepData can play an important role in deep-sea data resources while connected to existing genetic databases. Large data sets need robust tools for analysis and monitoring.
- h) The following key points were highlighted as possible next steps: association of genetic approaches with traditional methodologies is essential while setting the standards for assessing fauna composition, sampling efforts should be increased to understand natural variability in baseline studies, eDNA can be used to detect changes and to link with possible causes/drivers, association with computer tools, such as machine learning, to reveal and predict biodiversity patterns.

40. Workshop participants were invited to consider the results and provide comments and suggestions. They appreciated Dr. Genio's comprehensive and well-organized summary.

Item 8. Closure of the workshop – part I

41. The workshop closed at 17:30 on Thursday, 24 November 2022.

Group tour: MABIK collection facilities and museum

42. On Friday, 25 November 2022, participants were invited to a guided visit to the MABIK collection facilities and museum. The tour commenced at 09:30.

Part II: Hybrid session

Item 1. Opening of the workshop

43. The ISA OEMMR Environmental Coordinator, Dr. Luciana Genio, and the Chief Manager of MABIK, Dr. Yong-Rock An, opened the workshop at 14:00 (Republic of Korea; GMT+9) on Friday, 25 November 2022.
44. Their messages mirrored the opening remarks summarized in paragraphs 13 and 14 above.

Item 2. Enhancing genetic approaches to advance deep-sea taxonomy

45. Under this item, Dr. Luciana Genio presented the key outcomes of the technical meeting of the workshop (Part I).
46. Dr. Genio's summary can be found in Item 7 (Part I) of this workshop.
47. Participants were invited to ask questions and exchange insights, views and suggestions on the workshop outcomes in response.

Item 3. Effectively using genetic information for deep-sea biodiversity assessment and monitoring in support of sustainable ocean governance

48. Under this item, Mariamalia Chaves Rodríguez, ISA Legal and Technical Commission (LTC), presented the effective use of genetic information for deep-sea biodiversity assessment and monitoring in support of sustainable ocean governance.
49. Summary of the presentation is provided in Annex II of this report.
50. Participants were invited to ask questions and exchange insights and views in response to the presentation above.

Item 4. Exploring possible ways and means for collaboration to support the development of deep-sea taxonomic knowledge platform and necessary long-term capacity development within the context of ISA

51. Under this item, a panel discussion was organized with the following experts, who delivered brief presentations on collaborative opportunities to support the development of a deep-sea taxonomic knowledge platform and necessary long-term capacity development within the context of ISA:
- a) Samantha Smith, Global Seabed Resources NV, Belgium
 - b) Hye-Won Moon, MABIK, the Republic of Korea
 - c) Andrea Quattrini, Smithsonian Institute, United States of America
 - d) Valerie Allain, South Pacific Community, New Caledonia
 - e) Take Yamakita, Japan Agency for Marine-Earth Science Technology (JAMSTEC), Japan

f) Ward Appeltans, IOC-UNESCO, Belgium

52. Summaries of their presentations are provided in Annex II of this report.

53. Participants exchanged their insights and views in response to the presentations, including some points summarized below:

- **Collaboration efforts.** Some participants highlighted that this is a great opportunity to strengthen collaborations between ISA, academia and contractors, including collaboration to use research facilities.
- **eDNA approaches.** Participants asked how to effectively construct reference libraries to apply eDNA in underexplored areas. It was highlighted that this is a challenging task that sometimes allows for classification at higher taxonomic levels and that little progress would have been made in studying microbial diversity without eDNA. Participants also discussed that eDNA could be a valuable tool to detect environmental changes, which could lead to further and more focused work. This could provide more effectiveness to the extensive work done by taxonomists. This also highlights the importance of sample storage for future analysis. Biobanks are valuable resources for future studies.
- **Sample sharing and registration.** Participants discussed the challenges in data and sample sharing across institutions and countries. They also questioned how the development and maintenance of the sample registration platform could happen. It was highlighted that ISA could play an important role in facilitating access to samples collected in the Area by promoting partnerships between contractors, scientific institutions and international curated collection facilities. Samples collected during baseline and monitoring studies should be stored for long-term archive of voucher records according to the recommendations of the ISA LTC (ISBA/25/LTC/6/Rev.3).
- **DeepData.** DeepData does not store DNA sequence data. It creates interoperable links with existing biodiversity databases. For instance, ISA shares taxonomic and occurrence data with OBIS through the OBIS ISA node. Developing effective interoperable links with genetic databases can also be further advanced.
- **Training and capacity development.** Participants discussed the importance of recurrent training and the advantages of using existing platforms and available online resources. It was recalled that OBIS has courses in a hybrid format, with theoretical online modules and in-person practical modules.. These courses provide training to students and university professors, who can expand the trained public.
- **Functional traits.** The use of eDNA for detecting important functional traits was also discussed. This approach is widely used for microbial assessments, using target gene sequencing or metagenomics, and could provide valuable information for metazoan. The importance of functional traits was highlighted regarding corals with different morphologies, which have distinct sensitivity to environmental impacts. Expanding functional traits data and information is important for robust biodiversity assessment.
- **Machine learning.** Participants discussed using machine learning for prediction in baseline and monitoring studies. Regarding the number of samples required to keep high accuracy for the predictions, it was stressed that there is a trade-off between reducing sampling efforts/investments and accuracy.

