Appendix S5 – DNA barcode clustering (RAxML) for ant prey and non-ant prey

Hunting habits die hard: Conserved prey preferences in army ants across two distant neotropical rainforests

Philipp O. Hoenle, Christoph Merkel, David A. Donoso, Adriana A. Argoti, Nico Blüthgen, Christoph von Beeren

*Correspondence to:

Philipp O. Hoenle: philipp.hoenle92@gmail.com

Christoph von Beeren: cvonbeeren@gmail.com

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Figure S1. RAxML tree of ant prey.
Figure S2. RAxML tree of non-ant prey.

Figure S1. **RAxML tree of ant prey.** RAxML tree based on GTR GAMMA as substitution model of 523 *COI* sequences of ants collected as prey of army ants . We used the RAxML plugin for GENEIOUS PRIME (version 2020.2.1) to generate the tree. Terminal labels provide the following information: sample ID, BOLD BIN number, the order of prey items, and the species name as assigned in the present work. See also Appendix S4 for the comparison of sequences with a reference database of neotropical ant species. The scale bar indicates expected nucleotide substitutions per site as inferred by the RAxML algorithm. Bootstrap support values are shown at nodes (1,000 repetitions). Colors highlight the different species. For better visibility, this tree was rooted using the sequence of the paper wasps *Agelaia melanopyga*.

Figure S2. RAxML tree of non-ant prey. RAxML tree based on GTR GAMMA as substitution model of 120 *COI* sequences of non-ant army ant prey. We used the RAxML plugin for GENEIOUS PRIME (version 2020.2.1) to generate the tree. Terminal labels provide the following information: sample ID, BOLD BIN number, the order of prey items, and the species name as assigned in the present work. The scale bar indicates expected nucleotide substitutions per site as inferred by the RAxML algorithm. Bootstrap support values are shown at nodes (1,000 repetitions). Colors highlight the different species.