Join FunDive and help mycologists gain a deeper understanding of fungal diversity in Europe!

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Introduction

FunDive is a pan-European project funded by the Biodiversa+ partnership, launched in 2024 to improve awareness of fungal diversity in nature conservation (https://fun-dive.eu/). Upon its launch, 26 partners from 18 European countries were engaged, but since then, the consortium has expanded and currently includes a total of 42 partners across 26 countries (Fig. 1). This number includes the United Kingdom, with the University of Stirling, Royal Botanic Garden Edinburgh, and Royal Botanic Gardens Kew, joining the consortium as collaborating partners in 2025.

The overall project goal is to develop, improve, and compare methods for mapping and monitoring of fungal diversity and to analyse drivers of its patterns. In addition, we aim to assess how well current conservation strategies, which are typically based on plants and animals, target globally red-listed fungi (https://www.iucnredlist.org/). FunDive's focus is on engagement, with both policymakers and the broader mycological community. We aim to raise awareness about fungi as crucial components of ecosystems, and encourage people to become actively engaged in generating data to promote fungal conservation. While engagement is the focus of this article, Fig. 2 provides a graphical overview of how the project is organised more broadly.

To understand and monitor the drivers of fungal diversity patterns in Europe, high-quality mapping of species distributions is needed. To do so, we are combining two approaches: environmental DNA sequencing and occurrence recording mainly based on sporophores collected by participants across Europe. However, to be able

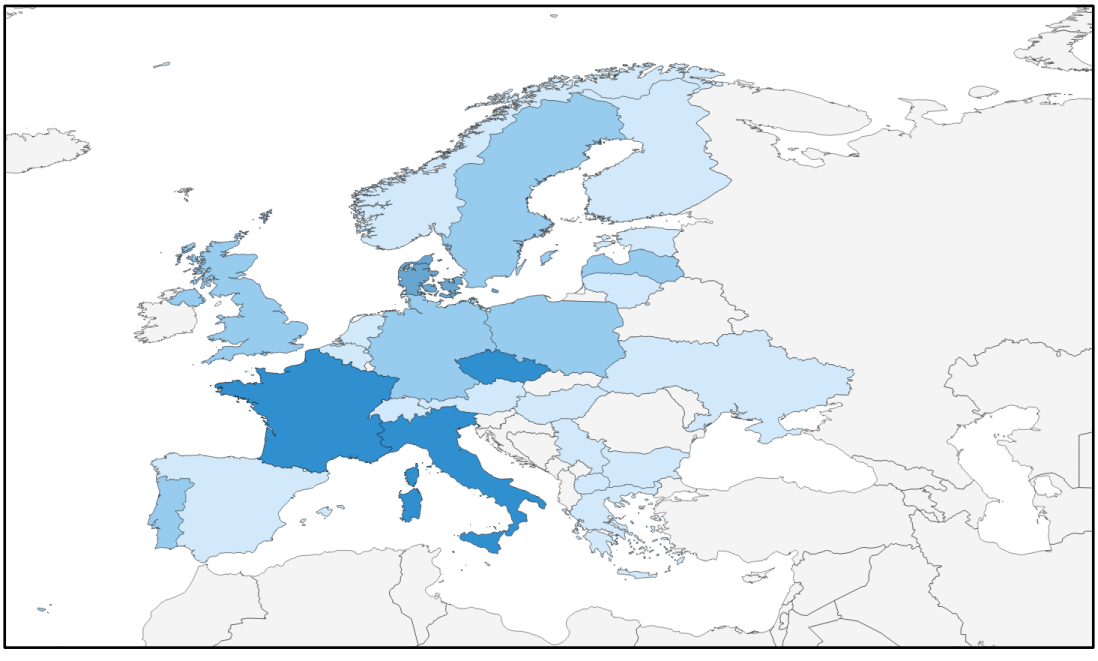

Fig. 1. Overview of the FunDive consortium. Currently, FunDive includes 42 partner institutions from 26 countries, and we are open to more. Darker shading means a higher number of partner institutions within individual countries.