Item 5. Summary and conclusion

54. Dr. Luciana Genio summarized the workshop results. She highlighted the opportunities for collaboration provided by the workshop, mainly regarding (i) standardizing methods and tools for species identification using genetic data, (ii) effective sharing of genetic data and biodiversity assessments and (iii) developing taxonomic capacity and deep-sea literacy. She reiterated some important points of discussion, including the need for reference genetic libraries for deep-sea, the available resources, such as major and interconnected databases that have a central role for deep-sea research; the demands for training opportunities, where a training platform linked to ISA could have an important task to address the needs.

55. In her closing remarks, Dr. Luciana Genio expressed her appreciation to the President of MABIK, Dr. Wan-hyun Choi, to the Chief Manager of MABIK, Dr. Yong-Rock An, and to the MOMAF for supporting ISA in the past years. She acknowledged that the partnership between ISA and the MOMAF had been renewed to continue the collaboration. She also stressed the importance of other collaborations and that these partnerships will take deep-sea research to a new level in the coming years and contribute to the implementation of the United Nations decade of ocean sciences and other important United Nations processes. She ended her remarks by thanking all the participants, speakers and partners to the workshop whose contributions will help ISA to advance deep-sea taxonomy knowledge used for effective protection of marine environment.

56. Dr. Yong-Rock An thanked the participants and speakers joining the workshop in-person or virtually. He stated that it was a pleasure for MABIK to host the workshop and wished to continue working closely with ISA.

Item 6. Closure of the workshop – part II

57. The workshop was closed at 18:00 (Republic of Korea; GMT+9) on Friday, 25 November 2022.

Annex I. List of participants

Part I: In-person technical meeting

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Part II: In-person/online hybrid session

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Annex II. Summary of theme presentations

Part I: In-person technical meeting

- *Presentation delivered under agenda item 2*

Workshop background, scope and expected outputs

Luciana Genio, ISA Secretariat

Protecting the marine environment from harmful effects that may arise from activities in the Area is at the core of ISA's mandate. To this end, ISA shall adopt appropriate procedures for effective environmental management. ISA is also responsible for promoting and encouraging marine research in the Area and coordinating and disseminating the results of such research. This workshop addresses one of the six strategic research priorities identified in the ISA's Strategic Plan and High-Level Action Plan for 2019-2023, focusing on standardization and innovation of methodologies for deep-sea biodiversity assessment, including taxonomic identifications and description in the Area.

During the exploration activities, ISA contractors are required to undertake comprehensive environmental studies to characterize the baseline conditions of the marine environments that are likely to be impacted by exploration and mining activities. The studies include a vast list of oceanographic, geological and biological scientific observations. The contractor shall use the best available technologies to collect biological data and submit a report describing their activities yearly. All the information is compiled in the ISA DeepData database, where environmental data, including taxonomic information, is made available to the scientific community and the general public.

To facilitate the integration of taxonomic knowledge, two workshops have been convened in collaboration with the MOMAF and the MABIK. In the first of these workshops, held in September 2020, several priority actions were identified for developing a collaborative platform to advance deep-sea taxonomic knowledge in the Area. The next workshop, held in October 2021, identified key elements for a standardized model of image data exchange, archiving and sharing to support biodiversity. This third workshop aims to identify key elements and technical means necessary for effectively sharing and using genetic data. The expected outcomes of this workshop include (i) developing methods and tools for species identification using genetic data, (ii) effective sharing of genetic data and biodiversity assessments, (iii) developing taxonomic capacity and deep-sea literacy and (iv) promoting opportunities for collaboration in deep-sea genetic research.

