

A preliminary morphological and molecular phylogeny of the rove beetle genus *Phlaeopterus* (Coleoptera: Staphylinidae: Omaliinae: Anthophagini)



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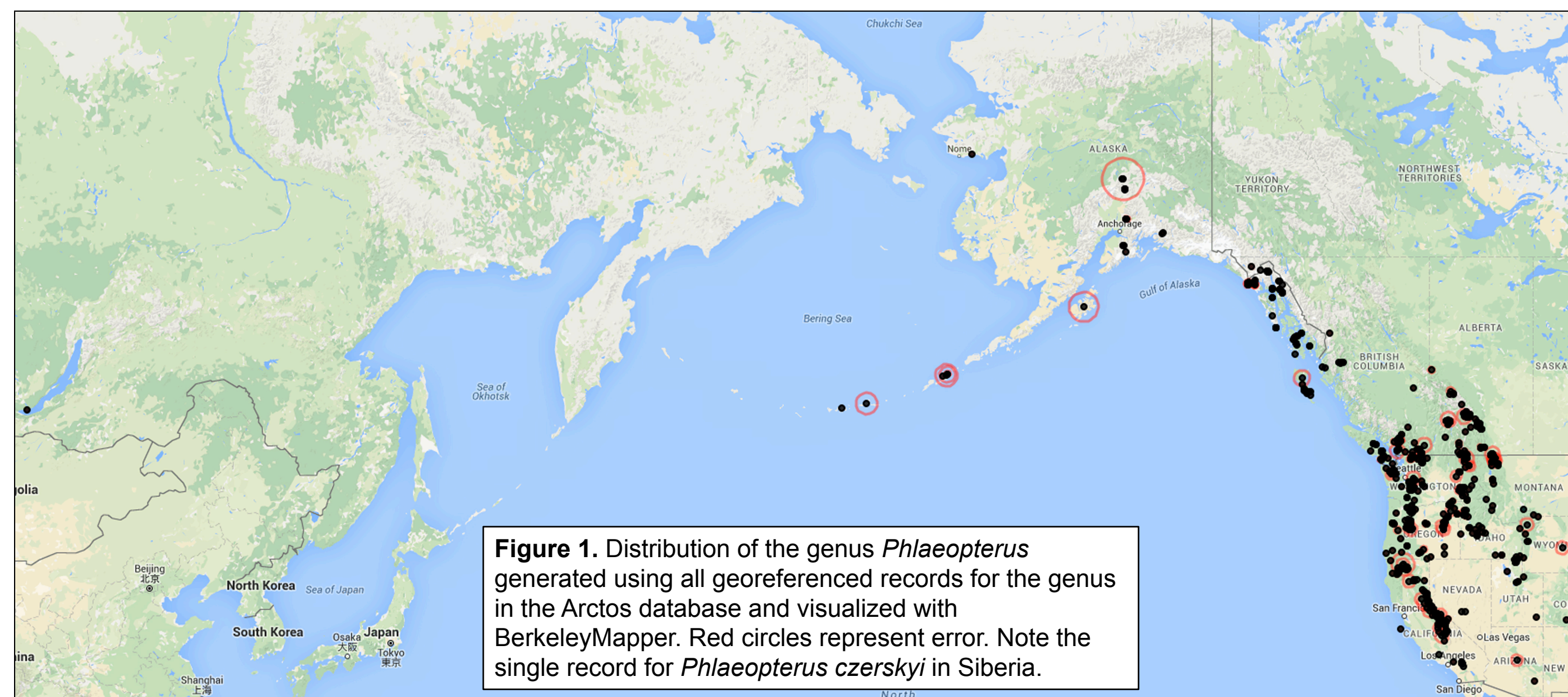
Introduction

The omaliine rove beetle genus *Phlaeopterus* Motschulsky 1853 contains 15 species, which are known from the northwestern United States, western provinces of Canada, Alaska, and Siberia. These beetles range in size from 3-10 mm in length, and seem to cluster in phylogenetically informative large- and small-bodied groups. Although *Phlaeopterus* has never been analyzed with modern phylogenetic methods, a taxonomic revision of the genus including 8 new species and the transfer of two *Phlaeopterus* species to the genus *Unamis* was drafted, but never published, by J.M. Campbell in the 1980's. Most recently a morphologically unique species from Siberia, *Lesteva czerskyi* Shavrin 2001, was moved into *Phlaeopterus* by Shavrin & Mullen (2015).

