



Monitoring Fungal Communities With the Global Spore Sampling Project

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OPEN ACCESS

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Specialty section:

This article was submitted to
Environmental Informatics,
a section of the journal
Frontiers in Ecology and Evolution

Received: 10 July 2019

Accepted: 17 December 2019

Published: 14 January 2020

Citation:

Ovaskainen O, Abrego N, Somervuo P, Palorinne I, Hardwick B, Pitkänen J-M, Andrew NR, Niklaus PA, Schmidt NM, Seibold S, Vogt J, Zakharov EV, Hebert PDN, Roslin T and Ivanova NV (2020) Monitoring Fungal Communities With the Global Spore Sampling Project. *Front. Ecol. Evol.* 7:511. doi: 10.3389/fevo.2019.00511

The kingdom Fungi is a megadiverse group represented in all ecosystem types. The global diversity and distribution of fungal taxa are poorly known, in part due to the limitations related to traditional fruit-body survey methods. These previous hurdles are now being overcome by rapidly developing DNA-based surveys. Past fungal DNA surveys have predominantly examined soil samples, which capture high species diversity but represent only the local soil community. Recent work has shown that DNA samples collected from the air with cyclone samplers provide information on fungal diversity at the scale of some tens of kilometers around the sampling location. To test the feasibility of air sampling for investigating global patterns of fungal diversity, we established a new initiative called the Global Spore Sampling Project (GSSP). The GSSP currently involves 50 sampling locations distributed on all continents, with each location collecting two 24-h samples per week. Here we describe the GSSP methodology, including the sampling, DNA extraction and sequencing protocols, and the bioinformatics pipeline. We further report results based on 75 pilot samples from five locations, of which three in Europe, one in Australia, and one in Greenland. The results show highly consistent patterns, suggesting that GSSP holds much promise for systematic global fungal monitoring. The GSSP provides highly standardized sampling across space and time, enabling much-improved estimation of total fungal diversity, the global distribution of different fungal groups, fungal fruiting phenology, and the extent of long-distance dispersal in fungi.

Keywords: biomonitoring, cyclone sampler, environmental DNA, fungi, global diversity

INTRODUCTION

Species in the megadiverse fungal kingdom play fundamental roles in ecosystem functioning as mutualists, decomposers, and pathogens. Over 80% of land plants establish mutualistic associations with mycorrhizal fungi (Wang and Qiu, 2006), which facilitate mineral and water uptake (Smith and Read, 2008). Saprotrophic fungi are primary decomposers of the organic matter in terrestrial ecosystems (Baldrian and Valášková, 2008). Pathogenic fungi have important implications for human health and food production (Almeida et al., 2019). Despite their importance, our knowledge of global fungal diversity and biogeography is minimal. While ca. 100,000 species of fungi have been described, estimates of global species richness vary between 0.5 and 10 million (Hawksworth and Lücking, 2017). Furthermore, current knowledge on the diversity and ecology of fungi is biased toward those groups producing macroscopic structures (mostly those producing visible fruiting bodies), even if the diversity of microscopic fungi is vastly greater.

The recent proliferation of environmental DNA based studies have overcome many limitations of fruiting body-based surveys, advancing knowledge of large-scale patterns of fungal diversity (e.g., Sato et al., 2012; Tedersoo et al., 2014; Barberán et al., 2015; Davison et al., 2015). To date, most fungal biogeographical studies have focused on soil communities (but see Barberán et al., 2015) even if different substrates (e.g., wood, litter) support very different assemblages. Furthermore, large-scale fungal studies have mostly been based on samples acquired from distant sites, although it is known that fungal communities can exhibit high spatial variation at very small spatial scales (Hazard et al., 2012; Kubartová et al., 2012). Thus, there are major knowledge gaps regarding the large-scale distributions of fungi, in particular of fungi other than those inhabiting soil.

Since many fungi disperse by windborne spores, DNA surveys based on aerial samples provide an alternative for characterizing the regional fungal composition. As demonstrated by Abrego et al. (2018), aerial sampling can simultaneously sample fungi growing on diverse substrates, while providing a regional scale perspective of some tens of kilometers. To test the feasibility of air sampling for investigating the global patterns of fungal diversity, we established an initiative called the Global Spore Sampling Project (GSSP). We first made a preliminary survey to identify researchers who would be interested in joining the project as sampling teams, and then selected the sampling teams so that we achieved maximal global coverage. Additional partners were encouraged to join if they were able to purchase the sampling equipment themselves. The GSSP currently involves fifty sampling locations distributed across all continents, with each location collecting two 24-h samples per week.

The GSSP project is designed to address research questions of both fundamental and applied nature. To start with, by examining accumulation curves for operational taxonomical units (OTUs) within and among locations, it will improve estimates of fungal diversity. With the help of taxonomic placement of the unknown OTUs (Abarenkov et al., 2018), GSSP will further help to reveal those groups of fungi that are least represented in taxonomy and sequence reference databases. Most

importantly, it will provide a much-improved view of global fungal biogeography, shedding light e.g. on how fungal diversity changes along latitude. Based on research on soil fungi, such patterns may deviate substantially from those in other organisms (Tedersoo et al., 2014). Furthermore, these global data may reveal the distributions and temporal dynamics of fungi affecting humans, such as pathogenic fungi causing diseases or infecting crop plants.