- *Presentation delivered under agenda item 3*

Using genetic information to advance deep-sea taxonomy and biodiversity assessment in the Area

Thomas Dahlgren, University of Gothenburg, Sweden

A new deep-sea blue economy will require long-term environmental monitoring of deep benthic ecosystems. We note that today's marine management practices need named species to assess rarity, endemism, connectivity and other parameters necessary to judge, e.g. extinction risks and the effectiveness of various conservation measures. If deep-sea mining commences, the means to monitor impact is also dependent on fauna catalogues and species lists. To achieve this, metabarcoding of eDNA samples has been suggested as a possible complement or alternative to current morphological methods to assess biodiversity. However, as about 95 per cent of the deep-sea fauna is yet to be described, let alone with molecular data, the use of existing taxonomic resources with this methodology may be

questioned. For the method to successfully characterize species assemblages, a public sequence database is necessary to match barcodes to species identity. However, these public sequence libraries must be expanded and subjected to at least some degree of quality control.

The oil and gas industry conducts large-scale environmental monitoring in the North Sea, one of the most heavily sampled marine areas worldwide. It could therefore be considered a ‘best-case scenario’ for macrofaunal metabarcoding. In a recent study, we investigated the database coverage for a complete list of 1,802 macrofauna taxa reported from the North Sea. We found that data did not represent 50 per cent or more of the species for both genes. This barcode coverage gap remains when looking at only the most common species in the data set, indicating that the problem is not limited to rare and cryptic species. Results from this study are contrasted with data from an emerging deep-sea industrial target – the CCZ in the equatorial Pacific. After a decade of intense work collecting baseline data, no less than 177 species have been described from this region, 40 per cent of which is accompanied by genetic barcode data. With increased support for integrated taxonomical work, we believe that fauna catalogues and barcode repositories could be achievable within the foreseeable future.

- ***Presentation delivered under agenda item 4***

Technological advances and methodological challenges in large-scale genetic surveys to assess deep-sea biodiversity

The European Marine Omics Biodiversity Observation Network

Nicolas Pade, EMBRC-ERIC, France

EMBRC is a research infrastructure that supports marine biological research, providing access to a broad suite of facilities, research platforms and biological resources. This research infrastructure connects more than 70 sites in 10 European countries through a joint governance and legal framework. Biodiversity observation in the ocean has previously been limited by the lack of shared protocols, proper operational framework and appropriate metadata due to the lack of enforcement of standards, protocols and documentation. As part of its mission to support and enable marine biological and ecological research, EMBRC has launched an omics-based observatory, the EMO BON, which aims at becoming the “best practice” observatory deploying open and shared protocols, setting high data and metadata standards and adhering to open science principles. EMO BON collects data from the water column, soft sediments and hard substrates and targets microbial communities using a metagenomic approach, sediment meio- and macrobenthos and sessile and mobile invertebrates using metabarcodes. The observatory has developed mock communities for positive controls and is working to develop data workflows to support data release and data analysis. It aims at providing a European contribution to global marine biodiversity research and observation with inclusive “low-tech” protocols. All documents and protocols related to the observatory can be downloaded for free from the EMBRC website or the Ocean Best Practices System. With the creation of EMO BON, EMBRC established comparable time series across multiple countries and institutions, fully enforced rules and standards, and centralized administration. This enables EMBRC to develop a structured biodiversity observation component, speaking with one voice to build collaborations and partnerships with other parts of the world and different communities. EMBRC contributes to the Ocean Biomolecular Observing Network United Nations Decade programme.

Molecular Techniques for Assessment of Deep-Sea Microbial Communities

Xue-Wei Xu, Second Institute of Oceanography, Ministry of Natural Resources, China

The deep-sea floor is rich in mineral resources, including polymetallic nodules, polymetallic sulphides and cobalt-rich ferromanganese crusts. Moreover, habitats such as abyssal plains, seamounts and mid-ridges provide a living paradise for diverse microbes. Currently, the vast majority of microbial species are “uncultured” and do not grow under laboratory conditions.

