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Bohmann, Kristine; Chua, Physilia; Holman, Luke E.; Lynggaard, Christina

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COMMENTARY

DNAqua-Net conference unites participants from around the world with the quest to standardize and implement DNA-based aquatic biomonitoring

Kristine Bohmann¹ | Physilia Chua¹,² | Luke E. Holman¹,³ | Christina Lynggaard¹

Abstract
The EU COST Action DNAqua-Net has since its start in 2016 gathered European researchers with the quest to standardize and implement DNA-based aquatic biomonitoring. On March 9–11, 2021, their work culminated in their first conference. Here, an astounding 1500 participants from around the world gathered virtually to share their research on DNA-based aquatic biomonitoring encompassing DNA reference databases, field and laboratory protocols, data analyses and storage, implementation strategy and legal issues, and biotic indices and metrics. The overwhelming interest in DNA-based aquatic bioassessment and monitoring strongly underlines its relevance and timeliness.

KEYWORDS
biomonitoring, environmental DNA, freshwater, marine, metabarcoding

1 | INTRODUCTION

We have all heard the saying "water is the giver of life." However, aquatic ecosystems are under pressure, and there is an urgent need to develop and implement methods to monitor their biodiversity. In recent years, DNA-based methods have proved to be a powerful tool to reveal the diversity of freshwater and marine ecosystems, and there has been growing interest in standardization and implementation to complement existing monitoring methods. To this end, the EU COST Action DNAqua-Net was established in 2016. To disseminate the latest results in DNA-based aquatic biodiversity monitoring, DNAqua-Net held its first international conference, DNAQUA2021, on March 9–11, 2021. The 3-day conference was initially to be held in Evian, France - a place known for its mineral water spring, which would have befitted the theme of this conference. However, due to the COVID-19 pandemic,
the conference was held virtually, allowing a large number of researchers and stakeholders from around the globe to participate. The conference had five sessions on DNA-based aquatic biomonitoring with themes ranging from field and laboratory protocols to strategies for implementation, and participants from around the world had the opportunity to connect virtually to present and discuss their research with the ultimate aim of standardizing and implementing DNA-based aquatic biomonitoring.

2 | DNAqua-NET

Just as the largest rivers begin as small streams, DNAqua-Net began as a small idea from a team centered around Professor Florian Leese, University of Duisburg-Essen, and Dr Agnès Bouchez, Research Director of the French National Institute for Agriculture. As others joined, the idea grew into an EU COST (European Cooperation in Science and Technology) Action (CA15219), and today, the DNAqua-Net stream has become a deep river of discovery and collaboration as researchers from all over Europe have joined to develop new genetic tools for the biomonitoring of aquatic ecosystems in Europe (Leese et al., 2016).

“As the managing team of DNAqua-Net, we could have hardly imagined the impact of DNAqua-Net back in 2015, when we wrote the proposal”, says the DNAqua-Net managing team in Leese et al., (2021).

Since the formation of DNAqua-Net in 2016, the managing team has led the network of over 400 members from 49 countries to work toward the goal of establishing a gold standard means of molecular biodiversity assessment for European waters (Deiner, 2021). To achieve this, members of DNAqua-Net are working in close collaboration with stakeholders to develop a legally binding conceptual framework for the standardization of DNA-based tools used in assessments. The progress of DNAqua-Net has been extremely fruitful, with more than 100 publications since its inception. Going beyond scientific impact, DNAqua-Net is a platform for capacity building by training the next generation of researchers to continue this crucial work. It has also acted as a springboard for the launch of various applied studies (Leese et al., 2021). Most importantly, the establishment of a DNA and environmental DNA-based methods working group within the European Standardisation Organisation CEN (CEN/TC230/WG28) is a marked testament to the impact of DNAqua-Net. One can only hope that the success and achievements of DNAqua-Net will inspire the establishment of EU COST Actions within related areas, such as DNA-based biomonitoring of terrestrial arthropods and vertebrates, fostering equally inclusive, open, and dynamic networks, and importantly giving us all an opportunity to stand on each other’s shoulders to strengthen our collective research and work toward common goals.