The objectives of this study are to test these published and unpublished taxonomic hypotheses of *Phlaeopterus* and develop a preliminary phylogeny of the genus using Bayesian analyses of morphological and molecular data.

Research Questions

- 1.) Do the small (<5 mm in length) and large (≥5 mm in length) *Phlaeopterus* species represent diagnosable monophyletic groups?
- 2.) Are the 8 new species proposed in Campbell's unpublished revision supported?
- 3.) Is Campbell's proposed transfer of *Phlaeopterus kootenayensis* and *Phlaeopterus stacesmithi* to the genus *Unamis* supported?
- 4.) How does the recently described and morphologically unique Siberian species *Phlaeopterus czerskyi* fit into the phylogeny of *Phlaeopterus*?



Methods

Morphological data

- 50 morphological characters were mined from Hatch (1957), Moore & Legner (1979), Campbell (unpublished), and Newton et al. (2000), and coded using MacClade 4.04 (Maddison & Maddison 2000)

Molecular data

- A 658 bp region of the mtDNA gene COI was sequenced for 66 specimens representing 10 species collected by the first author, donated by collaborators, or belonging to University of Alaska Museum Insect Collection
- Sequences were translated to amino acids, checked for stop codons and frameshifts, and aligned by eye using MacClade 4.04 and a reference sequence (Lunt et al. 1996)
- 38 additional sequences were downloaded from GenBank and BOLD

Model selection

- Morphology: Bayes Factors (Kass & Raftery 1995) were used to determine that gamma correction for among character rate heterogeneity was preferred with the MkV model (Lewis 2001)
- COI: Automated model selection in PAUP*4.0a136 (Swofford 2003) chose the general time reversal + proportion of invariable sites + gamma distribution (GTR+I+G) model under all criteria (AIC, AICc, BIC)

Tree searching

- Morphology, COI, and concatenated (morphology + COI) data sets were analyzed using MrBayes 3.2.0 (Ronquist et al. 2001), each retaining their respective best-fitting models
- MCMCMC chains were run for 2,000,000 steps sampled every 1,000 steps
- First 25% of samples were discarded as burn-in for each run, resulting in 1,500 trees sampled
- Tracer v1.6 (Rambaut et al 2014) was used to determine that runs had reached stationary (ESS values >1000 for all parameters)

Figure 2. Morphology: 50% majority rule consensus phylogram of 1,500 post burn-in trees using the MkV+G model in MrBayes 3.2.0 with all 18 *Phlaeopterus* species. Posterior probabilities are given above branches. Colored brackets indicate clades corresponding to species group hypotheses. All labeled subgenera and species groups are *sensu* Campbell (unpublished).