To overcome this problem, cultivation-independent methods, including amplicon sequencing and “omics” technologies, are invented and applied to deep-sea microbial study. Amplicon sequencing of marker genes can be classified into the operational taxonomic units grouped by DNA sequence similarity of a specific taxonomic marker gene. The previous study investigated the microbial community in polymetallic nodules and seamount using amplicon sequencings, highlighting that microhabitat is a major factor influencing microbial community composition. Applying “omics” technologies have immense potential in microbial community analysis at the composition and functional levels. Our group performed the metagenomic-resolved study in the hydrothermal vents, indicating that sulphur oxidation might be the major energy source for primary production. Novel chemoheterotrophic iron-oxidizing species in 12 phyla were identified. Furthermore, the application of other technologies, including microarray technology, stable isotope probing and fluorescence in situ hybridization, can be combined for measuring gene expression, detecting specific DNA sequences and separating the microorganisms responsible for the metabolism of a particular substrate.

Cultivation-independent methods revolutionized microbial ecology, as they provided direct access to the taxonomic classifications and ecological functions, promoting the development of deep-sea ecology and conservation. In the future, molecular techniques can have cross-fertilization with eDNA technologies. Also, the deep-sea microbial community can be deciphered at the single-cell level. Their interaction among species and with environments can be illustrated dynamically and in real time.

Mining eDNA and RNA: taxonomy and benchmark needs to understand and preserve deep-sea benthic life

Franck Lejzerowicz, University of Oslo, Norway

Nucleic acid sequencing is insightful yet an emerging technology in deep-sea research. Systematically freezing deep-sea samples would enrich knowledge in later studies and future researchers’ careers if complying with metadata and microbiology standards. Notably, shipboard PCR must be prohibited to prevent cross-expedition contamination. Standardization is warranted to build the large FAIR data needed to address taxonomic knowledge gaps and develop capacity globally. We initiated this for eukaryotes in the CCZ with >300 surface sediment samples sequenced for 18S ribosomal eDNA and rRNA. The huge unknown phylogenetic diversity of meiofauna (and, notably, foraminifera) confirms the need for well-trained taxonomists. Indeed, 63.3 per cent of CCZ metazoan meiofauna sequence diversity was only assigned to the family, and 74.5 per cent of foraminiferal sequence diversity is unknown.

Beta diversity analysis reveals CCZ uniqueness, where communities vary to an unexplored extent. A random sample from the well-explored human gut microbiome would resemble already-known samples. This precedent translates to oversight when predicting disturbance effects on a microbiome, e.g. surgery. Because no oversight is available for the deep sea, measuring mining disturbance effects on community composition is uncertain, and more samples must be sequenced to increase certainty of impact assessments. Moreover, current mining technologies are likely to resuspend large amounts of sediment that will resettle and blanket remote, undisturbed areas with allochthonous clays and their cohorts of

adsorbed, allochthonous DNA. Such contaminating effects of mining may jeopardize the applicability of eDNA for diversity estimation and monitoring. Given the importance of rare species in deep-sea sediments and the propensity for PCR-based eDNA sequencing to detect these, eRNA alternatives must be benchmarked. Indeed, eRNA data more accurately detect live, active species, which in the CCZ mainly corresponded to heterotrophs, while plankton prevailed with eDNA. Understanding deep-sea taxonomic compositions using genetic sequencing requires a dramatic sample size increase along all axes of diversity variation

- ***Presentation delivered under agenda item 5***

Promoting effective access and use of deep-sea genetic data and information

Integrating large metabarcode data sets and reference databases: probing the known and the unknown in the deep ocean

Tristan Cordier, Norce, Norway

Genomic assessments of deep ocean sediment biodiversity have failed to separate indigenous benthic organisms from sinking plankton. By comparing global-scale eukaryotic DNA metabarcoding data sets (18S-V9) from deep-sea sediments with publicly available data sets from the water column that included both euphotic and aphotic ocean pelagic layers, it was possible to distinguish sinking plankton from benthic diversity in sediment material. Based on 1685 samples collected worldwide and across the water column, our data show sediment diversity is at least threefold that in pelagic realms. Nearly two-thirds of benthic eukaryotes, representing half of the DNA reads obtained from sediment samples, could not be taxonomically assigned to any eukaryotic supergroups with the current reference barcoding database. This DNA-based meta-data set thus indicates that deep-sea benthic ecosystems host inconspicuous eukaryotes that are completely unknown to science. These benthic communities are spatially structured by ocean basins and particulate organic carbon flux from the upper ocean. Only the sustained combination of standardized and concerted sampling of deep-sea ecosystems, from microbes to megafauna, for both morpho-taxonomy and DNA barcoding work with an ever-growing number of environmental genomics data sets will allow shedding light on the functional role of benthic ecosystems and their sensitivity to human incursions.