In this paper, we describe the GSSP methodology, including the sampling, DNA extraction, sequencing, and concentration estimation protocols, and the bioinformatics pipeline. We further report results based on 75 pilot samples from five locations, of which three in Europe, one in Australia, and one in Greenland.

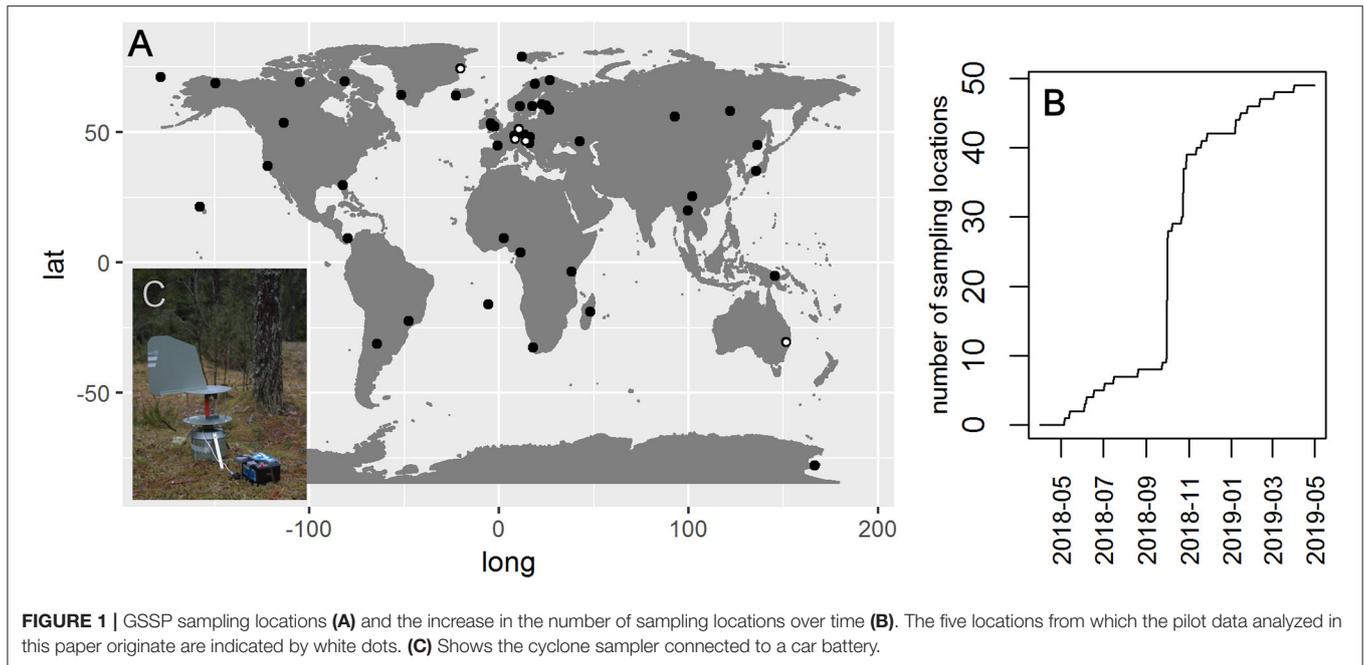
METHODS

The Global Spore Sampling Project (GSSP) is a globally distributed network of sampling locations (**Figure 1**) equipped with a cyclone sampler (Burkard Cyclone Sampler for Field Operation, Burkard Manufacturing Co Ltd; <http://burkard.co.uk/product/cyclone-sampler-for-field-operation>; Emberlin and Baboonian, 1995). The current network includes fifty sampling locations that cover all continents, but is most dense in Europe (**Figure 1**). At each sampling location, two 24-h samples are taken each week. Although sampling was planned to start synchronously in October 2018, realized sampling was initiated earlier at a few localities and later in some other localities (**Figure 1**). The sampling locations represent varying latitudes and altitudes. Some samplers are located in urban environments, while others are positioned in natural environments (e.g., forests, tundra).

In this paper, we utilize 75 samples collected during the pilot phase of GSSP from five sites (**Figure 1**). More details on these samples, such as the description of the sampling locations as well as the timing of the sampling, are given in **Supplementary Information**.

Sampling Protocol

Air DNA samples were acquired using cyclone samplers placed at ground level to ensure free airflow through the sampler. The cyclone sampler (shown in **Figure 1**) orientates itself in the direction of the wind and collects all particles from the air with a single reverse flow cyclone. The sampler collects particles with size $>1 \mu\text{m}$ from the air directly into a sampling tube, including spores, pollen, bacteria, and small insects. The sampler's average air throughput is 16.5 liters per minute for a total of 23,800 liters during each 24-h sampling period. Sterile 1.5 ml Eppendorf vials were used as sampling tubes. After sampling, the vial was removed from the cyclone sampler, the lid was closed, and the vials were labeled with the site code and week number. Likewise, the time and duration of the sampling, as well as notes about the presence of rainwater or larger objects (e.g., arthropods), were recorded. Every week, two 24-h samples (henceforth called Sample A and Sample B) were collected from each site. To avoid contamination, gloves were used while handling the samples or the device. Sampling teams were instructed to clean the cyclone part of the device monthly with water and soap and to rinse it



with ethanol, or to sterilize it with dry-heat, chlorine or UV when such equipment was available.