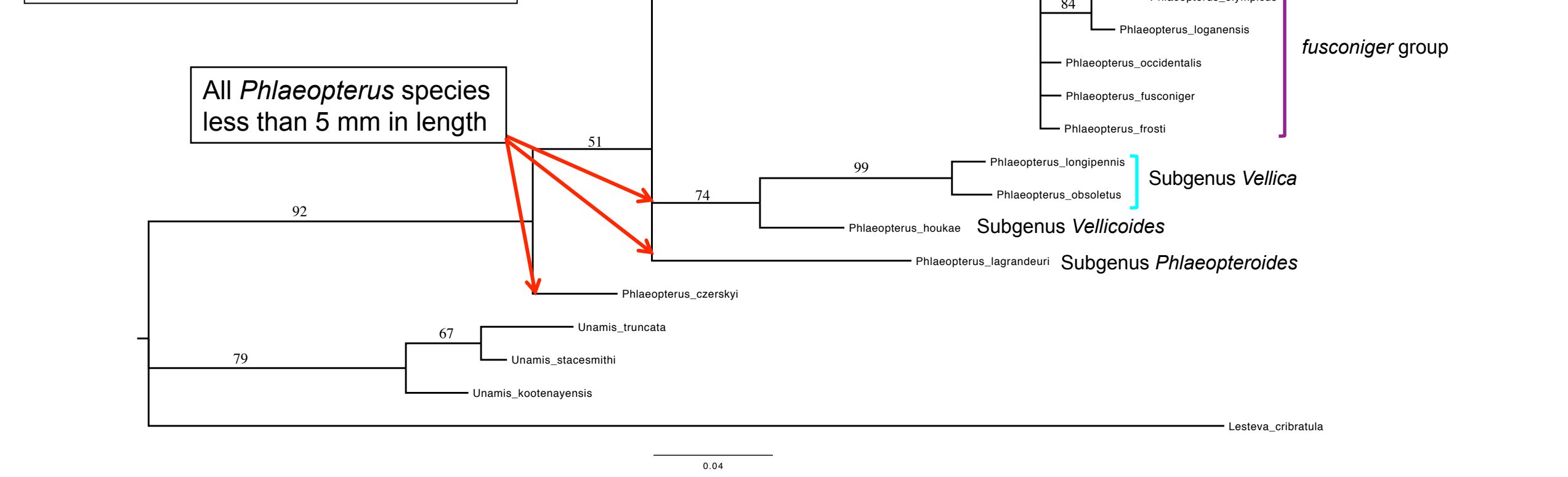


Figure 3. COI: 50% majority rule consensus phylogram of 1,500 post burn-in trees using the GTR+I+G model in MrBayes 3.2.0 with 9 *Phlaeopterus* species. Posterior probabilities are given above branches. Colored brackets indicate clades corresponding to subgenus and species group hypotheses from Figure 2. All labeled subgenera and species groups are *sensu* Campbell (unpublished).

