of microscopic diversity and reduces the well-known taxonomic bias in favour of easily identifiable taxa and against cryptic biodiversity. By combining morphological and molecular biodiversity in a single taxonomic backbone using Linnaean names, OTU codes, and molecular occurrence data from BOLD, UNITE, EMBL-EBI, and SILVA, the GBIF network will address major spatial, temporal, and taxonomic biases while supporting scientific efforts to understand functional biodiversity. GBIF promotes open data while protecting data provenance through data citation, and new API-based tools will further scale up cross-platform data integration and data indexing. These efforts address the growing need for easily accessible molecular biodiversity evidence.

Effects of climate-induced tree-dieback on freshwater and Malaise trap communities in the Bavarian Forest National Park

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Background: Mountain forest ecosystems are under increasing pressures. Rising global temperatures lead to increased frequency of droughts and pathogen outbreaks, which in turn lead to drastic changes in forest structure and widespread die-off of key tree species. How these forest die-offs affect arthropod communities and biodiversity overall is not well understood, and current biomonitoring methods are inadequate for large-scale quality assessments. The Bavarian Forest National Park has a long history of research on mountain forests, in particular on spruce (*Picea abies*), and an ongoing insect monitoring program. **Results:** We used Malaise traps to sample invertebrates in 30 plots within three different forest habitats (intact, naturally disturbed, salvage-logged) along an elevational gradient over four months in summer 2017 for a total of 240 samples. We used kick-netting to sample invertebrates in 30 stream sites within the same forest habitats. DNA was extracted from subsamples and metabarcode libraries (313 bp COI) were sequenced with Illumina MiSeq. We used replicate PCRs ($n = 3$) and twin-tagging, together with a mock community and negative controls, in order carry out stringent filtering. To date, >4000 operational taxonomic units (OTUs) have been identified for the Malaise traps, with >70% belonging to Diptera or Hymenoptera and Ichneumonidae being the most diverse family (>800 OTUs). **Significance:** The project is part of a larger effort that combines ecological and socio-economic approaches to understand mountain forest die-back and its implications for biodiversity. Our specific goal is to develop a fast, repeatable, and reliable method for biomonitoring of terrestrial and aquatic invertebrates in mountain forests that will help practitioners such as national parks and forest owners. We hope to further our knowledge of methodological processes and techniques to make monitoring results in the future more comparable and standardized, and to gain additional insights into the ecology of invertebrate communities in mountain forest habitats.

Multiplexed chloroplast and nuclear marker sets for differentiation of 19 relevant poplar species for breeding

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Background: The genus *Populus* includes about 30 species classified in six sections, where some are cross-compatible even between sections. Therefore, many naturally and additionally, due to breeding programs, artificially produced hybrids exist, often without any information about involved species. Due to the very high variability of *Populus* hybrids, species identification using morphological characters is sometimes difficult. For this reason, we combined classical barcoding markers with newly designed chloroplast and nuclear markers with the aim to develop sets of markers for the differentiation of the 19 most widely used poplar species. **Results:** We used 1–32 individuals per species for sequencing of a total of nine chloroplast and four nuclear regions. Overall, we found species-specific SNPs or indels for 14 of the 19 species in chloroplast and 17 out of 19 species in nuclear regions. Nucleotide diversity in the analysed regions varied among species and was highest for the three species of the section *Populus* (*P. alba*, *P. tremula*, *P. tremuloides*) followed by the Aigeiros species *P. nigra*. We developed methods to identify species by either species-specific nucleotide variations or, without initial information for the species, by using markers either in a step-wise procedure of exclusion or in a multiplexed marker set. The two species *P. koreana* and *P. ussuriensis* are not distinguishable by applying both procedures. **Significance:** Hybrids between various *Populus* species belonging to the same or different sections are commonly used in short rotation coppices for biomass production because of their superior growth and advanced resistance traits. We present a comprehensive study on the identification of a high number of *Populus* species that, to our knowledge, have not been performed across such a wide range and with feasibility in any laboratory.

Barcoding Canada's ecozones: past progress, future steps

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DNA barcode reference libraries are the foundation for scalable, high-resolution biosurveillance systems. Over the past 15 years, 2.1 million Canadian specimens have been barcoded, providing coverage for 77 391 BINs and 31 253 named species. Most of these records (95.2%) derive from terrestrial settings; just 4.8% derive from the marine environment although it comprises more than a third of Canadian territory. The differences are even more profound when one considers coverage from an ecozone perspective. Coverage for the 15 terrestrial ecozones averages 129 909 records but ranges from 2463 records (Taiga Shield) to 582 663 (Mixed Wood Plain). Coverage for the 12 marine ecozones is far lower, averaging 5591 records and ranging from a low of just 58 (Arctic Archipelago) to a high of 22 617 (Strait of Georgia). The average number of records on an areal basis differs by more than an order of magnitude between marine and terrestrial settings (1.2 vs. 19.5 records per 100 km²). When viewed at a species level, coverage for marine phyla ranges from near zero for bryozoans, ctenophores, and nematodes to 56.6% for arthropods. Moreover, many species in the oceans await discovery as metabarcoding studies on marine benthos indicate high diversity. Studies are now underway to strengthen coverage in marine environments through studies on hyperdiverse groups such as harpacticoid copepods and nematodes that have seen little prior investigation.

Identification of tree species in wood composite products by DNA barcoding

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Background: In Europe and in the USA, the detailed labeling of imported wood is an attempt to control illegal logging. Finding out the mixture of species in wood composite products poses a great challenge due to the use of different wood species in one product; the exposure of wood to chemicals, heat, and pressure during the production process; and the restricted applicability of wood anatomical methods. **Results:** Wood composite products often consist of wood from several tree species, which may belong to the group of angiosperms as well as to the gymnosperms. We are developing a set of genetic markers for the differentiation of kinds of frequently used wood on different taxonomic levels. The combination enables the development of an application protocol for an individualized and minimized marker set for each genus and species of interest. The marker development is based on a genome-wide identification of SNPs and InDels in chloroplast and mitochondrial genomes. For the differ-