The samples were stored at -20°C until they were shipped to the University of Helsinki, Finland. Shipping was at room temperature as the shipping time was relatively short and refrigerated transport would be costly. In Helsinki, visible arthropods were removed from the samples. To avoid losing fungal spores attached to the arthropod bodies, their surface was rinsed by adding sterile water into the sample tube and vortexing. After washing, the arthropods were removed with sterile tweezers. Samples with rainwater were dried in a freeze drier (24 h, -80°C , 0.57 mbar) covered with a porous Parafilm to avoid cross-contamination between samples. After drying, all samples were sent to the University of Guelph, Canada, for DNA extraction and sequencing.

DNA Extraction, Primers, and Sequencing

Upon receipt, each sample tube was accessioned and assigned a unique Process ID. DNA extraction followed Ivanova et al. (2008) with minor modifications. Two hundred seventy microlitre of ILB (700 mM GuSCN, 30 mM EDTA pH 8.0, 30 mM Tris-HCl pH 8.0, 0.5% Triton[®] X-100, 5% Tween-20) with 30 μl Proteinase K (20 mg/ml) was added to each collection tube before it was gently rotated to wash spores off the tube walls and lid, and the tube was then centrifuged at 11,000 g for 5 s. The resultant pellet was re-suspended by gentle pipetting, and the entire volume was transferred to a Lysing Matrix A tube (MP-BIO). Tissue was ground in a TissueLyser (Qiagen) for 2 min at 28 Hz. Samples were then incubated for 1 h at 56°C , followed by 1 h at 65°C . Lysates were transferred to a MN block containing 600 μl of 5M GuSCN Binding Buffer (5M GuSCN, 16.66 mM EDTA pH 8.0, 8.33 mM Tris-HCl pH 6.4, 3.33% Triton[®] X-100), and the entire volume was transferred in two equal aliquots of 350 μl (each followed by centrifugation

at 5,000 xg) onto AcroPrep 96 Filter Plates with 3.0 μm glass fiber media/0.2 μm Bio-Inert membrane, followed by two washes with WB buffer (60% ethanol, 50 mM NaCl, 10 mM Tris-HCl pH 7.4, 0.5 mM EDTA pH 8.0). DNA was eluted in 45 μl of 10 mM Tris-HCl pH 8.0.

Synthetic Positive Control

We applied a synthetic positive control approach (also called spiking approach), with the aim of translating the raw sequence counts into more quantitative estimates of DNA amount. The nine positive control plasmids were prepared from synthetic sequences that are generally consistent with fungal ITS sequences, yet different from all known natural sequences (Palmer et al., 2018). These contained ITS3 (GCATCGATGAAGAACGCAGC) and ITS4 (TCCTCCGCTTATTGATATGC) priming sites (White et al., 1990), and were synthesized as gBlocks at Integrated DNA Technologies (IDT). PCR products were amplified using Platinum Taq and cloned into TOPO4 vector using TOPO[™] TA Cloning[™] Kit for Sequencing, with One Shot[™] TOP10 Chemically Competent *Escherichia coli* (Invitrogen) following manufacturer's instructions. Resulting clones were validated by Sanger sequencing, and each selected clone containing the desired insert was grown in 100 ml of liquid LB media with 150 $\mu\text{g}/\text{ml}$ ampicillin. Plasmid DNA was extracted as described using standard protocols (Sambrook et al., 1989) with minor modifications. Plasmid DNA concentration was normalized using BR Qubit dsDNA kit and qPCR, resulting in a pool containing all nine plasmids at 0.01 ng/ μl .

Estimating DNA Concentration With qPCR

As an alternative approach to the synthetic positive controls, we also estimated the DNA concentration on each sample

using qPCR with a serial dilution of AMPtk plasmids. The target genetic marker ITS2 rDNA for fungi and plants was amplified using the Polymerase Chain Reaction (PCR) for 45 cycles on LightCycler96 (Roche). Each of the 12 μl reactions contained 6 μl of FastStart Essential DNA Green Master (Roche), 1.2 μl of each 10 μM primers (forward primer consisted of a cocktail of ITS_S2F and ITS3 mixed 1:1, ITS4 was used as single reverse primer), 1.6 μl of ddH₂O and 2 μl of genomic DNA. Standard curve DNA dilutions for 0.01 ng/ μl , 0.001 ng/ μl , 0.0001 ng/ μl were generated in three replicates using AMPtk plasmids DNA. The thermocycling profile consisted of denaturation at 95°C for 10 min; 55 cycles of 95°C for 10 s, 51°C for 10 s, 72°C–40 s; melting: 95°C for 10 s, 65°C for 60 s, 97°C–1 s. Absolute quantification analysis was performed in LightCycler96 software v1.1.

