institutions to set up the German Barcode of Life (GBOL) initiative. The main goal was to establish a network of professionals and non-professionals to begin with the construction of a DNA barcode reference library for the fauna, flora, and fungi of Germany. Most project goals of the first phase (2011–2015) have been achieved: a national web portal for DNA barcodes and specimen data was developed and is continuously improved (www.bolgermany.de); over 250 independent scientists provide their taxonomic expertise and over 50 institution-based taxonomists contribute to GBOL. Especially, the engagement of external experts contributed significantly to the project's success: of the 48 000 animal and 10 000 plant species (excluding algae and fungi) present in Germany, over 23 000 different species plus a few selected rust fungi (Pucciniales) have been processed, and DNA barcodes for them were generated. In total, 295 000 specimens were submitted to GBOL institutes, and after choosing (usually) up to 10 individuals per species from throughout their distribution range in Germany, over 145 000 of them delivered a DNA barcode. The second phase of the initiative (2016–2018) is now focusing more on applications of DNA barcoding with seven dedicated PhD students working on specific aspects from metabarcoding for water quality assessments to developing a diagnostic microarray chip for the detection of phytopathogenic fungi. As a prerequisite for the successful implementation of the new techniques, a core team and network of taxonomists are further expanding the reference library with DNA barcodes for another 13 800 species. With this target the database will be filled with about half of the known metazoan species of German animals and plants and be operable to identify the vast majority of organisms in terrestrial and aquatic environmental samples.

Testing the Global Malaise Trap Program: how well does the current barcode reference library identify flying insects in Germany?

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Background: Biodiversity patterns are inherently complex and difficult to comprehensively assess. Yet, deciphering shifts in species composition through time and space are crucial for successful management of ecosystem services, as well as for predicting change. To better understand species diversity patterns, Germany participated in the Global Malaise Trap Program, a worldwide collection program for arthropods using this sampling method followed by DNA barcode analysis. Traps were deployed at two localities: Nationalpark Bayerischer Wald in Bavaria, the largest terrestrial Natura 2000 area in Germany, and the nature conservation area Landskrone, an EU habitats directive site in the Rhine Valley. Arthropods were collected from May to September to track shifts in the taxonomic composition and temporal succession at these locations. **Results:** In total, 37 274 specimens were sorted and DNA barcoded, resulting in 5301 different genetic clusters (BINs, Barcode Index Numbers) with just 7.6% of their BINs shared. Accumulation curves for the BIN count versus the number of specimens analyzed suggest that about 63% of the potential diversity at these sites was recovered with this single season of sampling. Diversity at both sites rose from May (496 and 565 BINs) to July (1236 and 1522 BINs) before decreasing in September (572 and 504 BINs). Unambiguous species names were assigned to 35% of the BINs (1868), which represented 12 640 specimens. Another 7% of the BINs (386) with 1988 specimens were assigned to genus, while 26% (1390) with 12 092 specimens were only placed to a family. **Significance:** These results illustrate how a comprehensive reference library can identify unknown specimens, but also reveal how this potential is constrained by gaps in the quantity and quality of records in the Barcode of Life Data System (BOLD), especially for Hymenoptera and Diptera. As voucher specimens are available for morphological study, we invite taxonomic experts to assist in the identification of unnamed BINs.

Authenticating fish and seafood products for sale on the Belgian market

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Background: Due to the international importance of fish and seafood trade, there is a large potential for (un)intentional misidentification and (or) deliberate fraud through species substitution. Several studies worldwide indicate that this is common practice, especially for processed products that lack characterizing morphological features (e.g., fillets). More stringent regulation on foodstuff labelling is supposed to enhance traceability, and protect consumers and the seafood industry from (un)intentional mislabeling. For Belgium, which has a higher per capita fish consumption than the EU average and a seafood import rate of 54% (42% of the total import comes from outside the EU), a study on samples collected from restaurants exposed a 32% incidence of fish mislabeling. In the present study, we sampled fish and seafood at various supermarkets and fishmongers to evaluate the frequency of seafood mislabeling on the Belgian retail market including a broad range of taxa and processing methods (e.g., fresh, frozen, smoked, pickled, cooked, fried). **Results:** Due to the large range of taxa being analyzed, several technical aspects concerning marker choice, primer selection, protocol optimization, and interference as a result of food processing are being encountered, analyzed, and improved. Preliminary identification results uncovered mislabeling of several samples; however, at this stage, there does not yet appear to be a pattern towards specific taxa or treatments. **Significance:** Although past seafood fraud studies investigated different taxa, processing methods, and purchase locations, they all seem to indicate that the scale, as well as the product most prone to mislabeling, differs by country. The present exploratory survey, including a broad taxonomic range of seafood species, therefore aims to identify those fish and seafood products (species and processing) most subjective to mislabeling in Belgium, while also further optimizing the identifications techniques.

Aliens in Europe

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Background: An increasing number of species are being introduced into Europe, either by accident or deliberately. Some are able to establish viable populations and may outcompete other species or disrupt ecosystem functioning: these species are called invasive alien species (IAS). In order to (i) protect native biodiversity and ecosystem services, and (ii) mitigate potential impacts on human health and socio-economical activities, the European Commission issued *Regulation 1143/2014*, reporting on 37 IAS. The Regulation foresees three types of interventions: (i) prevention, (ii) early detection and rapid eradication, and (iii) management of established populations. Aside from compiling this list and gathering information on presence, distribution, ecology, impacts, and management, accurate methods for rapid identification are required when suspicious biological material is being encountered. In cases where a morphological identification is problematic (e.g., cryptic species, trace material), DNA-based identifications may represent an alternative method. The purpose of the present work is, therefore, to investigate and evaluate the available molecular identification techniques for each IAS in silico. **Results:** We investigated the usefulness and accurateness of the Barcode of Life Data System (BOLD) (COI for animals; *rbcL*,