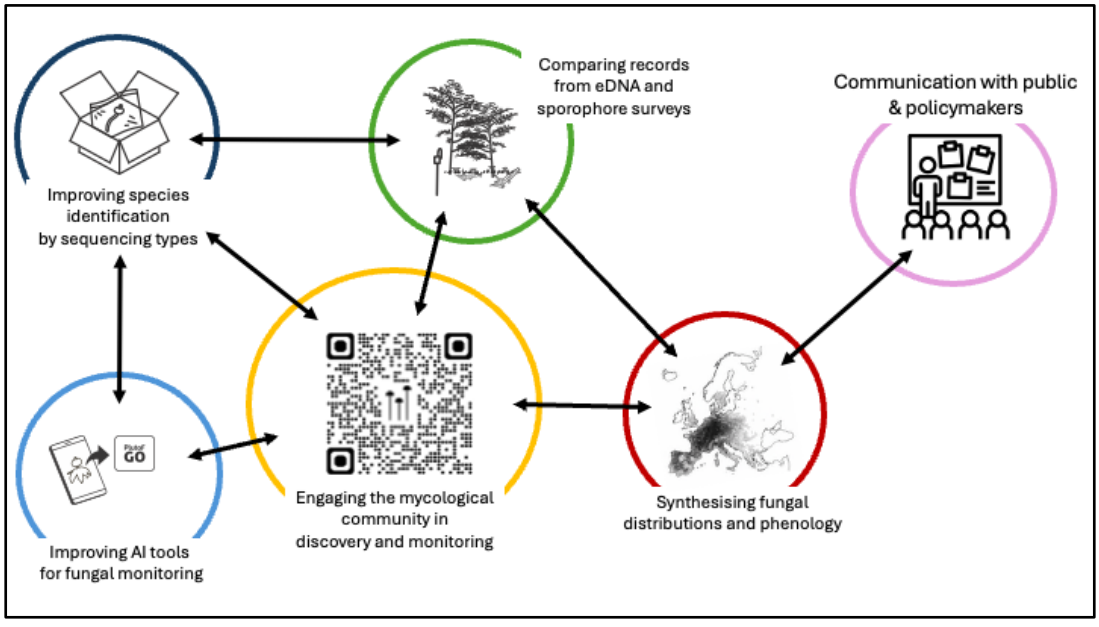

Fig. 2. FunDive is focused on fungal records collection, data curation, and the development of tools to aid mycologists. This schema will inform data analysis and synthesis, which can be relayed to the public and policy-makers. The arrows represent synergies among work packages within FunDive.

to combine these reliably, development of several other components is needed. Besides providing access to DNA barcoding of fungal specimens to the broader audience, we also focus on developing molecular protocols, sequencing old fungarium specimens that are representative of described species (called "type specimens"), and enhancing identification tools based on artificial intelligence (AI). A fungal species recognition system built by applying machine-learning models on photographs and metadata in the Atlas of Danish Fungi (https://svampe.databasen.org/en/; Picek *et al.*, 2022) is being developed further and incorporated into the biodiversity recording app PlutoF GO (http://plutof.ut.ee/go) to assist users in documenting their findings. We hope that the readers of this paper share our consideration of fungi as much as we do and want to join our efforts to incorporate fungal diversity into European conservation strategies.

Citizen science has always played an important role in fungal research (Watling, 1998). For centuries, some of the leading taxonomic experts in mycology did not have academic positions. For example, one of the most famous Italian mycologists, Giacomo Bresadola (1847-1929), who described more than 1000 new fungal species, served as a priest. As in earlier centuries, but even more nowadays, the availability of proper equipment could limit the engagement of enthusiasts in mycology. Molecular tools and protocols (including DNA barcoding) have become a standard in fungal research but these techniques are usually not available to the broader audience, creating a growing lack of comparability of data originating from professional and non-academic mycologists. The targets of FunDive include closing this gap by providing access to DNA barcoding using Oxford Nanopore Technology, standardising protocols, and training the broader mycology community. Nanopore sequencing can process long stretches of DNA in real time by measuring electrical signals as molecules pass through nanopores. Among the benefits of this high-throughput sequencing technique are its portability and independence from full sequencing facilities.

The British Mycological Society (BMS) has played a pioneering role in making DNA barcoding more accessible to non-professional mycologists. For example, the BMS established a DNA barcoding network across the UK in collaboration with local groups of field and amateur mycologists. In addition, the Lost and Found Fungi (LAFF) project, coordinated by BMS, the Royal Botanic Gardens Kew, and the British Lichen Society, further broadened access with easy-to-use DNA extraction kits (Douglas, 2020).

