

Within the context of a species description or revision, the relevant information here is that:

- 1) The CO1 barcode was very easy to generate. While the majority of specimens analyzed here are between 1–2 years old, we did generate full length barcodes (>600 bp) for specimens up to 14 years old. Barcodes were generated with the same primers and reaction conditions. Alternatively, rRNA data, variable at a species level, was often challenging to generate (i.e. sequence) due to long regions of t-repeats and uncharacterized intra-individual variation (in ITS1).
- 2) We found no evidence for Numts [54] or other misplaced nuclear markers that would introduce conflict into our analysis if not spotted.
- 3) CO1 sequences never showed intra-individual variation as did some of the rRNA markers.
- 4) Although the species described here (especially *O. coquereli*, *A. goodmani* and *A. boltoni*) contain large CO1 divergences, such variation is always geographically segregated, as one might expect from a species where the queens (when known) are ergatoid.

In the worst-case scenario, by describing species containing large intra-specific CO1 divergences, we have missed morphologically cryptic diversity within these species. However, the DNA data, collection records, measurements and photo-digital accessions are all preserved in publicly accessible databases, facilitating the testing (and potential refutation) of our one-species hypothesis in the traditional, iterative, process of alpha-taxonomy.

### Collaborative Taxonomy

Species inventories are essential for documenting global diversity and generating necessary material for taxonomic study. However, for inventories to be relevant in the short term, the taxonomic process must reduce the bottlenecks in describing and identifying specimens. The sheer diversity of arthropods can easily overwhelm an inventory system with too many specimens, the bulk of which are outside the focal expertise of the taxonomists. As an example, the NSF-funded Arthropod Inventory of Madagascar has shipped over a third of million specimens to over 150 participating taxonomic collaborators [5]. Major taxonomic products from these inventories, which will take decades to produce, represent only a fraction of the diversity collected, and provide no short-term return of biodiversity data to Madagascar.

The development of “collaborative taxonomy” would permit researchers to participate collectively in an accelerated team-driven taxonomic process. Key participants in collaborative taxonomy are (i) inventory teams led by conservationists, ecologists, and taxonomists, (ii) traditional morphology-based taxonomists equipped with imaging tools, and (iii) geneticists. Under this plan, inventory teams would generate specimens and sequence data in collaboration with geneticists. Geneticists, in turn, would work directly with the taxonomist who identifies the need for additional sequencing of specimens. Taxonomists would then combine extensive sequencing data with their morphological and ecological analysis, assisted by new technologies in digital

imaging and web-based delivery (e.g. [www.antweb.org](http://www.antweb.org) and [www.barcodinglife.org](http://www.barcodinglife.org)), to infer species limits and frame evolutionary context for species.

Nothing can replace the countless hours of careful observation necessary to understand variation and to delimit species boundaries. However, the addition of sequence data provides a means to create short-term results from inventories and at the same time generate data helpful to taxonomists. For taxonomists, sequencing highlights the specimens most deserving of focused study. We tested this collaborative model by revising the ant genera *Anochetus* and *Odontomachus* of Madagascar using a combination of morphological and genetic character sets based on inventories in Madagascar.

### Future

This study demonstrates how sequence data, combined with morphological analysis and innovations in imaging and web delivery, have set the stage for accelerated discovery and documentation of global species diversity. The combination of DNA sequence data with inventory and traditional taxonomy is a model that can be applied across disciplines and will allow analytical needs to scale to the enormity of the biodiversity crisis [55]. It will help in the identification and conservation of the evolutionary processes that generate and preserve biodiversity.

Little time remains to document and protect global biodiversity. Taxonomists, equipped with modern tools and collaborations, have a chance to move systematics to the forefront of conservation and the public’s attention. With increased taxonomic output and improved public access and visibility, public support for the discovery of life on this planet will follow.

### Supporting Information

**Appendix S1** Accessions and collection information for all sequences created in this study.

Found at: doi:10.1371/journal.pone.0001787.s001 (0.64 MB XLS)

**Appendix S2** This is the current article provided as a TaxonX XML document. TaxonX models taxonomic treatments and allows semantic enhancement so machines can understand, mine and extract the content (see <http://plazi.org>).

Found at: doi:10.1371/journal.pone.0001787.s002 (0.11 MB RTF)

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### Author Contributions

Conceived and designed the experiments: BF MS. Performed the experiments: BF MS. Analyzed the data: BF MS. Contributed reagents/materials/analysis tools: BF MS. Wrote the paper: BF MS.

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