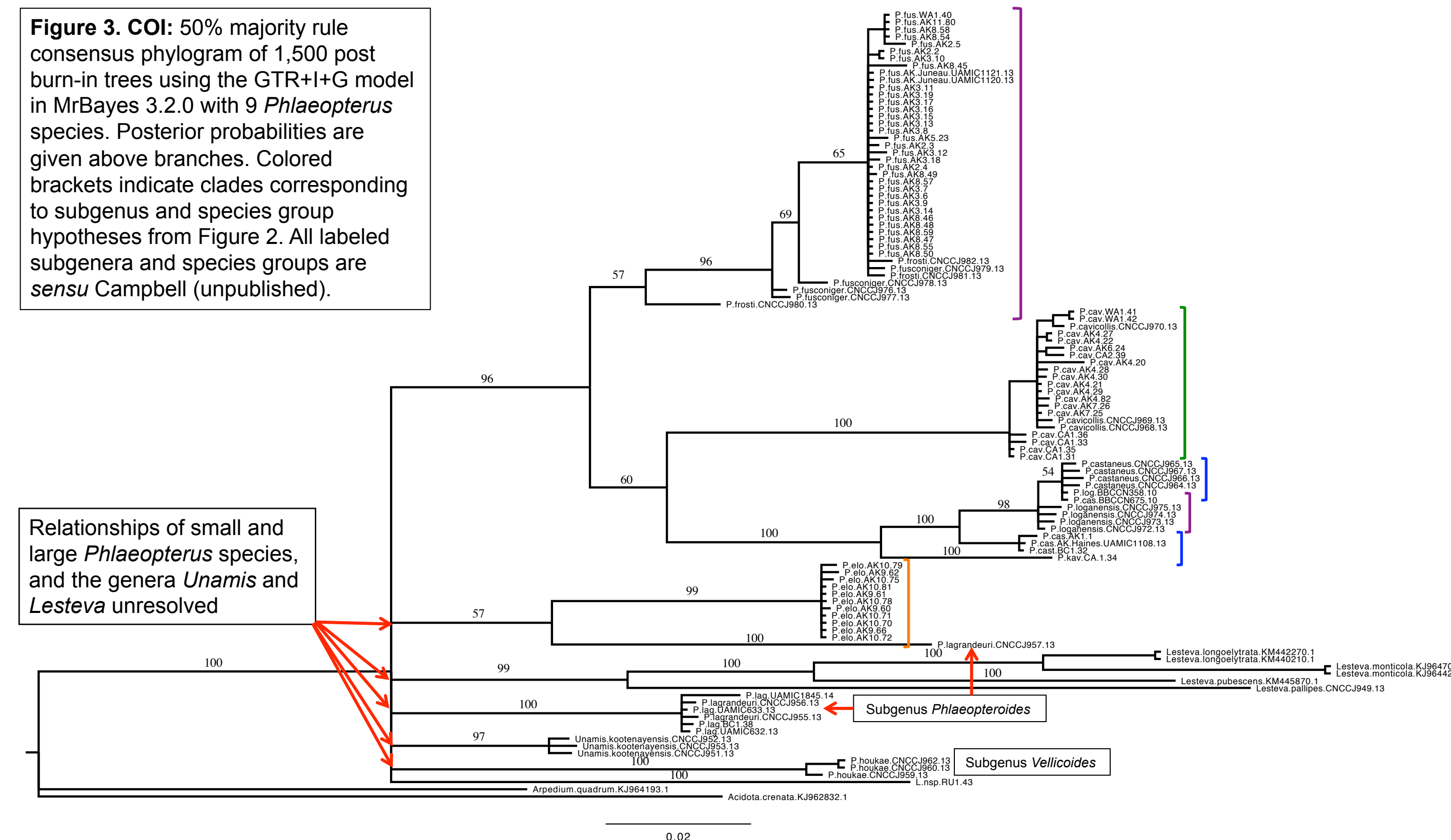


Figure 4. Morphology + COI: 50% majority rule consensus phylogram of 1,500 post burn-in trees of a concatenated analysis using the MkV+G model for the morphology partition and the GTR+I+G model for the COI partition in MrBayes 3.2.0 with 9 *Phlaeopterus* species. Posterior probabilities are given above branches. Colored brackets indicate clades corresponding to species group hypotheses as labeled in Figure 2. All labeled subgenera and species groups are *sensu* Campbell (unpublished).

