However, data analysis procedures and assignment tools can influence species detection ability. In a previous study, we tested five COI primer pairs in two mock communities (MC1 and MC2), each containing 21 macrobenthic species in different proportions, using a Roche-454 platform. **Results:** Here, we compare the detection success obtained for the same communities with an Illumina-MiSeq platform using (*i*) one of the five COI primer-pairs (ArF2/ArR5) and (*ii*) a primer pair targeting an alternative marker (V4 region of 18S rDNA). Furthermore, in both platforms we tested the impact of species assignment tools using two different approaches: read-based assignment and OTU-based assignment. BOLD and SILVA databases were used, respectively, for taxonomic assignment of COI reads/OTUs and 18S OTUs with ≥97% similarity. Compared to 454, in MiSeq platform the detection success increased in both communities (MC1: 43% vs. 52%; MC2: 43% vs. 62%). Using the V4 region, species-level resolution was only attained for *Lepidochitona cinerea*. Moreover, some taxa were detected solely by V4, demonstrating a tendency to detect preferentially other taxa than target macrobenthic species. Compared to the individual read-based assignments, OTU-based assignments resulted both in a lower detection success of the target species, together with an excess of putative taxonomic units, i.e., multiple OTUs produced for the same species, resulting in an overestimation of species richness. **Significance:** High-throughput sequencing (HTS) platforms with deeper sequencing capacity can improve species detection success. COI performance in macrobenthos detection remained superior to V4, showing higher recovery rates and species-level resolution. To avoid potential operational artifacts, circumvent OTU-clustering, and to improve the performance of HTS-based macrobenthos monitoring, more efforts should be allocated to the completion of reference libraries.

The mystery of muthi: unveiling the identity of bulbous and perennial plants traded at the Faraday Medicinal Market, Johannesburg, using DNA barcoding

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Background: The South African medicinal market generates ~2.9 billion ZAR per annum, providing a fundamental source of income but comes at the expense of the environment. Most plants traded at these markets are harvested from wild resources, resulting in noticeable levels of species depletion. Adulteration, trade using vernacular names, and morphological similarities of plants, or lack thereof, make identifying samples on a taxonomic level challenging. In this study, DNA barcoding was implemented to rapidly identify bulbous and perennial plants traded at Faraday, South Africa. A list of species traded, including their conservation status, was compared against a known published checklist. **Results:** Sixty samples were collected and sequenced for the core barcoding regions. Three identification methods were used namely, BLAST (Basic Local Alignment Search Tool), Tree-based, and BRONX (Barcode Recognition Obtained with Nucleotide eXposés), permitting 76%, 64%, and 88% of the samples to be identified to species level, respectively. When comparing the final vernacular identities to the proposed scientific names, 20% of the samples matched to species level and 17% matched to genus level. Of the samples, 37% did not link to proposed scientific names, although sharing the same vernacular names, and 26% of the given vernacular names had no proposed scientific names. **Significance:** The high level of disagreement between the vernacular and scientific names indicate instances of misidentification or substitution, emphasising the eminent threat of health risks for end users. Results from this study reveal a noticeable increase in the number of species traded with the majority of sought-after species being of Least Concern. However, 10% of the species are Declining or Near Threatened in the wild, posing serious conservation issues. A prolonged unsustainable trade of these plants could lead to more Critically Endangered species status in future.

Museum harvesting in major natural history collections

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Background: Large natural history collections are a crucial resource of diverse and rare specimens, but their genetic reserves are underutilized. For the last decade, the Centre for Biodiversity Genomics (CBG) has worked to reverse this trend and has set the standard for DNA barcode-based museum processing pipelines. Past efforts were often limited by specimen age, preservation method, and ultimately DNA quality. However, recent advances in high-throughput sequencing (HTS) technologies have made it possible to amplify and sequence DNA from old and rare specimens, even with very limited quantities of DNA. CBG's partnership with the National Museum of Natural History (NMNH) in Washington DC is an exemplar of this system, which incorporates both Sanger- and HTS-based methods to maximize sequencing success rates based on predicted DNA quality. **Results:** To date, over 120 000 specimens from the NMNH have been DNA barcoded and deposited in the Barcode of Life Data System (BOLD). The current focus of this partnership remains on building the barcode reference library of North American Lepidoptera, which is nearing completion. However, efforts have recently expanded to include barcoding the world genera of Lepidoptera, where significant progress can be made at the NMNH due to its vast archives of authoritatively identified material from around the globe. In parallel, the CBG is also working towards completing barcode coverage for every insect family with the assistance of the NMNH. **Significance:** While contributing valuable digitization services to participating institutions, the CBG's museum harvesting pipeline is also producing an invaluable reference barcode library for BOLD, and for the community as a whole. This resource is of critical importance for parameterizing the BOLD Identification Engine, and it will undoubtedly assist its users with the discovery of new, rare, and exciting taxa.

The application of DNA barcoding for the identification of invertebrates, at the Ministry for Primary Industries, New Zealand

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Background: Since DNA barcoding was proposed in 2003, its application for the identification of invertebrates has increased dramatically. It is now widely used as an effective tool that enables rapid and accurate identification of invertebrates for diagnostic purposes. **Results:** Since 2008, DNA barcoding has been applied for routine identification of border interceptions and surveillance samples by the entomology team at Plant Health & Environment Laboratory (PHEL), Ministry for Primary Industries (MPI), New Zealand (NZ). DNA barcoding has provided species-level identification for immature stages and damaged specimens where identification with morphological characters was impossible. DNA barcoding was applied by PHEL for the following: (*i*) Border interceptions: Since 2015, around 500 individual specimens were barcoded each year, which has greatly assisted in the identification of the immature stages of intercepted organisms. Each species-level identification allows the assignment of accurate regulatory status, thus reducing fumigation, which is beneficial to both importers and environment; (*ii*) General surveillance: A DNA barcoding reference library was constructed for samples collected from various locations in NZ. To date, this library includes around 400 sequences, with novel DNA barcode sequences endemic to NZ, building up baseline information for NZ species, and providing a reference for identifying new to NZ species; (*iii*) DNA barcoding