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The complete picture: An update on the rapid biological inventory of a temperate nature reserve using DNA barcoding

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Abstract

In 2015 a rapid, barcode-assisted all taxon biodiversity inventory was completed at the *rare* Charitable Research Reserve in Cambridge, Canada. Two approaches were used – a seven-month sampling program and a 24 hour bioblitz, each employing a variety of collecting techniques. 48,551 specimens were processed resulting in 5,440 BINs (Barcode Index Numbers). A complete checklist of all taxa was produced with 4,276 distinct taxa, making *rare* one of the best inventoried protected areas in North America. This study demonstrates how DNA barcoding can complement traditional surveys and provide valuable occurrence data for difficult and small-bodied groups often disregarded.

Introduction

An all taxon biodiversity inventory (ATBI) is a comprehensive census of life for a given area. While informative for tracking changes over time and space, these inventories are difficult and rarely completed due to a substantial bottleneck at the identification stage.[1,2,3] DNA barcoding has proven invaluable for accelerating this task, allowing for rapid assessment of protected areas.[4,5]

Materials & Methods

Sampling sites were chosen to represent a wide variety of habitats situated on the ***rare*** property. Comprehensive passive sampling using Malaise traps and pitfall traps were run from April to October 2015. A standardized sampling regime was deployed for two seven day periods that included Malaise, pan, pitfall, intercept, Berlese and sweep trapping methods.

A 24 hour bioblitz occurred on August 15, 2015 to coincide with the 6th International Barcode of Life Conference. Over 100 delegates participated by collecting, sorting and identifying organisms of animals, plants and fungi.

Samples were selected for processing and subjected to arraying, databasing, tissue sampling, DNA extraction, PCR amplification and sequencing of the COI barcode region, and data analysis.

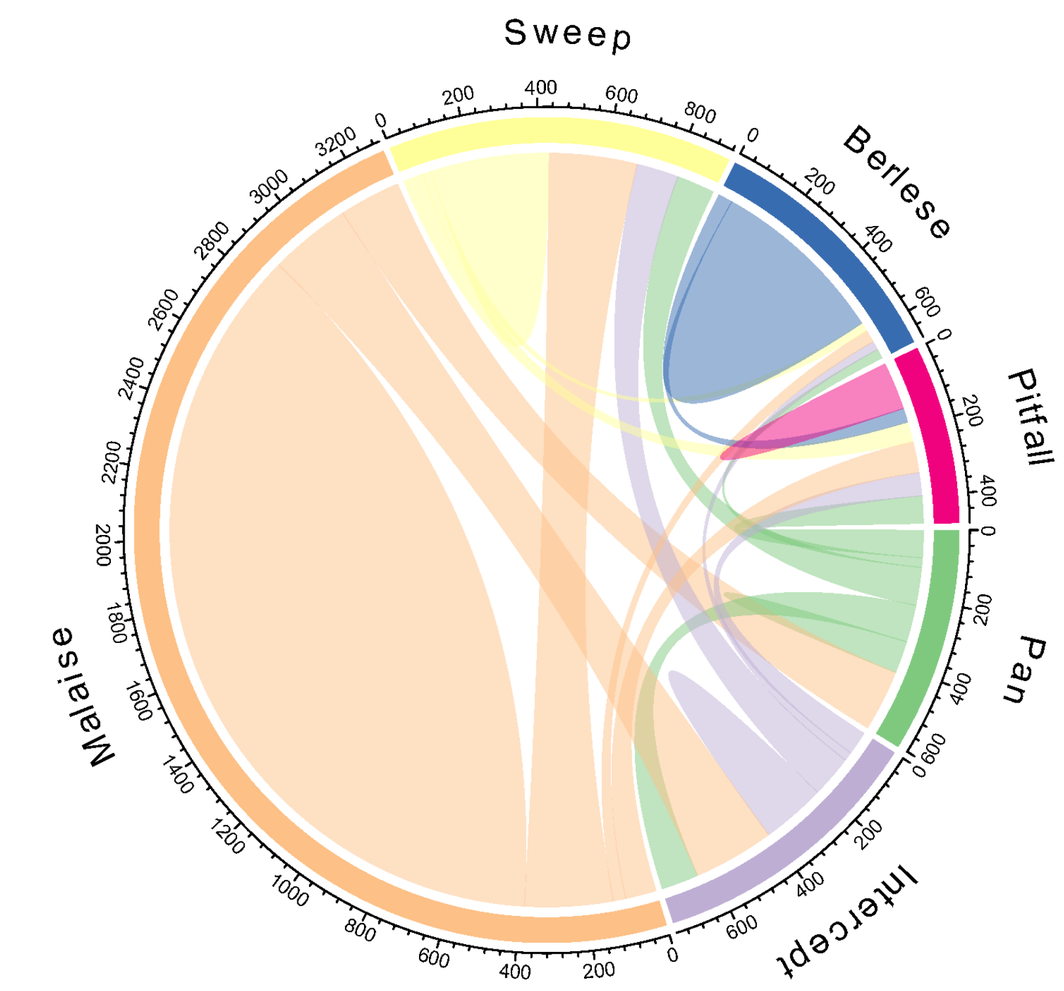

Figure 1: Chord diagram showing species overlap between trap types.