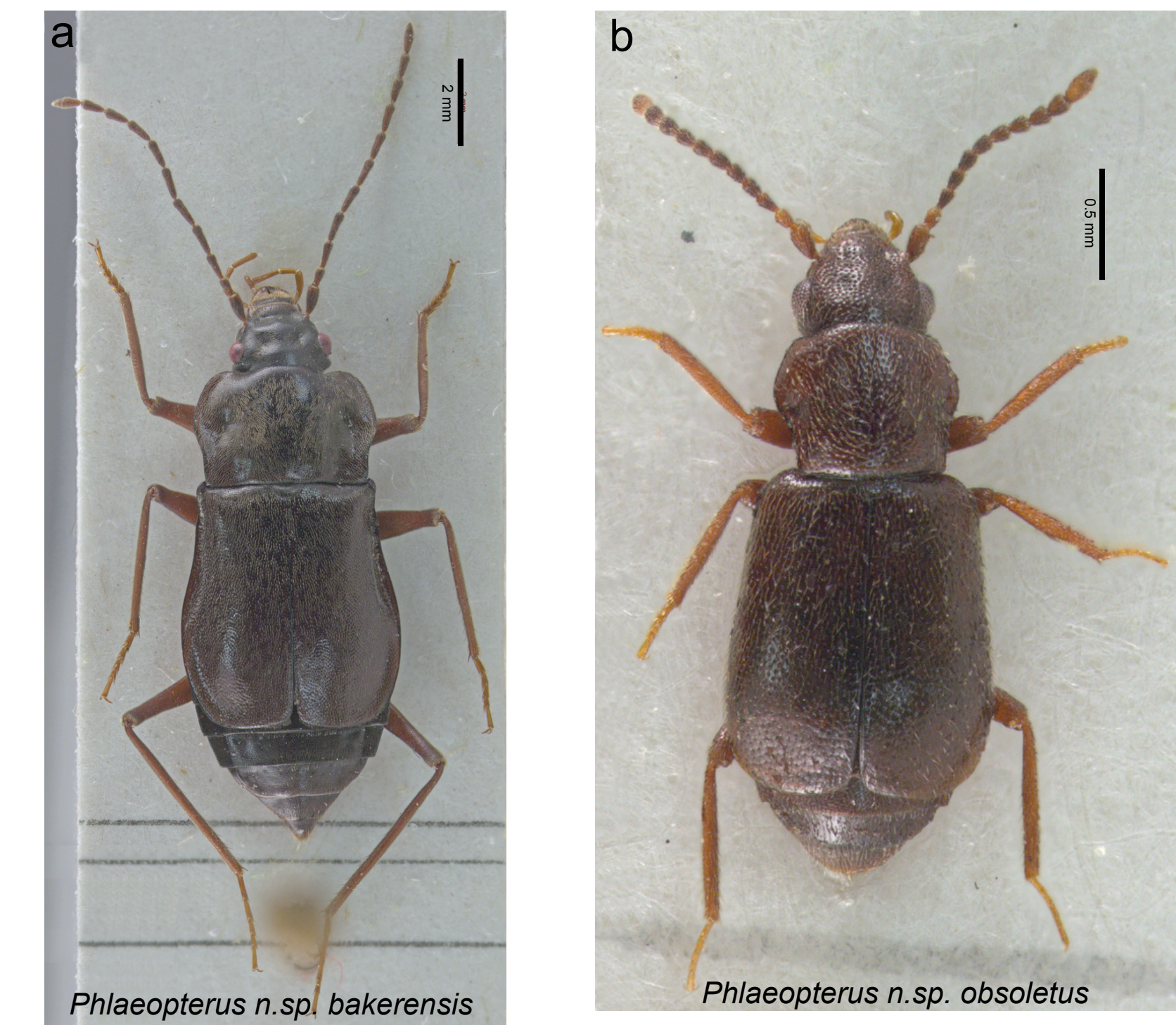
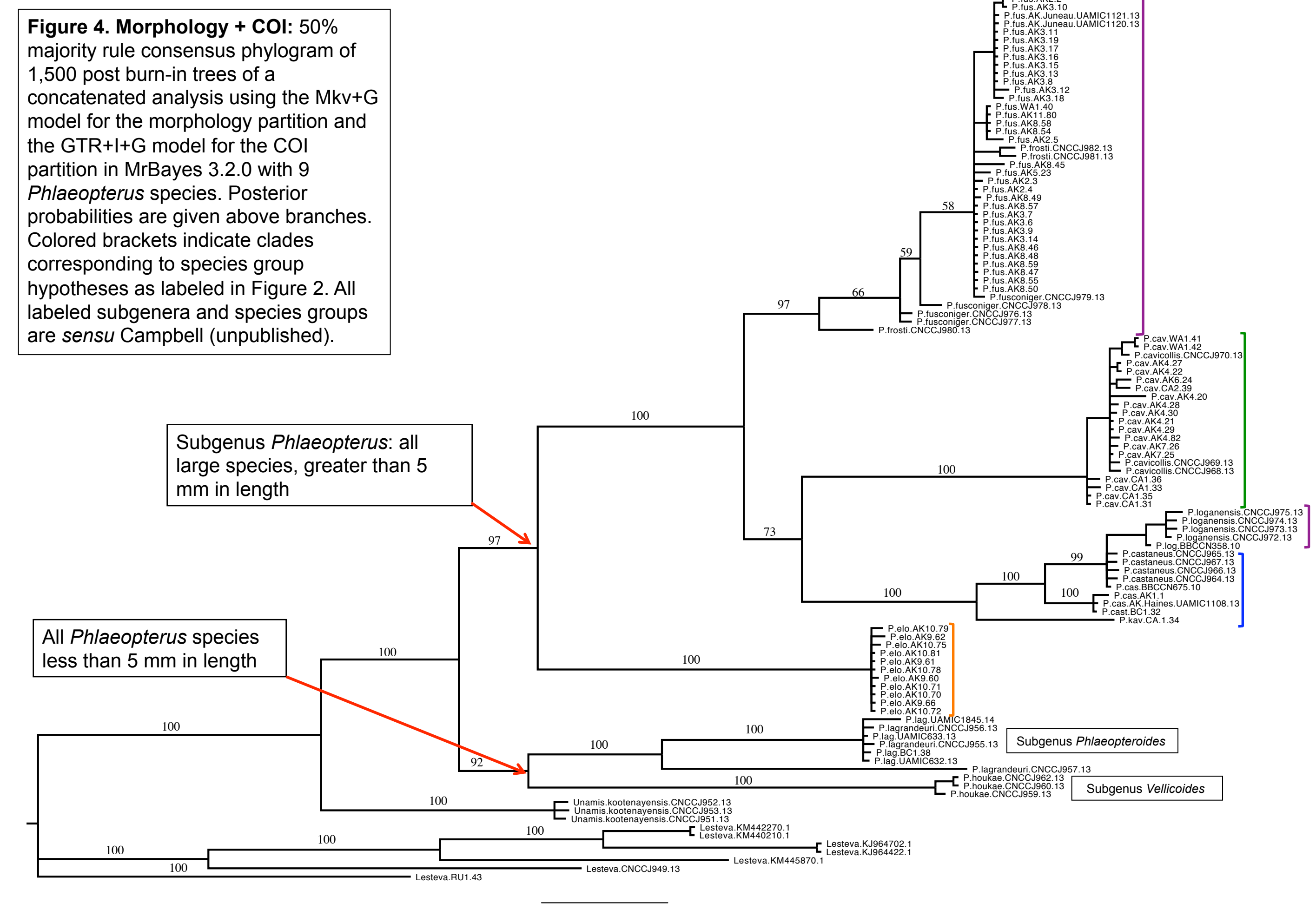