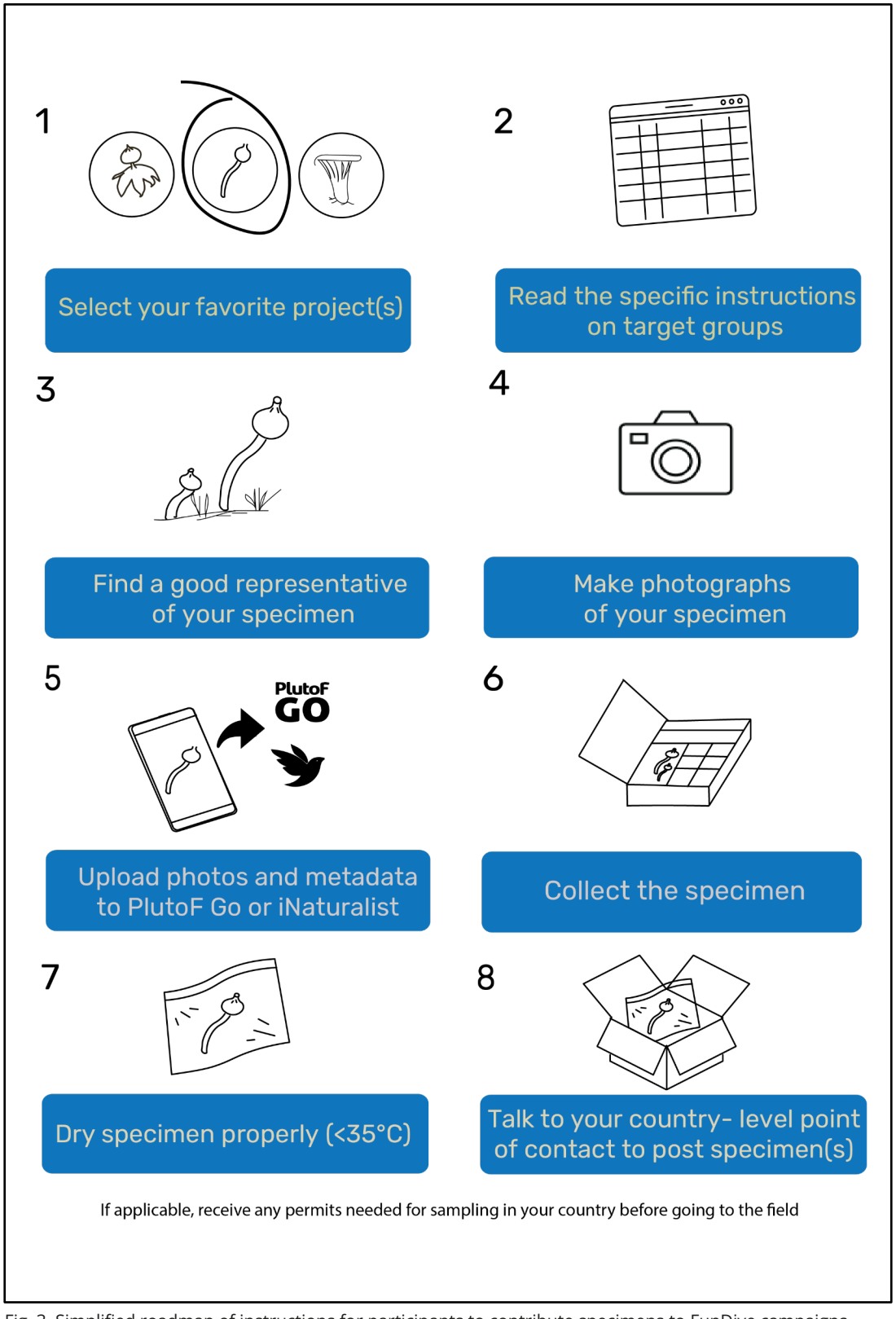

Fig. 3. Simplified roadmap of instructions for participants to contribute specimens to FunDive campaigns.

How can you become involved in FunDive?

FunDive strives to bring together everyone interested in mycology from across Europe (Haelewaters *et al.*, 2025). We encourage you to visit the project webpage, https://fun-dive.eu/, and to follow us on social media. There you will find instructive materials, such as sampling protocols and identification keys but also information about upcoming mycological meetings, conferences, and events across the continent. Most importantly, we use these online platforms to announce our sampling campaigns and communicate their outcomes.

Due to the huge diversity of the fungal kingdom (Blackwell, 2011; Niskanen *et al.*, 2023), we needed to create a step-by-step approach. Each season, we launch centrally coordinated campaigns targeting specific groups of fungi, led by experts. The ongoing campaigns vary widely. Some are easy to attend, whereas others require more extensive mycological experience. For some campaigns, recording and sharing observations is enough, while for others we ask you to sample specimens to sequence and confirm their identification. You can find all ongoing campaigns on our website, https://fun-dive.eu/en/get-involved/current-projects/.