Biodiversity of the CCZ – from field sampling to data-sharing: an SGN perspective

Magdalini Christodoulou, Senckenberg Museum, Germany

The CCZ is an area spanning about 6 million km² in size located at a depth of 4,000-6,000 metres in the Northeast Pacific Ocean. It holds the world's largest deposits of polymetallic nodules and is targeted for potential mining. Polymetallic nodules are rock formations containing valuable metals and minerals such as cobalt, nickel and manganese, but they also support a rich sessile and mobile fauna. Very little is known about these deep-sea animals' taxonomy, natural history and biogeography, which is vital for accurate risk assessment of species extinctions from large-scale mining. For this reason, the Senckenberg – Leibniz Institution for Biodiversity and Earth System Research (SGN) is developing a curated DNA reference library based on mitochondrial cytochrome c oxidase subunit I for the fauna in the CCZ that could serve as a backbone for taxonomic, phylogenetic and environmental studies. Material collected during numerous exploration cruises throughout the CCZ is being examined. The specimens are processed following a series of standardized workflows covering sampling, morphological

identifications, molecular lab processing and data handling. Currently, the CCZ reference library holds DNA barcodes for over 5,400 specimens comprising over 1,140 barcode index numbers from throughout the animal kingdom and it continues being enriched. All specimens are photographed and, together with the accompanying sequences, collection and taxonomic data are archived in a dedicated BOLD database project, while voucher specimens are archived. The reference library has supported reverse taxonomy studies on *Echinodermata* and *Crustacea* that led to species descriptions. Once available, this DNA library will support the implementation of faster and more reliable DNA-based identifications and, subsequently, environmental health assessments for the CCZ. Finally, this study provides the foundation for biogeographic and functional analyses that will provide insight into the drivers of species diversity and its role in ecosystem function.

OBIS and genetic data

By Saara Suominen, OBIS Secretariat, IOC-UNESCO

OBIS is a global biodiversity database that provides free, accessible, open and reliable marine data. Species occurrence data in OBIS is collected from many different sources, studies and surveys. OBIS provides long-term, sustainable storage of that biodiversity data in a machine-readable and comparable format. The data in OBIS is stored in a standard format with controlled vocabularies. The standard is the Darwin Core Archive format upheld by Biodiversity Information Standards. It consists of core data in a table format with species information and an extension table where specific metadata on the collection method and data can be shared. Different extension table types exist for data collected with different methods.

Recently, DNA-derived data extension has been enabled in OBIS, allowing the flexible collection and sharing of genetic data. Genetic data has enormous potential to increase our access to biodiversity data globally. It is very important that this data is shared according to the FAIR principles so that its benefit can be reaped. Luckily, data-sharing is common within the genetic sciences. However, currently, this data does not allow search through time and space, especially if one is not an expert in the field. Now, biodiversity data from genetic studies can be easily and efficiently shared through biodiversity databases like OBIS.

The extension allows recording all metadata from the choices made during sample and data processing. Key metadata allowing the user to understand how the data was collected is especially important in the case of DNA-derived data, as it represents highly processed data. For example, the data quality is directly linked to the reference databases used for data analysis; there are still a lot of unknowns. Most importantly, the sequences from which the species information is derived are directly shared with the DNA-derived data extension, enabling future users to confirm the results, update analyses based on new evidence, and search for similar sequences around the globe. When carefully done, sharing genetic data will enable an unprecedented overview of global biodiversity.

The DeepData platform

Luciana Genio, ISA Secretariat

The ISA mandate is to regulate and control activities in the Area to ensure effective protection of the marine environment and biodiversity from potentially harmful effects that may arise from seabed exploration and exploitation activities. In addition, ISA is responsible for promoting and encouraging the conduct of marine research in the Area and coordinating and disseminating the results of such research.

