From BINs to biodiversity: rapid arthropod assessments using DNA barcodes

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The vast majority of animal species in terrestrial ecosystems are arthropods, yet contemporary environmental assessments all but ignore this massive assemblage, and its susceptibility to disturbance is unmeasured. We address this shortfall through a time- and cost-efficient approach for terrestrial arthropod assessments based on DNA barcode analysis of specimens collected by Malaise traps. In a study we conducted in 2012 comparing several standardized techniques, Malaise traps were found to be the most efficient sampling method in terms of capturing the largest proportion of the arthropod assemblage with minimal effort. The material collected by Malaise traps are currently individually sorted, analyzed in a 384-well pipeline, and Sanger-sequenced; this approach permits the link between each barcode record and its source specimen to be maintained, and facilitates the construction of a barcode reference library based on carefully identified specimens. The assignment of taxonomy following analysis is achieved through matches with authoritatively identified records on Barcode of Life Data Systems (BOLD 2014, http//www.boldsystems.org/) and by collaborating with taxonomic specialists. This approach is currently employed in several ongoing studies, including a multi-year project inventorying arthropods in all of Canada's 45 National Parks (CNP). The CNP project is currently running in its third year, and has completed analysis for the first year of field collection. In 2012, 14 sites and 189 weekly malaise samples were processed, to reveal nearly 150 000 specimens, and over 15 000 distinct Barcode Index Numbers (BINs), a reliable proxy for species. Another effective application of this approach involves the early detection of non-indigenous species (NIS) at Canada's ports. The Halifax Port project has analysed 20 weekly samples from a single Malaise trap in the vicinity of the port, and revealed several potential and known NIS, including the recently discovered beech flea weevil (*Orchestes fagi* (Linnaeus, 1758)). In the near future, this approach will require a shift to Next Generation Sequencing (NGS) to facilitate time- and cost-efficient sequencing of bulk samples. Initial NGS trial runs have resulted in high BIN recovery for bulk samples (> 95 %), but some analytical biases (such as amplification and body mass bias) require further fine-tuning of protocols. The integration of NGS analyses with DNA barcode reference libraries could ultimately set the global standard for rapid biodiversity assessment, one that finally includes the terrestrial arthropod component.

BOLD 2014. Barcode of Life Data Systems. http//www.boldsystems.org/ [accessed 06-Oct-2014]

DNA barcode enabled ecological research on Geometridae in Papua New Guinea

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DNA barcoding of the Geometridae of Papua New Guinea provides a framework for multiple lines of systematic and ecological research, as part of a large-scale study of insect-plant ecology and biogeography in forests in Papua New Guinea by the Binatang Research Centre (Novotny et al. 2010). The foundation of the program has been characterization of the insects reared from woody plants, but we are increasingly combining those data with bioassessments of adults using light traps (Pagi et al. in preparation). DNA barcoding provides a rapid and accurate taxonomic framework, which is also instrumental in analysis of phylogeographic patterns (Craft et al. 2010), identifying caterpillars (Miller