To celebrate the achievements of DNAqua-Net and the researchers who use DNA-based methods for assessing biodiversity, researchers and stakeholders came together in the first DNAqua-Net international conference for three days of remarkably interactive talks and insights. Following the conference, on March 12, 2021, DNAqua-Net members offered 13 stakeholder workshops for end-users and policymakers, bridging the gap from academic progress to application. This attracted over 900 participants from 15 European countries.

3 | THE CONFERENCE

The DNAQUA2021 conference offered an opportunity for scientists and stakeholders alike to get up to date with the latest research on DNA-based aquatic biomonitoring and the achievements of DNAqua-Net. The conference gathered a large number of participants from around the world with 1498 registered participants from 79 countries spanning taxonomists, ecologists, geneticists, bioinformaticians, policymakers, conservation managers, and more. The popularity of the conference underlines the relevance and timeliness of DNA-based aquatic bioassessment and monitoring, which we have also seen in the ever-increasing numbers of articles published on the topic. Furthermore, the virtual conference format likely boosted participation, allowing people to take part from the comfort of their work-from-home office.

The conference had one track, allowing participants to follow all talks, and the session themes mirrored the work packages in the DNAqua-Net COST Action. With this structure, the conference successfully guided participants through all the steps of a DNA-based aquatic bioassessment and monitoring workflow represented by DNAqua-Net’s working groups (WGs). In order of occurrence, (a) DNA barcode references (WG1), (b) field and laboratory protocols (WG3), (c) data analyses and storage (WG4), (d) implementation strategy and legal issues (WG5), and (e) biotic indices and metrics (WG2). In the first two evenings of the conference, there were two-hour poster sessions held on the SpatialChat platform, spanning the topics of all five sessions. SpatialChat enabled attendees to move around as avatars to view the posters or meet and chat in various settings. Between them, the five presentation sessions and two poster sessions offered participants a chance to see no less than 12 keynotes, 56 talks, and 136 posters on DNA-based aquatic bioassessment and monitoring.

4 | HIGHLIGHTS FROM DNAqua2021

The conference was kicked off by Agnès Bouchez and Florian Leese, who warmly welcomed the conference participants, gave a short presentation about the achievements of DNAqua-Net, and introduced the first two keynote speakers. Both keynote speakers presented their research regarding improvements in eDNA methods and touched upon the need for protocol standardization. The first keynote was by a member of DNAqua-Net, Assistant Professor Kristy Deiner, ETH Zurich (Switzerland), who presented an overview of eDNA, outlined key knowledge gaps,
and shared her view on the future and the direction of the field (Deiner, 2021). The second keynote lecturer, Associate Professor Hideyuki Doi, University of Hyogo (Japan), presented a range of studies using different eDNA sources, such as water and sediment cores, to demonstrate methodological and fundamental advances for understanding the distribution and abundance of aquatic species (Doi, 2021). These two keynotes set a welcoming tone for the following sessions.

The first session of the conference was on DNA barcode reference libraries and was chaired by Professor Torbjørn Ekrem, NTNU University Museum (Norway), and senior researcher Fedor Čiampor, Slovak Academy of Sciences. The quality, accuracy, and comprehensiveness of the reference database are of critical importance, regardless of whether a researcher chooses to employ quantitative single-species detection, barcoding, metabarcoding, or shotgun sequencing. This is crucial not only for accurate taxonomic assignment of sequences but also for applications such as robust primer design and specificity testing. Given that DNA reference data are the foundation of DNA-based aquatic biomonitoring, the conference naturally started with a session appropriately entitled “The endless quest for completeness and curation of reference libraries.” The first keynote for the session was given by Dr Hannah Weigand, Musée national d’histoire naturelle de Luxembourg, who presented a gap analysis of DNA barcode reference libraries for monitoring aquatic species in Europe (Weigand, 2021). The second keynote, presented by Associate Professor Filipe O. Costa, University of Minho (Portugal), discussed the revision, curation, and annotation of marine invertebrate reference libraries, stressing the need for automated reference library auditing and curation systems (Costa, 2021). These keynotes were accompanied by 13 talks and 23 posters, detailing a wide array of presentations on the curation, expansion, and gap assessment of reference data relevant for aquatic biomonitoring.