In 20 years, more than 100 cruises were undertaken in the abyssal plains of the Pacific and Indian oceans. In addition, over 30 cruises occurred in the North Atlantic and Indian oceans for polymetallic sulphide exploration and 22 cruises for exploration of cobalt-rich ferromanganese crusts in the Northwest Pacific and South Atlantic.

DeepData is a geospatial database where all the information related to contractor activities is stored and compiled. Since its launching in 2019, DeepData has been continuously updated with the information generated during almost 40 years of scientific activities undertaken by pioneer investors and contractors during the exploration of deep-sea minerals.

As defined in the exploration regulations, some information is confidential and only accessible to the Secretariat and by the LTC. In contrast, environmental information, including biological data, is open and free to the scientific community and the general public. The reporting uses standard templates for digital data, including geological and environmental data and associated metadata. DeepData also contains GIS functionalities, allowing for the visualization of contract areas, reserved areas and areas of particular environmental interest.

To expand the potential of DeepData, it is essential to establish best practices and data standards to follow FAIR data principles. Efforts are already made in this direction, including linking with relevant databases, such as the World Register of Marine Species and OBIS.

Efforts will be made to expand the capacities and functionalities of the ISA DeepData and establish its position as a key data platform for the deep ocean. Creating effective collaborative linkages for data exchange between DeepData and other global databases will substantially catalyse the utility of data and information contained in DeepData. It will also enable the development of information products and communication tools to facilitate knowledge uptake by all ISA stakeholders. In line with this, special emphasis will also be placed on increasing deep-sea literacy of the general public.

- *Presentation delivered under agenda item 6*

Use of genetic information for environmental baseline studies and monitoring

Gustavo Fonseca, USP, Brazil

The best practices in ecosystem conservation use all available information for baseline and environmental monitoring. Baseline and monitoring studies have different objectives. While the first aims at characterizing an ecosystem, the second aims at anticipating changes based on a selected set of indicators. Both need a curated database with the raw data and associated metadata and a derived “analytical” database, where some processing steps are already performed to support further analysis. Given the eminent anthropogenic and climate pressures on marine ecosystems and the amount of data that has to be collected to understand spatial-temporal dynamics, machine learning techniques are becoming recurrent in monitoring programmes. Different types of algorithms can be used, compared and even combined to get the most accurate predictions. Applying machine learning modelling methods already at the beginning of a project improves data acquisition, guides sampling campaigns and optimizes the selection of essential environmental variables for monitoring programmes. When the model becomes highly accurate, its predictions can be extrapolated to unsampled sites. Additionally, each newly collected data can be used to test the model and improve the predictions. The whole process could be automated and visualized through a user-friendly dashboard, from raw data to the final prediction. This end-to-end approach will guide the best management decisions.

Part II: In-person/online hybrid session

- ***Presentation delivered under agenda item 3***

Effectively using genetic information for deep-sea biodiversity assessment and monitoring in support of sustainable ocean governance

Ocean governance developments and the use of genetic information for deep-sea biodiversity assessment and monitoring

Mariamalia Chaves Rodríguez, ISA LTC

The current negotiation of the Treaty for the conservation and sustainable use of marine biodiversity in areas beyond national jurisdiction (BBNJ Treaty) will provide provisions on access to marine genetic resources and sharing of benefits, area-based management tools including marine protected areas, environmental impact assessment and capacity-building and the transfer of marine technology to the international community.

More specifically, the further revised text of the BBNJ Treaty on ocean governance and the use of genetic information develops in Part II related to Marine genetic resources, including the fair and equitable sharing of benefits. In addition, under Part VI on Institutional arrangements, a clearing house mechanism is proposed to be established as an open access and centralized platform to enable Parties to access, provide and disseminate data, including information regarding marine genetic resources of ABNJ.

The United Nations Regular Process and one of its key outputs, the World Ocean Assessment, aim to support actions for achieving Sustainable Development Goals and implementing the United Nations Decade of Ocean Science. Within World Ocean Assessment II, some chapters highlighted challenges and needs of interest to the use of genetic information

- key knowledge and capacity-building gaps in the description of taxonomic units, as well as an urgent need to list species
- gaps of knowledge and consequences of changes in ecosystems due to future mining operations
- lack of information on deep-sea ecosystems, species, life history and biological traits, connectivity, ecosystem services, and the need for a robust collection of baseline ecological data for predictions of future seabed mining activities.