Next Generation Sequencing Workflow

CCDB PCR Master Mix with Platinum Taq was prepared as described in Hebert et al. (2013). The total reaction volume was 12.5 μl and contained 10.5 μl of MMix and 2 μl of DNA template. The positive synthetic control (0.01 ng/ μl) containing nine plasmids was spiked into the PCR mastermix at a 1:100 ratio. The target genetic marker ITS2 rDNA was amplified using the Polymerase Chain Reaction (PCR) for 20 cycles with fusion primers ITS_S2F (Chen et al., 2010), ITS3 and ITS4 (White et al., 1990) tailed with Illumina adapters:

ITS_S2F-mis

TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATG
CGATACTTGGTGTGAAT

ITS3-mis

TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCA
TCGATGAAGAACGCAGC

ITS4-mis

GTCTCGTGGGCTCGGAGATGTGTATAAGAGACA
GTCCTCCGCTTATTGATATGC

PCR products were diluted 2x, and a volume of 2 μl of the diluted product was used in second round PCR amplification with Index 1 and Index 2 fusion primers containing i5 and i7 Nextera indices for dual-indexed PCR: https://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/experiment-design/illumina-adapter-sequences-100000002694-11.pdf.

The thermocycling for Platinum Taq PCR1 consisted of initial denaturation at 94°C for 2 min followed by 20 cycles of: denaturation at 94°C–1 min; annealing at 51°C– 1 min; extension at 72°C for 1 min; final extension at 72°C for 5 min. PCR2 with indexed Illumina primers consisted of 30 cycles of initial denaturation at 94°C for 2 min followed by 20 cycles of: denaturation at 94°C–1 min; annealing at 60°C– 1 min; extension at 72°C for 1 min; final extension at 72°C for 5 min. DNA template and indexed primer transfers were done on a Biomek FXP robot.

The library was pooled without normalization and purified using Ampure beads (Agencourt, Beckman Coulter) with 0.8:1

beads/PCR product ratio and sequenced on Illumina MiSeq following manufacturer's instructions with 25% spike of PhiX.

Bioinformatics Pipeline

Raw Illumina data were paired using Geneious Prime 2019.0.4, short sequences (<100 bp) were discarded and 5'-end and 3'-end were trimmed by quality (QV20) using BBDuk. The following bioinformatics workflow was used to process paired-end data: Cutadapt (v1.8.1) was used to trim primer sequences; Sickle (v1.33) was used for filtering (<200 bp) and Uclust (v1.2.22q) was used to cluster OTUs with 98% similarity threshold and minimum coverage 2.

We denote the total number of sequences obtained for sample i by n_i and henceforth refer to it as the sequencing depth. Only those samples for which the sequencing depth was at least 10,000 were included. Clusters that corresponded to the spikes were identified using Ublast with 95% similarity threshold. We denote by s_{ij} the number of sequences that were assigned to the spike j (with $j = 1, \dots, 11$), by $s_i = \sum_j s_{ij}$ the total number of spike sequences in sample i , and by $m_i = n_i - s_i$ the number of sequences not assigned to the spikes. The amount of fungal DNA in each sample was estimated by $w_i = m_i/s_i$, with the caveat that some m_i sequences may not represent fungal DNA. With this definition, w_i measures the amount of fungal DNA in units relative to the spike (presuming no inhibition or competition for PCR reagents). As the total input of spike DNA was ca. 0.001 ng (1/100 volume of 0.01 ng/ μl (10.4 μl) spiked into 1,040 μl PCR mix before adding DNA), e.g., $w_i = 24$ would theoretically correspond to a sample containing 0.024 ng of DNA in 2 μl of template DNA added to the reaction, indicating a DNA concentration of 0.012 ng/ μl . During DNA extraction 78% of lysate was used for binding so total DNA yield can be calculated as 0.012 ng/ μl *45 μl (elution volume), resulting in 0.54 ng in the 78% of the used lysate or 0.69 ng in the total initial sample. As the cyclone sampler processes 24 m³ of air in 24 h, the value of $w_i = 24$ would theoretically correspond to 0.029 ng of fungal DNA per cubic meter of air. However, we note that this calculation assumes that all DNA amplifies equally across spikes and species, whereas many factors may cause variation in it (Polz and Cavanaugh, 1998; Sipos et al., 2007; Berry et al., 2011; Kennedy et al., 2014).

