The Ontario Bioblitz: Exploring Biodiversity and Connecting a Community

Applications
Searching for Substitutions in a Natural Sweetener

Research
Uncovering the Truth About the Moa

Cover Photo: Vincent Luk
Planning is now underway for the 6th International Barcode of Life Conference which will be held from August 18th to 22nd, 2015 at the University of Guelph in Ontario, Canada. The conference will feature four full days of plenary and parallel sessions, a poster session, an evening keynote address, and multiple excursions to renowned Ontario destinations. A range of pre-conference workshops will also be offered to attendees. Additional details will be made available on the conference website, dnabarcodes2015.org, as they emerge.

Through a $2.5 million project launched on the International Day of Biodiversity, researchers aim to enhance our understanding of Australian biodiversity using DNA barcoding. Andrew Lowe at the University of Adelaide will lead this highly collaborative project, which involves partnerships among numerous institutions: Kings Park Botanic Garden, CSIRO, Australian Tropical Herbarium, the South Australian Museum, ARC Centre of Excellence in Plant Energy Biology, and WA Department of Parks and Wildlife. Bioplatforms Australia, a research infrastructure organization, will manage the project and provide genomics and bioinformatics support. Specific research themes of this project include mapping biodiversity of plants and invertebrates for environmental impact assessments in mining and farming localities, promoting conservation of Australia’s orchids, and combating illegal logging as well as mislabeling in seafood markets.

An international group of researchers led by Marko Mutanen at the University of Oulu has received €570K from the Finnish Academy to explore several phenomena of barcode datasets. This research aims to better understand non-monophyly, deep splits, and barcode-sharing, among others, through genomic scans of selected target species using next-generation sequencing and methods such as RAD-Seq.
If staying enigmatic would warrant evolutionary success, they would be among the most successful animal groups on Earth; Protura, also referred to as coneheads, are a group of primarily wingless insects. First described just over a century ago, a concealed distribution of morphological diversity motivated only a handful of committed taxonomists to carve out phylogenetic signal from cryptic characters.

Our recent study thus aimed to test the accuracy of these inconspicuous diagnostic characters by a barcoding approach based on two independent markers: the standard barcoding fragment and a fragment of the nuclear 28S rDNA gene after Non-Destructive DNA-Extraction. Not only is the signal from both markers fully congruent with the current taxonomy, we likewise were able to characterize a species new to science with both morphological and molecular characters.

The most interesting outcome, however, lies in the distances among different populations of what is currently assessed to be the same species. Not surprisingly, populations of proturan species can be differentiated by both markers, given that the dispersal ability of these animals is highly limited by both their small size (with body lengths of 1mm and below) and their hidden life style in the soil. With intraspecific distances of up to 21.3%, coneheads are among the record holders of within-species variability. This is even more remarkable considering that the three populations chosen for this study by far do not cover the distributional range of the studied species.

Two of the most important lessons we can learn from coneheads are: Firstly, even a high mismatch regarding observable diversity between morphological and molecular data does not necessarily result in incongruent phylogenetic signal from these data sets. Secondly, the restriction of biodiversity to species numbers is highly prone to underestimations, especially in organisms with restricted dispersal ability.

Future work will focus on some important points: (i) The protocol will be improved to allow for a more standardized barcoding approach for Protura. (ii) The range of sampled localities will be widened, both to cover more species and a higher number of populations within each species. (iii) The results will be compared to other groups of soil-living arthropods. All of these studies will be incorporated into the newly launched ABOL-Initiative (Austrian Barcode of Life).