You can participate in FunDive campaigns, either individually or by joining country-level organised activities. The process to record fungal specimens for FunDive campaigns is simple (Fig. 3): (1) select your favourite project(s), (2) read the specific instructions, (3) find a representative of a target species, (4) make a photo of your specimen, and (5) document it in a biodiversity recording platform, *e.g.*, PlutoF GO or iNaturalist (https://www.inaturalist.org/). If sampling of specimens is required: (6) collect the specimen that you documented, (7) dry it properly, and (8) send it to a FunDive country-level point of contact following online instructions (https://fun-dive.eu/en/get-involved/how-to-engage/). A unique code needs to be physically attached to the specimen and its digital record to which the DNA barcode will be added. Your specimen will be processed in our molecular lab and identified based on the resulting DNA sequence. You can follow the progress of your (and other FunDive) fungal specimens in this workflow on our website: https://fun-dive.eu/dataportal/.

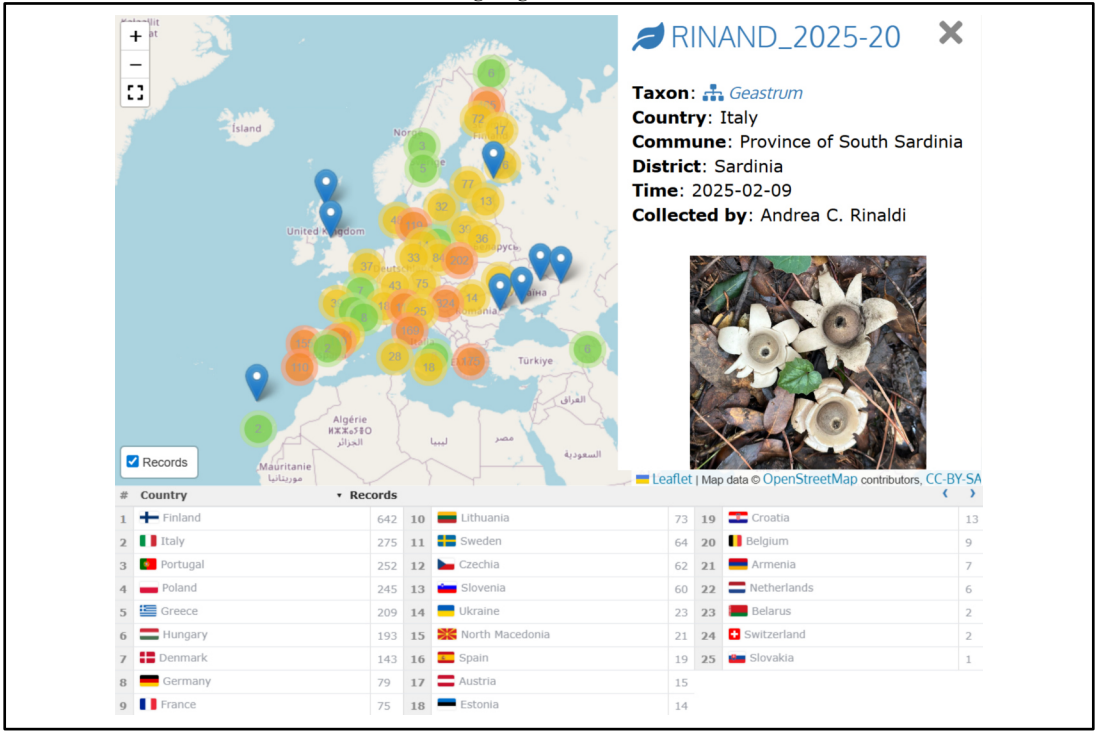

Fig. 4. Visual summary of the 2024–2025 sampling season. Left, map representing all 2504 fungal records from the last season. Blue icons represent individual records; coloured circles represent multiple records in a given area (green <10 records, yellow 10-99 records, orange ≥100 records). Right, example of a fungal record, a collection of *Geastrum* sp. from Sardinia (Italy), photo by Andrea Rinaldi. Bottom, summary of records made in 25 countries.