For the m_i sequences that were not assigned to the spikes and thus represented DNA, a probabilistic taxonomic placement was performed with PROTAX (Somervuo et al., 2017). The specific implementation of PROTAX to fungal identification (Abarenkov et al., 2018) is based on a taxonomy database that includes ca. 130,000 species, and a reference database with about 420,000 reference sequences that represent 22,300 species. We recorded for each query sequence the most likely taxonomic identity at the levels of phylum, class, order, family, genus, and species, and the uncertainty in these assignments as measured by probabilistic placement. We note that the uncertainty estimates of PROTAX account for the possibility that the species might be unknown to science (i.e., not included in the taxonomy database), or known to science but lacking reference sequences (Somervuo et al., 2017; Abarenkov et al., 2018). We

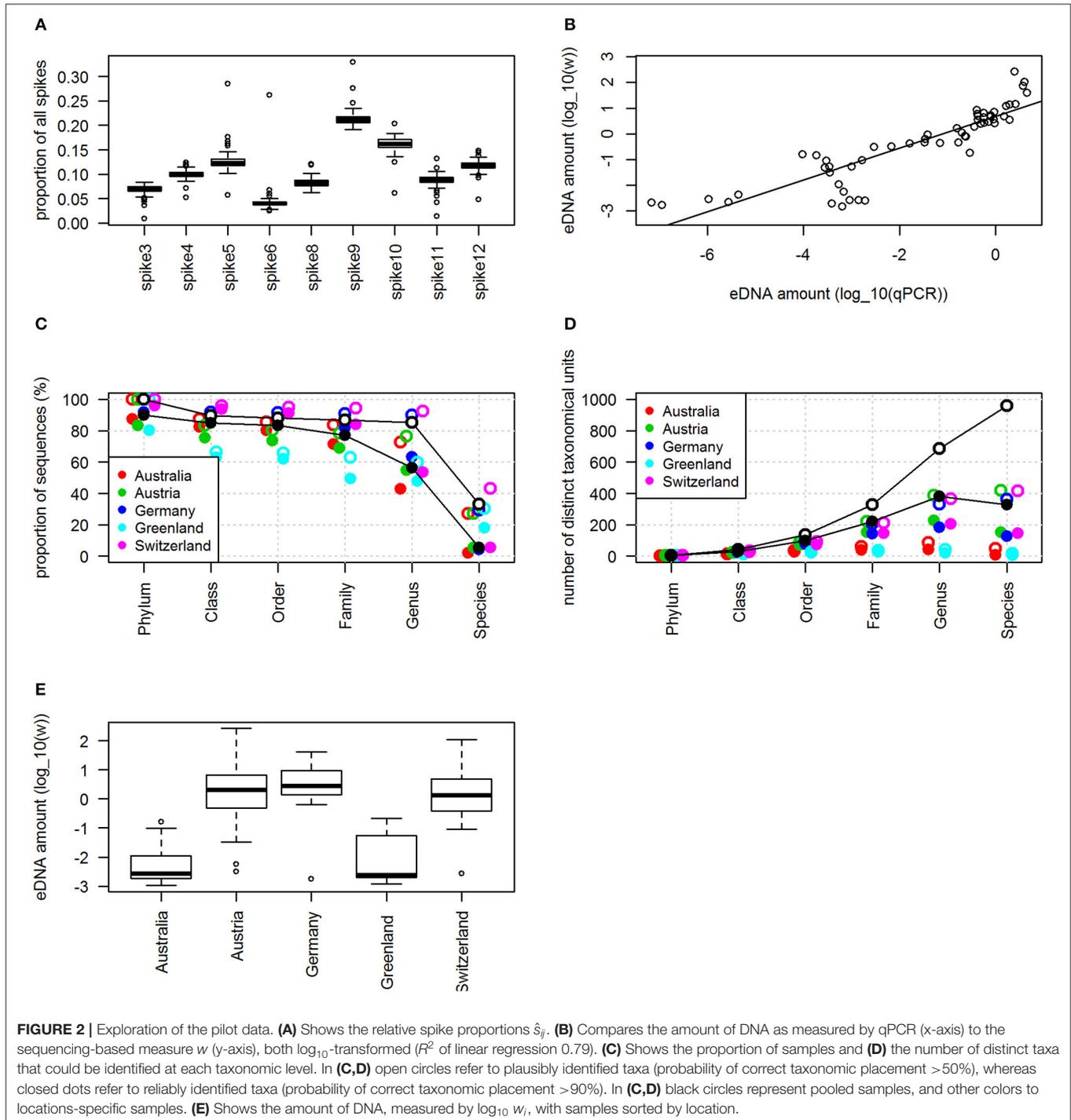
followed Somervuo et al. (2017) in treating an identification as plausible if the probability of taxonomic placement was >50%, and reliable if the probability of taxonomic placement was >90%.

Statistical Analyses of the Pilot Data

The statistical analyses were aimed at testing the feasibility of the method in surveying local species communities. Given the lack of controlled mock-community data, the assessment on the

reliability of the GSSP pipeline is based on the consistency of observed patterns, especially on the comparison of samples from the five sampling locations.

First, to examine how consistently different spikes were captured among the samples, we defined the relative spike proportion as $\hat{s}_{ij} = s_{ij}/s_i$. We performed an analysis of variance to examine how much of the variation among the relative spike proportions was explained by spike identity j .



Second, to validate the accuracy of the sequence-based estimate of fungal DNA amount (w_i), we compared it to the qPCR-based estimate of fungal DNA amount (see above) with the help of linear regression. To identify variation in DNA amount over orders of magnitude, we \log_{10} transformed both the sequence- and the qPCR-based estimates.