- ***Presentations delivered under agenda item 4***

Exploring possible ways and means for collaboration to support the development of deep-sea taxonomic knowledge platform and necessary long-term capacity development within the context of ISA

Samantha Smith, Global Seabed Resources NV, Belgium

Dr. Smith focused on challenges and opportunities in collaborations involving academia and industry for deep-sea taxonomic research. She shared two previous experiences, one related to deep-sea research in a national jurisdiction territory and another related to work in the CCZ. She highlighted that in all her

collaborations involving sending biological specimens to experts, the samples remained stored in the universities without advertising their location to the scientific communities.

In the first example, Dr. Smith shared an experience of industry-academia partnership in deep-sea research in Papua New Guinea. The main academic partner was Duke University, USA. She mentioned that no information about where samples were stored was shared. She highlighted, however, that the partnership was advantageous to provide capacity-building for students from Papua New Guinea. She also stressed the challenges in performing analyses of species' global distribution, as it depends on other research groups to enter information into databases.

In her experience working in the CCZ, which is mainly in collaboration with Ghent University, Belgium, the samples are kept at the university. Although there is a centralized database, it is not accessible to the public.

Finally, Dr. Smith referred to the BOLD database and its functionalities, including the possibility of making the data private. This is often used by scientists who want to publish the study before making the data available to others, preventing further data analysis.

Hye-Won Moon, MABIK, the Republic of Korea

The North Pacific Ocean supports some of the world's most productive and diverse fisheries. During the past decade or so and largely in response to regional and global concerns about the toll these fishing activities have had on the ecosystems that support them, Korea and other North Pacific States have established joint projects to identify, research and conserve vulnerable marine ecosystems. We know vulnerable marine ecosystems (VME) species are particularly sensitive to disruptive activities, especially fishing. We have a general understanding of the biology and ecology of VME organisms to predict which faunal groups are at high risk of significant adverse impacts from fishing.

Successful by-catch monitoring programmes will require the completion of VME field guides specific to each region. We are constructing a comprehensive coral guide to aid fisheries observers in identifying coral by-catch, specifically from fisheries operating in the Emperor Seamount region. We also try to improve the quality of the specimens by training scientific observers twice a year. Hundreds of coral specimens were collected and examined in 2014 and 2018, leading to scientific papers on new species of corals and sponges. We will continue to monitor the by-catch collected during fishing operations in the Emperor Seamount region and update the coral field guide. Unknown specimens will be sampled and sent to the appropriate taxonomic authorities for genetic work. Experience from the VME project has demonstrated the importance of collaborative work to enhance deep-sea taxonomy in species identification.

Andrea Quattrini, Smithsonian Institute, USA

The utility of museum specimens for genomic approaches has become more apparent over recent years, particularly with decreasing sequencing costs and the advent of novel methods, such as target-capture enrichment. The Department of Invertebrate Zoology at the Smithsonian National Museum of Natural History is trying to capture genomic data for various deep-sea specimens in their collections. This critical data can be used to resolve evolutionary relationships, delimit species and determine the connectivity of populations. With these types of data, we can also obtain conventionally used DNA barcodes to help build voucher-based reference libraries for eDNA studies. There has been an uptick in using eDNA to characterize deep-sea biodiversity, yet, many deep-sea species have never been sequenced before or may be species new to science. Thus, eDNA cannot yet offer definitive

identification of biodiversity in a particular area. An emphasis on well-curated physical specimens entrusted to museums and the principles of open data-sharing will overcome this bottleneck to identifying many deep-sea species.

