



Conference Abstract

Welcome to DNAQUA2021 International Conference

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Abstract

Dear participants of DNAQUA2021 International Conference,

Undoubtedly, DNAQUA2021 is a major highlight of the EU COST Action DNAqua-Net (CA15219). Even though we cannot claim that the organisation of DNAQUA2021 was a piece of cake, it is simply wonderful to see the great interest in this event. With 1,498 registered participants from 79 nations, 204 contributed talks and posters for only two and a half days, the conference shows how timely and relevant research on DNA-based aquatic bioassessment and monitoring is.

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 (Leese et al. 2016). Yet, the more we are now delighted and thankful to see the success. Together with many experts from many different countries, taxonomists, ecologists, geneticists and bioinformaticians, we have made significant methodological progress. Above all, we have succeeded in connecting biomonitoring experts all across Europe and beyond. With more than 100 scientific publications from DNAqua-Net's five working groups, the research impact of the network is obvious. Furthermore, with "Metabarcoding and Metagenomics" ([MBMG](#)), we have established an international journal for basic and applied aspects of genetic bioassessment and monitoring. However, in many ways, the impact of DNAqua-Net goes far beyond the mere scientific progress. Capacity building e.g. via barcoding projects have

been initiated in many countries, validation studies were co-designed by researchers and stakeholders from the applied sector and launched - even across several countries as for example the SCANDNet project shows. DNAqua-Net has supported over 50 research exchanges that fostered close cooperation among the institutions and countries. Also, DNAqua-Net accompanied the fourth Joint Danube Survey (JDS4) and conducted the (e)DNA-based surveys for fish, benthic invertebrates, phytobenthos and the sediment community. Last but not least, we have developed many essential pieces of an applied concept for future implementation of DNA-based methods together with various stakeholders at national and international level. Here, of particular importance was the establishment of a working group within the European Standardisation Organisation CEN on DNA and eDNA-based methods (CEN/TC230/WG28).

We are particularly grateful also to our colleagues from 'beyond Europe' that have supported us, participated in workshops, discussions and training schools, invited us to their national meetings on DNA and eDNA-based biomonitoring on five continents. 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 (Fig. 1).



Figure 1. [doi](#)

Concept and vision of DNAqua-Net to link traditional and novel bioassessment approaches with the aim improve monitoring of aquatic ecosystems around the globe. Source: <https://dnaqua.net>

Many of the findings from basic to applied research will be presented at DNAQUA2021. We are particularly pleased that so many early career researchers present their findings. Please take the chance and discuss with them (but not only with them) about their findings. With "Spatial.Chat" we offer you a nice and intuitive environment that allows for some 'real' conference spirit even in these COVID-19 virtual meeting times.

Now enjoy two and a half days packed with fascinating insights from (e)DNA-based aquatic biomonitoring. Take the chance, foster and extend your collaborations. We hope to see and discuss with you over the next days at DNAQUA2021 and beyond.

THANK YOU!

Florian, Agnès, Charly & Alex (Fig. 2)



Figure 2. [doi](#)

Best regards from the current DNAAqua-Net managing team: Florian Leese, Agnès Bouchez, Charlotte Frie and Alexander Weigand.

Keywords

aquatic ecosystems, biomonitoring, COST, DNAAqua-Net, environmental DNA, metabarcoding

Presenting author

Florian Leese & Agnès Bouchez

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