Third, we used generalized linear models to examine variation in the estimated amount of DNA (w_i) and OTU richness among the samples. For amount of DNA, we fitted a linear model where the response variable was $\log_{10} w_i$. For OTU richness, we fitted a negative binomial model. In both models, the explanatory variables were the sampling location, the presence of insects in the sample, the presence of water in the sample, and the \log_{10} transformed number of sequences, i.e., the sequencing depth. While the samples were collected over several months and thus contain seasonal variation, we expected that most of the variation would be explained by the sampling location and that the three European sampling locations would yield similar amounts of DNA and OTU richness compared to the Greenland and Australian samples. We further expected that the treatment of the samples due to insects or water might influence the amount of fungal DNA and consequently OTU richness. As we normalized the samples by the spiking approach, we did not expect sequencing depth to have an influence on the estimated amount of DNA, but we expected that OTU richness may increase with sequencing depth.

Fourth, to examine how reliably the sequences could be identified, we computed the proportion of sequences that could be either plausibly or reliably identified for each taxonomic level and each sampling location. To examine how much diversity the samples contained, we computed for each taxonomic level and each sampling location the numbers of distinct OTUs that could be plausibly or reliably identified.

Fifth, to examine how community composition varied among the five locations, we employed a non-metric multidimensional scaling. For the community data we used g_{ij} , defined as the number of sequences in sample i that were plausibly (with probability >50%) identified to the genus j . To account for sequencing depth and the variation that covered many orders of magnitude, we transformed the data as $y_{ij} = \log((g_{ij} + 1)/(n_i + 1))$. The non-metric multidimensional scaling was performed using Euclidian distance by the sammon function of the MASS R-package with the default settings as `sammon(dist(y))`. We further used the `anosim` function to test whether the five locations separated in the ordination space. We note that the NMDS analyses are aimed primarily for illustrating the data, and that we plan to apply more rigorous model-based analyses (see e.g., Gloor et al., 2017; Ovaskainen et al., 2017) after we have obtained data from all localities.

RESULTS

Among the 75 samples, 73 yielded >10,000 sequences with a mean of 52,000 sequences (standard deviation = 10,000; range = 25,000–67,000). The results below are based on the 3.8 million

sequences represented by the 73 samples, whereas the two samples with <10,000 sequences are excluded.

Does the Use of Spikes Allow Accurate Estimation of DNA Amount?

Different spikes generated very different sequence proportions, ranging from ca. 0.05 to 0.20 (Figure 2A). These proportions were found to be stable since in the linear model spike identity explained $R^2 = 0.88$ ($p < 0.001$, $df = 8$, df -residual = 648, $F = 646$) of the variance among the proportions (reflected by the clear separation of the boxes in Figure 2A). The use of the spikes allowed very accurate estimation of the amount of fungal DNA, shown by the fact that the sequence-based estimate correlated very closely with the qPCR-based estimate (Figure 2B). The proportion of fungal DNA sequences (i.e., non-spike sequences) varied greatly among the samples: the median proportion was 24.9%, the minimum proportion 0.1%, and the maximum proportion 99.7%. Consequently, the estimated amount of DNA varied by five orders of magnitude among the samples, ranging from 0.001 to 264 units of spike DNA, corresponding to from 1.2×10^{-6} to 0.3 ng of fungal DNA per cubic meter of air.

How Much Diversity Was Detected in the Samples?

The taxonomic placement was generally successful up to the family level, as 75% of the sequences were reliably, and 85% were plausibly, identified (Figure 2C). As expected, due to the incompleteness of the reference databases (Abarenkov et al.,