The second session, held on day two of the conference, concerned field and laboratory protocols and was chaired by Dr Kat Bruce, founder and Chief Technical Officer of NatureMetrics (UK), and Associate Professor Emre Eskin, Ankara University Agricultural Faculty (Turkey). Ultimately, the protocols used in field and laboratory work make or break our sequence data, and if not carried out properly, even the best bioinformatician would struggle to make sense of the data. Therefore, work toward standardization and implementation of DNA-based aquatic biomonitoring requires solid groundwork with respect to protocol development and validation. The session was entitled “The search for one (or none) protocol to rule them all!”, and the first of the two keynotes was given by Associate Professor Xavier Pochon, University of Auckland (New Zealand). Dr Pochon outlined the development, validation, standardization, and implementation of a protocol for monitoring marine benthic ecosystems around coastal salmon farms using eDNA (Pochon et al., 2021). The second keynote was given by Associate Professor Kristine Bohmann, University of Copenhagen (Denmark), who outlined the main labeling strategies in metabarcoding studies and talked about how to both account for and avoid tag-jumps (Bohmann & Caræ, 2021). The keynotes were accompanied by 12 talks and the 60 posters dealing with the development and exploration of protocols for sampling, water filtration, DNA extraction, primer design, blocking primers, quantitative PCR, eDNA/eRNA target capture, metabarcoding, and more.

The third session on data analyses and storage was chaired by Dr Alain Franc, Research Director at INRAE BIOGECO (France), and Dr Diego Fontaneto, Research Director at National Research Council of Italy. There is a need to store and maintain the ever-increasing amounts of sequencing data generated and to use pipelines that allow for cross-comparison between studies. This session, therefore, focused on current and future data analysis pipelines and was titled “Revealing, comparing, and storing biodiversity patterns in massive amplicon datasets”. The first keynote speaker was Assistant Professor Benjamin Callahan, North Carolina State University (USA), who talked about new sequencing technologies for highly accurate long-read sequencing, and presented a comparison with previous high-error rate technologies (Callahan, 2021). The second keynote speaker, Assistant Professor Holly Bik, University of Georgia (USA), touched upon the bioinformatics hurdles of working with meiofauna and nematode holobionts, and presented recent work improving current bioinformatics workflows (Bik, 2021). These keynotes were followed by 13 talks comparing existing tools and presenting new bioinformatic pipelines.