Results

48,551 specimens were processed resulting in 5,440 individual BINs. Diptera and Hymenoptera dominated by representing 40% and 19% of BINs, respectively. Malaise traps were the main source of specimen collection and caught the highest proportion of BINs (Figure 1). Berlese funnels resulted in the most BINs unique to a single collecting method.

An updated checklist was generated adding 1841 species to the existing list of 2130, an increase of 48%. The number of species added for some taxa was significant; arachnids for instance added 224 species (Figure 2). Accumulation curves indicate that sampling is nearly complete for most major taxa, with the exception of Diptera and Acari (Figure 3).

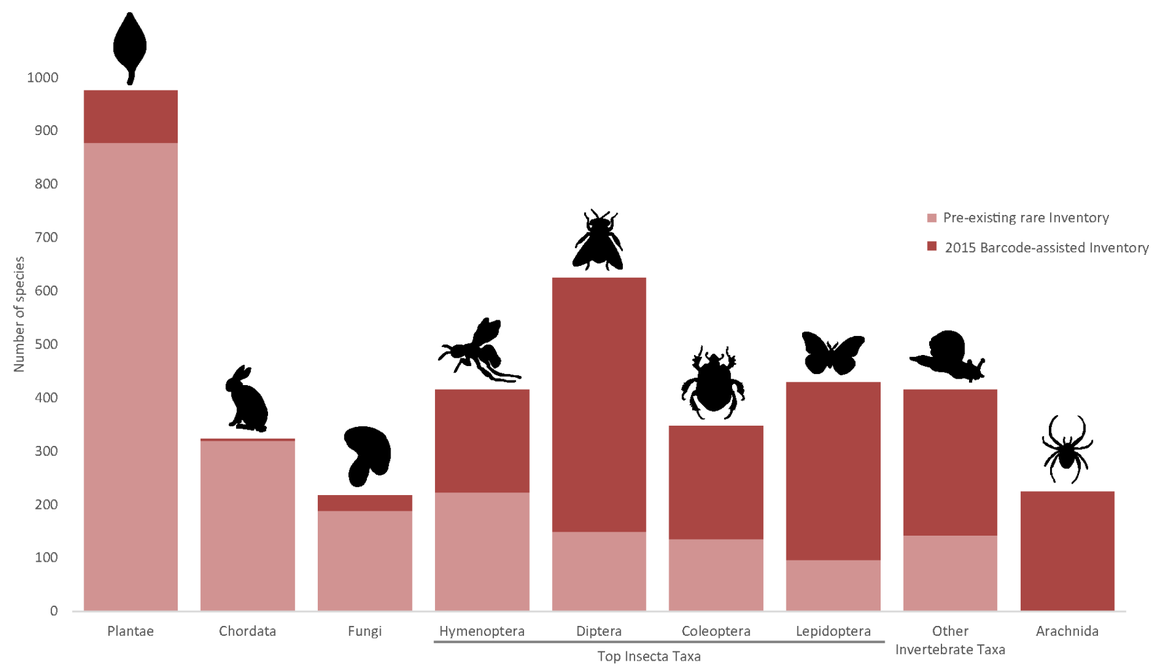

Figure 2: Breakdown of named species following the recent barcode-assisted survey at ***rare***.