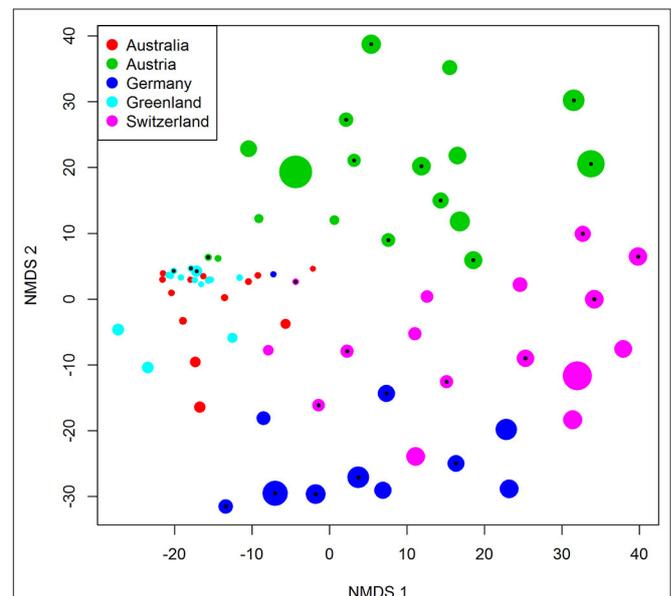
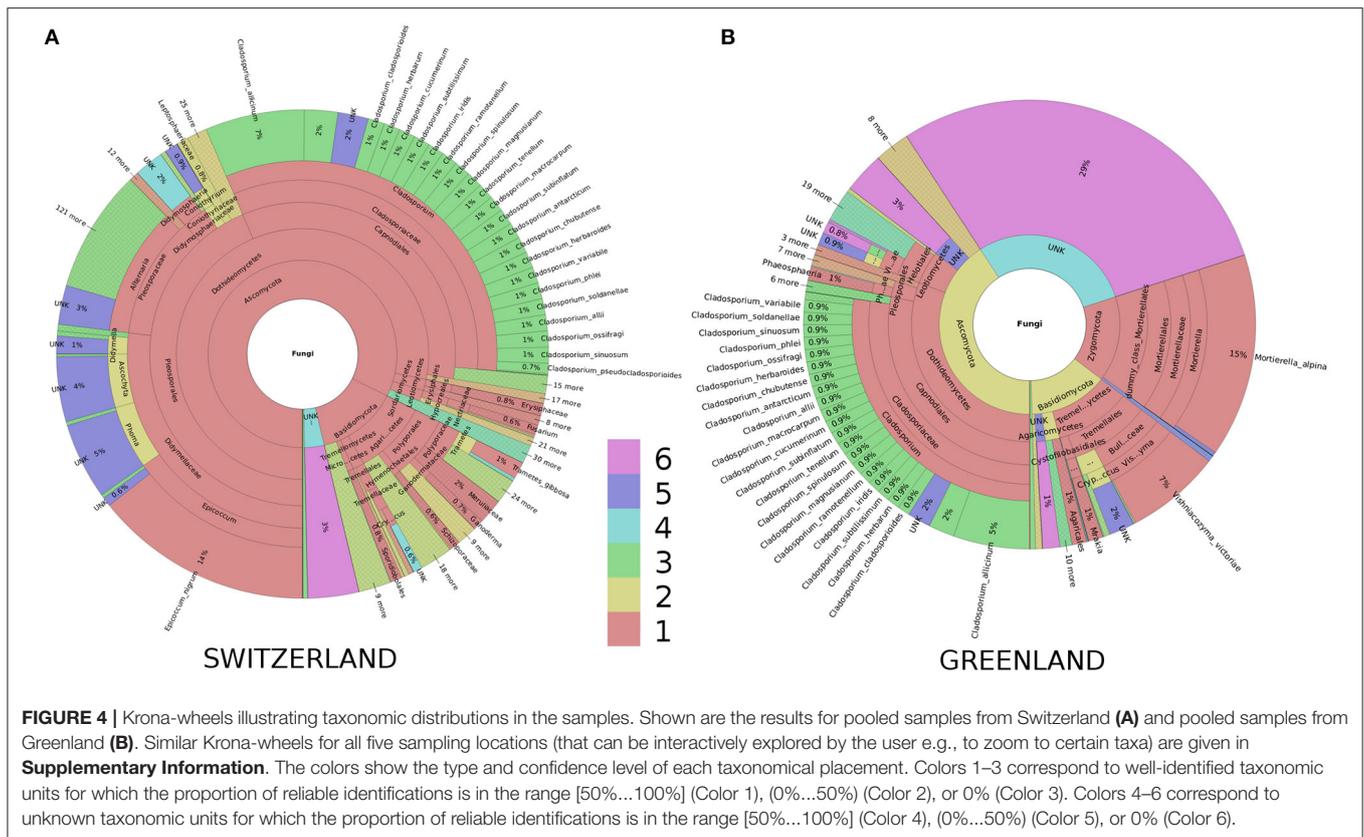


FIGURE 3 | NMDS ordination of the pilot data. Each dot corresponds to one sample. The color indicates sampling location, the size of the sample corresponds to the amount of DNA (measured by w_i), while the black dots mark samples that contained an insect. The final stress achieved in the NMDS was 0.061.



2018), a large proportion of the sequences remained unidentified at the genus and especially species levels. The samples yielded considerable taxonomic diversity, totalling about 1,000 species that could be plausibly identified (Figure 2D). The true diversity is likely much higher as many sequences remained unidentified at the species level and thus were not included in this estimate.

4088 OTU sequences representing 130,309 sequences (3.5% of all sequences) were assigned to unknown phyla in fungal classification. The best BLAST hits of these sequences against Genbank suggest that 66% of them belong to Viridiplantae, 18% to Fungi, 11% to Metazoa, 3% to Oomycetes, and 1% to Alveolata.

How Did Fungal Communities Vary Among the Sampling Locations?

The samples from the three European locations had consistently high levels of fungal DNA, whereas those from Australia and Greenland did not (Figure 2E). Variation in DNA amount was not explained by the presence of water ($p = 0.50$), insects ($p = 0.49$), or sequencing depth ($p = 0.19$), but location had a major effect ($p < 0.001$, $R^2 = 0.56$, $df = 4$, df -residual = 68, $F = 22$). Similarly, variation in OTU richness was not explained by the presence of water ($p = 0.08$), insects ($p = 0.69$), or sequencing depth ($p = 0.99$), but location had a major effect ($p < 0.001$, $df = 4$, df -residual = 68, null deviance = 161, residual deviance = 87). The NMDS suggested consistent variation in fungal community composition, as the five locations separated in the ordination space (anosim, $p < 0.001$), including the three

European samples from neighboring countries (Figure 3). The Australian and Greenland samples were close in the NMDS plot because we chose to use a Euclidean distance metric and samples from both of these locations contained little DNA and low species diversity. The NMDS further suggested that the removal of insects did not influence the fungal communities e.g., due to introducing contamination, as the samples that contained insects did not deviate systematically from those that lacked them (Figure 3).