Figure 5. Different types of FunDive activities engaging the broader audience. A. The Muurola hospital area in Rovaniemi (Finland) is built on a pine heath, where mushrooms were collected for FunDive. From left to right Tapio Kekki and Raisa Sunnari. Photo © Merja Lipponen. B. A group of citizen scientists admiring earthstars in the Cabour Dunes (Belgium). Photo © Martine Decoussemaeker. C. Participants of the Micocosmo festival, sampling in Capo di Ponte, Lombardy (Italy), 2–6 October 2024. Photo © Simone Graziosi. D. Excerpt of a sketchbook with drawings made during a mushroom walk. Photo © Lindsay Robbins. [*Caption continued on page 83 ...*]

The first FunDive campaigns were announced in August 2024. During our first sampling season, which ended in July 2025, 2504 fungal records (186 observations, 2316 specimens) from 25 European countries were made by 309 participants (Fig. 4). Most records originated from Finland (642), followed by Italy (275), Portugal (252) and Poland (245). Although DNA barcoding of these specimens is still ongoing, 849 ITS sequences have been generated. Preliminary analysis of these sequence data has already uncovered species that are new to science, as well as new records for several countries. These are exciting results that will undoubtedly lead to multiple academic papers, including formal descriptions of new species (*e.g.*, Marxmüller *et al.*, 2025) and molecular phylogenetic inferences.

One of the first campaigns we launched deals with the distribution of earthstars (*Geastrum*) in Europe. As most of the 37 *Geastrum* species currently known in Europe are rare and occur in declining habitats, species in this genus are under assessment for the IUCN Red List. To perform these assessments, reliable data on species distribution are needed. After only one season, we collected 324 specimens that were all DNA-barcoded. Most of these specimens originated from Poland (124), Greece (53), and Hungary (24), broadening the known distribution to southeastern European countries, where fungal distribution data are particularly scarce.

Additionally, in several countries, sampling activities were organised by local mycological organisations and working groups. For example, guided excursions were organised in Belgium, Finland, Greece, Italy, and Poland (Fig. 5F). FunDive partners also gave open lectures (in person and online), presented during scientific conferences (*e.g.*, the International Mycological Congress in The Netherlands), and organised stands during mycological events such as the "Micocosmo" festival in Italy (Fig. 5C). Finally, a DNA barcoding workshop was organised in Poland for the exchange of knowledge between 38 participants, including researchers, lab technicians, students, and amateur mycologists (Fig. 5G–I).

From basic research to public engagement and policy recommendations

In FunDive, we aim to (1) examine temporal changes in fungal phenology and community composition in a spatial context, (2) compare the potential of sporophore- and environmental DNA-based approaches for fungal monitoring and conservation, and (3) analyse whether existing international conservation areas are effective in protecting fungal biodiversity. To do this, we combine three different sources of data. First, occurrence records generated by citizen scientists have leveraging power in that they capture a spatiotemporal range that professional researchers are unable to reach (Haelewaters *et al.*, 2024). Second, other occurrence records are based on sequencing of environmental DNA (eDNA) from soil, dead wood, air etc. This approach usually yields a higher number of species allowing for a greater understanding of diversity patterns (*e.g.*, Tedersoo *et al.*, 2014; Van Nuland *et al.*, 2025). Finally, data are also collected from existing datasets published previously in the Global Biodiversity Information Facility (https://www.gbif.org/).

To achieve our goals, we need reliable fungal names that can be linked to different data sources, including specimens, environmental samples and their respective DNA barcodes. This can be challenging as new fungal species are continuously being discovered, especially from eDNA data, and many classical fungal taxa are revealed to represent species complexes. For

[*... cont. from page 82*]: E. *Xylaria longipes*, documented during the "Summer School 2024: From Fungal Morphology to Genotype" in Skryje (Czechia), 1–7 September 2024. Photo © Danny Haelewaters. F. Presentation of fungal specimens collected during guided walk at the Pietraporciana Nature Preservation, Tuscany (Italy) where the Italian Mycology Union and Italian Botany Society organised Mycological Days, 18–20 October 2024. Photo © Simone Graziosi. G. Visit in the WA fungarium at the University of Warsaw (Poland) during the FunDive barcoding workshop, 17–21 March 2025. Photo © Mathias Rocheleau-Duplain. H. Participants of the FunDive barcoding workshop in Warsaw, 17–21 March 2025. Standing from left to right Mathias Rocheleau-Duplain, Marta Tischer, Christos Asimakopoulos, Dominik Knop, Karolina Grabowska, Vasco Fachada, Kinga Walczak, Aneira Williams, João Silva, Anna Mostowska, Heidi Tamm, Marcin Mazurkiewicz, Ana Posta, Anna Galińska, Balázs Palla; sitting from left to right Michał Kochanowski, Julia Pawłowska, Agnieszka Grochowska, Ariadne Furtado, Ivana Kusan, Katarzyna Szlendak, Maria Furman, Sara Piechota; on the floor Beniamin Abramczyk. Photo © Mathias Rocheleau-Duplain. I. Karolina Grabowska-Grucza handling a MinION device in the mobile molecular laboratory in Góry Stołowe National Park (Poland). Photo © Julia Pawłowska.