Valerie Allain, South Pacific Community, New Caledonia

The Pacific Community is a regional organization created in 1947 with 27 members (22 oceanic states and territories and five founding countries). It is the principal scientific and technical organization supporting the development of the Pacific region. The Pacific Community works in different domains, such as climate change, agriculture, public health or fisheries. Tuna fisheries represent an important resource in the region for food security. Tuna fishing licensing contributes to more than 50 per cent of the government revenues in some countries. The Pacific Community conducts research in monitoring the pelagic ecosystem that sustains the important tuna fisheries. It conducts research cruises at sea to collect data and specimens of marine organisms from the pelagic domain, including in the deep mesopelagic area (down to 600 m depth), which could potentially be impacted by deep-sea mining activities (e.g. plumes). Marine specimens (micronekton = 2-20 cm fish, crustaceans, molluscs, gelatinous organisms) are collected and identified based on their morphology. DNA barcoding is a work in progress to build a barcode reference to develop eDNA solutions for biodiversity monitoring and contribution to global databases. The Pacific Community is also building a Pacific Marine Specimen Bank to make samples available to the scientific community.³ For the development of a deep-sea taxonomic knowledge platform, it is crucial to associate DNA barcoding and morphological taxonomy, to improve expertise in taxonomy by training, to develop best practices, to enhance observations and the collection of specimens, to build a bank of samples and deposit reference organisms in appropriate institutes, as well as to contribute to publicly available global databases of DNA and taxonomy with strong quality control.

Takehisa Yamakita, JAMSTEC, Japan

Dr. Yamakita presented the activities and work of JAMSTEC and noted that the Global Observation Network of Marine Biodiversity began with the Global Ocean Observing System (GOOS) and was fully developed with the biological monitoring project, Census of Marine Life, formerly organized by the Marine Biodiversity Observation Network (MBON). There is a programme under the United Nations Decade called Marine Life 2030, which provides a framework to connect different organizations, multiple regions and ecosystems.

There is a common interest between GOOS and MBON in developing high priority observations using essential ocean and biodiversity variables. The linkage with OBIS for data and products was highlighted, as well as the expectation that the information will be used for indicators, long-term observation, conservation and management. It was noted that OBIS can already access eDNA data. However, since data standardization was still under discussion, persons with particular interests in this area were encouraged to join this group.

Regarding Asia Pacific MBON and JAMSTEC activities, it was reported that under Marine Life 2030 and United Nations Decade, JAMSTEC has a project which involves monitoring deep-sea organisms in marine protected areas. With a focus on newly established marine protected areas, under a new role to protect offshore seabed, images from seamounts are taken using autonomous underwater vehicles and

³ The Pacific Community. Pacific Marine Specimen Bank. Available at: <https://www.spc.int/ofp/PacificSpecimenBank>.

are analysed manually and automatically. As an Asia Pacific regional activity, APMBON facilitates information-sharing and networking among interests in seagrass, coral reefs and coastal ecosystems. There is ongoing work involving remote sensing, surveys and genetic analysis.

JAMSTEC's work on eDNA analyses for deep-sea fishes was also highlighted. Since the concentration of eDNA was very low in deep waters, methods were developed and improved to extract six times more eDNA when compared to conventional methods. Developing cost-effective equipment, such as the new pump system (full-depth pump), was also highlighted. Using these methods, JAMSTEC has advanced efforts to evaluate the biodiversity of deep-sea fish.

Finally, the ongoing work of OBIS was lauded, and all interested parties were encouraged to join the community and become more involved in data standardization while building a strong network.

Ward Appeltans, IOC-UNESCO/OBIS, Belgium

Dr. Appeltans delivered his presentation focusing on work developed by OBIS regarding molecular and genetic approaches. He highlighted that OBIS is a platform that provides free access to world ocean biodiversity and biogeographic data. In addition, OBIS promotes cooperation and capacity development programmes. Thirty-two OBIS nodes, including the ISA node, were created in June 2021.

He highlighted that the OBIS database contains over 100 million observations of 160,000 marine species. Those include more than 17 million records of more than 95,000 species from deep-sea benthic ecosystems. He also noted a clear trend towards increasing records from the deep ocean in recent years.

Dr. Appeltans expressed great interest in developing capacity using eDNA technologies and provided examples of two ongoing UNESCO projects. One is in citizen science, engaging local communities in 25 marine world heritage sites. The collection of eDNA samples to evaluate the ability of these sites can act as a refuge for species. The project aims to raise the next generation of marine scientists. The other project is called PacMAN (Pacific Islands Marine Bioinvasions Alert Network). Training local technicians and applying eDNA tools for early detection of invasive species includes a theoretical part, laboratory and OBIS bioinformatics pipeline. OBIS has the capacity to manage DNA-derived species occurrence data and metadata standards, bioinformatics pipeline and FAIR data platform. Dr. Appeltans concluded his presentation by reiterating that OBIS is a trustworthy partner and can collaborate on projects to develop capacities worldwide.