In terms of taxonomic composition, all samples were dominated by Ascomycota, but they also contained a substantial proportion of Basidiomycota, and the Greenland samples also Zygomycota (Figure 4). We note that samples from all five locations consistently contained a high proportion of the genus *Cladosporium*.

DISCUSSION

The results of the present pilot study are encouraging in three ways. First, DNA was obtained from nearly all samples, and sequence characterization recovered a substantial taxonomic diversity despite the small number of samples. Second, we could quantify DNA concentrations consistently by two methods, even if DNA amount was generally low and varied over five orders of magnitude. Third, the results showed a strong biological signal as samples were consistent at each site, suggesting low levels of contamination or other problems related to the workflow.

Community composition was well separated over space among the three neighboring countries of Europe. This result is consistent with an earlier study (Abrego et al., 2018), which showed that air samples represent the regional diversity of fungi procuding airborne spores at some tens of kilometers around the sampling site. However, the more precise spatial scale represented by the samples needs to be determined by further studies, such as sampling at different distances from known point sources.

The success of the pilot study suggests that the GSSP project has great promise for improving knowledge of fungal diversity and distribution at a global scale, with the caveat that GSSP is limited to those fungi only that can be sampled from the air. Importantly, the results are quantitative in the sense that one can ask how many times more common (in terms of the number of ITS sequences) a species is in a sample from a particular location and time than in samples from another location and time. This will allow incorporating abundance information in many kinds of analyses. Since spores may disperse over very long distances, the presence of the species in a sample does not necessarily mean that it is part of the local fungal community. Thus, if using the data to construct “species lists,” it will be important to separate local spore sources from long-distance dispersal. This can be done by accounting for sequence abundance, and in particular repeated occurrence of species at the same location. Conversely, examining the amount and origin of DNA that does not originate from the local community (e.g., samples acquired during winter in the arctic regions) will allow quantitative estimation of long-distance dispersal in fungi under current air circulation patterns.

The abundance of *Cladosporium* species at all sampling locations raises the possibility of contamination (Czurda et al., 2016). What speaks against this is that the total amount of DNA varied by five orders of magnitude among the samples, while the proportion of *Cladosporium* remained relatively stable. If its presence is due to contamination, one would expect the Greenland and Australian samples (with little DNA) to be dominated by it, whereas the other samples with much DNA would be less influenced. However, no such pattern was observed. *Cladosporium* spores are wind-dispersed and they are known to be very abundant in outdoor air (Harvey, 1967; Kurkela, 1997), and thus we consider their consistent presence in our samples biologically plausible.

To conclude, our pilot study suggests that the GSSP will contribute a fungal dimension to the increasing number of global trapping efforts combined with DNA methods, such as the Global Malaise Trap Program (<https://biodiversitygenomics.net/projects/gmp/>) or the African Soil Microbiology Project (Wild, 2016). Within the fungal realm, the program will add an important airborne perspective to ongoing perspectives

focused on soil (Tedersoo et al., 2014; Bahram et al., 2018) and water (<http://pk.emu.ee/en/structure/hydrobiologyandfishery/research/projects/international-projects/funaqua/>). While we have focused here on fungal diversity, samples collected by the GSSP network can potentially also be utilized for other taxonomic groups such as plants where the same sampling method has been successfully applied (Brennan et al., 2019). The GSSP network is open to new sampling teams, and thus we encourage new members to join (<https://www.helsinki.fi/en/projects/lifeplan>), especially from locations that are currently poorly covered.

DATA AVAILABILITY STATEMENT

Raw sequence data were deposited into ENA, accession PRJEB33255 (<https://www.ebi.ac.uk/ena/browser/view/PRJEB33255>).

AUTHOR CONTRIBUTIONS

OO, NA, PS, BH, and TR initiated the GSSP network. NRA, PN, NS, SS, and JV collected the data. IP, BH, and J-MP acted as project coordinators, and IP processed the samples in Helsinki. EZ and NI conducted DNA extraction, sequencing, and bioinformatics analyses. PS and OO conducted the statistical analyses. OO, NA, IP, and NI wrote the first draft of the manuscript. All authors contributed substantially to the revisions.

FUNDING

The research was funded by the Academy of Finland (Grant 309581 to OO, and postdoctoral Grant 308651 to NA), the Jane and Aatos Erkko Foundation, and the Research Council of Norway (SFF-III Grant 223257), the Australian Discovery Grant DP160101561 to NRA.

ACKNOWLEDGMENTS

We thank Victoria Eisenbach for acquiring the samples from Hainich, and Arusyak Abrahamyan for preparing plasmids for the synthetic positive control.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fevo.2019.00511/full#supplementary-material>

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