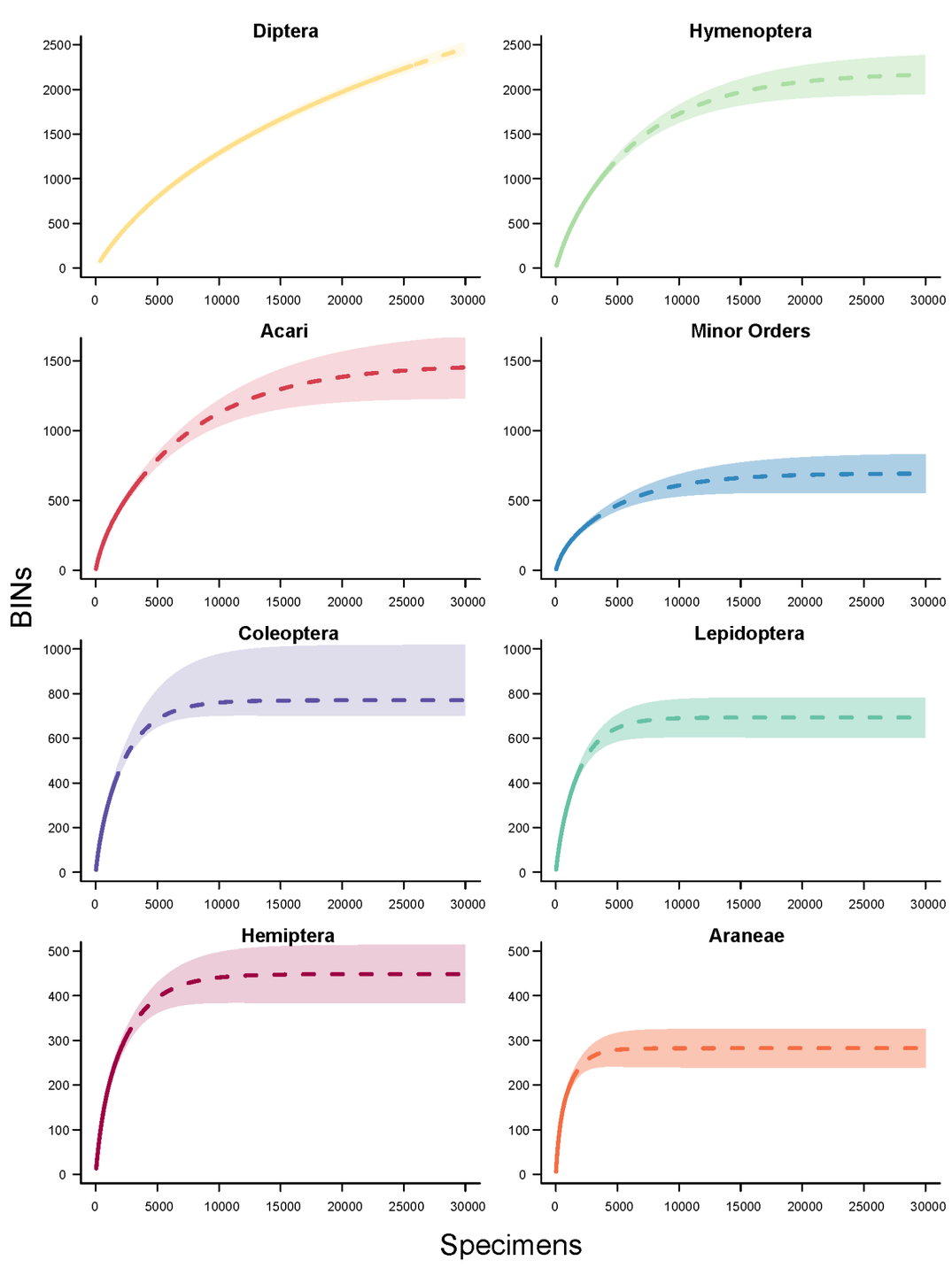

Figure 3: Species accumulation curves for the eight main taxa at ***rare***.

Discussion

DNA barcoding provides a significant advance for biodiversity inventories and assessments. By accelerating and automating the identification process, comprehensive taxon lists can be compiled in the absence of considerable resources and expertise.

Mass sampling, particularly with Malaise traps and other passive collection techniques, is important for maximizing taxon coverage in barcode-assisted surveys.

Combining the new 2015 inventory with the existing, traditional checklist has now made ***rare*** Charitable Research Reserve one of the best inventoried protected areas in North America.

References 1 Janzen D (1993) In: Sandlund OT, Schei PJ (Eds) Proc. Norway UNEP Expert Conference on Biodiversity, Trondheim. **2** Lawton JH, et al. (1998) Nature 391: 72-76. DOI: 10.1038/34166. **3** Janzen D (2004) Journal of Applied Ecology 41: 181-187. DOI: 10.1111/j.1365-2664.2004.00879.x **4** Hebert PDN, et al. (2003) Proceedings of the Royal Society B: Biological Sciences 270 (1512): 313-321. DOI: 10.1098/rspb.2002.2218 **5** Packer L, et al. (2009) Molecular Ecology Resources 9: 42-50. DOI: 10.1111/j.1755-0998.2009.02631.x

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