The fourth session was held on the third and final day of the conference, and concerned implementation strategies and legal issues. It was chaired by Dr Patricia Mergen, Liaison Officer at the European Commission Royal Museum for Central Africa, Dr Pieter Boets, Senior Researcher at Ghent University (both Belgium), and Professor Daniel Hering, University of Duisburg-Essen (Germany). The implementation and uptake of DNA-based technologies into routine monitoring depends on communication with stakeholders including policymakers. Hence, this session focused on the legal issues of technological implementation and stakeholder communication. It was entitled “Neglected, feared but indispensable: standardization and tailored communication”, and included 2 keynotes and 14 talks. Professor Florian Altermatt, University of Zurich and Swiss Federal Institute of Aquatic Science and Technology (Switzerland), was the first keynote speaker. He discussed the challenges and opportunities for the implementation of eDNA biomonitoring in riverine systems. Due to the potential pitfalls when comparing traditional sampling with eDNA approach, Dr Altermatt recommended that the particular strengths of eDNA biomonitoring should be the focus to avoid inheriting some of the built-in limitations of existing methods (Altermatt, 2021). The second keynote speaker, Dr Kristian Meissner, Director of the Finnish Environment Institute, talked about how to advance molecular methods used in research to enable routine use in biodiversity monitoring. To achieve this, Dr Meissner outlined the need for common guidance, networks, pilot studies, and collaboration with natural resource managers and regulators (Meissner, 2021). The 14 talks and 5 posters from this session presented experiences in implementing DNA-based approaches into routine aquatic monitoring, collaborating with regulatory bodies to help inform decision-making, and identifying the various legal issues, threats, and opportunities associated with the uptake of these techniques.
Rounding off the final day of the conference was the fifth session, on biotic indices and metrics chaired by Dr Maria Kahlert, a researcher at the Swedish University of Agricultural Sciences, and Professor Jan Pawlowski, University of Geneva (Switzerland). Traditionally, aquatic ecosystems are assessed using selected groups of organisms that are identified based on morphotaxonomy. With the advance of DNA tools, the biotic indices and metrics we use have to evolve to fit the tool. This session was therefore entitled “New trends in bioassessment of aquatic ecosystems: from organisms to DNA-based metrics”. It included 2 keynotes and 17 talks. The first keynote speaker, Dr Isabelle Domaizon, Research Director at the French National Institute for Agriculture, spoke about the opportunities and challenges of using lake sedimentary DNA to reveal long-term changes in aquatic biodiversity and ecosystem functioning. She highlighted best practices for DNA analyses and emerging topics that could potentially be addressed using sedimentary DNA (Domaizon, 2021). The second keynote speaker, Dr Maria Joana Feio, a researcher at the University of Coimbra & Marine and Environmental Sciences Centre (Portugal), gave an interesting talk on how predictive machine learning models can be used to assess river quality using molecular data derived from diatoms. Her work gives promising insights for the future of bioassessment in rivers, but critically noted that further studies would be required to test the accuracy of this approach on other taxa such as invertebrates (Feio, 2021). The following 17 talks and 51 posters highlighted how advances in high-throughput sequencing have presented new opportunities for biodiversity monitoring and the assessment of ecological status. Following the sessions, 13 prizes of 500 € were awarded to students and early-career researchers, 11 selected by expert reviewers and 2 selected by the audience.

5 | VIRTUAL TAKE-HOME MESSAGES

"Instead of focussing on what we disagreed on, we started focussing on what we agreed on", said Dr Kat Bruce at the beginning of the Field and Laboratory Protocols session in reference to her work leading the DNAqua-Net WG3 on the same theme. Here might lie the secret to the success of DNAqua-Net’s hundreds of members driving DNA-based aquatic biomonitoring toward standardization and implementation.

Focusing on common ground may have also contributed to the positive community atmosphere of the DNAQUA2021 conference. Hosting a virtual conference with a large number of participants runs the risk of technical disaster or long lonely days in front of the computer. Instead, the positive, dynamic, and inclusive atmosphere from the DNAqua-Net network carried over into the conference, everything ran without technical issues, and people from across the world shared their knowledge as a community. Thereby, the conference opened the door for synergy and collaboration between research groups. As the DNAqua-Net managing team says in the welcome statement in the abstract book:

“The implementation of (e)DNA-based methods into bioassessment and monitoring programs of our rivers, lakes, oceans and the groundwater, will be particularly successful if we sustainably stay connected across countries, generations, cultures and disciplines” (Leese et al., 2021).

Following the DNAQUA2021 conference, it became clear that the participants agreed: a community vote resulted in an overwhelming majority in favor of having another international conference in 2023. The broad support for maintaining this community is a testament to the significant methodological progress that has been made since the inception of DNAqua-Net, and it will be exciting to see the progress toward standardization and implementation of DNA-based aquatic biomonitoring at the next conference. With more biomonitoring experts now connected across Europe and beyond, the impact of the work contributed by everyone, no matter the research background, will be felt for years to come.

6 | RESOURCES

Conference website: https://symposium.inrae.fr/dnaqua-conference-evian2021
DNAqua-Net website: https://dnaqua.net/
Abstract book: https://aca.pensoft.net/collection/244
Recorded presentations: https://www.youtube.com/channel/UC3EtwRbadjz-dBH4c30xEow (available for one year).

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CONFLICT OF INTEREST

The authors of this meeting report are not part of DNAqua-Net. Chair of DNAqua-Net Florian Leese and DNAqua-Net member and WP3 leader Kat Bruce have read and approved the meeting report.

AUTHOR CONTRIBUTIONS

KB led the work. All authors contributed to writing and editing.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed.
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