example, the names *Paxillus involutus* (Batsch) Fr. and *P. rubicundulus* P.D. Orton [= *P. filamentosus* (Scop.) Fr.] have been applied to two species complexes, each consisting of multiple species, potentially with overlapping geographic distributions (Hedh *et al.* 2008; Jargeat *et al.*, 2016). To better understand species distribution patterns and host ranges, this genus is one of the FunDive target taxa for the upcoming sampling season.

Species in such complexes can often be separated morphologically by trained field mycologists, whereas in other cases, only DNA can distinguish closely related species. In contrast, species identification in studies of fungal communities based on environmental samples is based solely on DNA sequence data, typically a fragment of the internal transcribed spacer (ITS) barcode region of the nuclear ribosomal DNA. When species are being described, it is recommended that a DNA sequence is linked to the holotype collection (Aime *et al.*, 2021). For many classical taxa, this is difficult to achieve either because the type specimen cannot be barcoded or because no type specimen exists at all. Again, in FunDive, we are running a "typification campaign" to address this issue. The goal of this specific campaign is to identify and barcode specimens that can serve as nomenclatural and interpretive types for fungal species currently based on ambiguous or missing original material.

We aim to sequence as many type specimens of fungi as possible from fungaria across Europe and make the resulting data available in public repositories to improve DNA-based delimitation of fungal taxa. Currently, no comprehensive database of fungal type specimens exists. We have access to ~10,000 type specimens deposited at 31 of the total 274 European fungaria (Thiers, continuously updated). We are also collaborating with researchers at the Royal Botanic Gardens Kew, who are undertaking similar work on their extensive fungal collections.

To compare the diversity captured by sequences generated from sporophores and eDNA, we have designed a comprehensive study in pine forests. Using sequences generated from soil, dead wood, passive spore traps, bulk sporophore samples in 200 pine forest locations across Europe, we will (1) analyse how fungal species composition and diversity in pine forests differ across a broad climatic range and (2) compare how different sample types represent fungal communities.

Finally, DNA barcodes of reference specimens and those collected during sampling campaigns will be uploaded via the PlutoF platform and mapped to UNITE Species Hypotheses (Kõljalg *et al.*, 2020). These, alongside newly generated eDNA-based sequences and existing datasets on fungal occurrences (*e.g.*, GBIF), will be analysed to understand drivers of fungal phenology, diversity, and species composition across Europe. Based on the results of these studies we hope to be able to formulate recommendations for eDNA-based and sporophore fungal monitoring and conservation to policymakers and stakeholders.

Acknowledgements

We thank the following people for allowing us to use their photos in this paper: Martine Decoussemaeker, Simone Graziosi, Merja Lipponen, Lindsay Robbins, and Mathias Rocheleau-Duplain. This research was funded by Biodiversa+, the European Biodiversity Partnership, in the context of the "FunDive: Monitoring and mapping fungal diversity for nature conservation" project under the 2022–2023 BioDivMon joint call. It was co-funded by the European Commission (grant agreement No. 2128-00020A - Biodiversa2022-640) and the following national funding agencies: Research Foundation Flanders (Belgium), Technology Agency of the Czech Republic (Czechia), Innovation Fund Denmark (Denmark), Estonian Research Council (Estonia), Republic of Estonia - Ministry of Climate (Estonia), Academy of Finland (Finland), Agence National de la Recherche (France), German Research Foundation (Germany), Bundesministerium für Bildung und Forschung (Germany), General Secretariat for Research and Innovation (Greece), National Research, Development and Innovation Office (Hungary), Ministero dell'Università e della Ricerca (Italy), Netherlands Organisation for Scientific Research (the Netherlands), Research Council of Norway (Norway), National Science Centre (Poland), Fundação para a Ciência e a Tecnologia (Portugal), Agencia Estatal de Investigación (Spain), and Swiss National Science Foundation (Switzerland). This work was supported by the project with grant no. PCI2023-146021-2, funded by MCIN/AEI/ 10.13039/501100011033 and the European Union.

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