Figure 5. a) *Phlaeopterus n.sp. bakerensis*, the largest *Phlaeopterus* species: length = ~10 mm
b) *Phlaeopterus n.sp. obsoletus*, the smallest *Phlaeopterus* species: length = ~3 mm.

Table 1. Testing previous taxonomic hypotheses of the genus *Phlaeopterus* using Bayesian morphological (Fig. 1), molecular (Fig. 2), and concatenated (Fig. 3) analyses. Posterior probabilities are given as percent values. g = genus, subg = subgenus, sg = informal species group, - = untested due to monotypy, and NA = untested due to lack of molecular data.

Hypothesis	Citation	Posterior probability morphology	Posterior probability COI	Posterior probability morphology + COI
<i>Phlaeopteroides</i> subg (monotypic)	Campbell (unpublished)	-	-	-
<i>Vellicoides</i> subg (monotypic)	Campbell (unpublished)	-	-	-
<i>Vellica</i> subg	Campbell (unpublished)	99	NA	NA
<i>Phlaeopterus</i> subg	Campbell (unpublished)	98	<50	100
<i>castaneus</i> group sg	Campbell (unpublished)	96	<50	99
<i>cusconiger</i> group sg	Campbell (unpublished)	95	NA	NA
<i>filicornis</i> group sg	Campbell (unpublished)	<50	<50	<50
<i>Phlaeopterus</i> g (including <i>czerskyi</i>)	Shavrin & Mullen (2015)	93	-	-
		92	NA	NA

Summary

- 1.) Reciprocal monophyly of small (<5 mm in length) and large (≥5 mm in length) *Phlaeopterus* species is supported in morphological and concatenated analyses.
- 2.) One of the 2 proposed new species of Campbell (unpublished) for which molecular data are available, *Phlaeopterus n.sp. elongatus*, is supported by the mtDNA and concatenated phylogeny. A second, *Phlaeopterus n.sp. kavanaughi*, is represented by a single specimen that shows a large enough genetic distance to its nearest relatives to support its species status.
- 3.) The transfer of *Phlaeopterus kootenayensis* to the genus *Unamis* of Campbell (unpublished) is supported in the morphological and concatenated analyses. The transfer of *Phlaeopterus stacesmithi* to the genus *Unamis* is supported in the morphological analysis.
- 4.) The Siberian species *Phlaeopterus czerskyi*, recently transferred to *Phlaeopterus*, appears to represent a basal lineage.

Discussion

The COI only phylogeny (Fig. 2) is less well resolved than the morphology or concatenated phylogenies, and has a 6-branch polytomy at the base of the *Phlaeopterus* clade. This could be due to saturation, which often confounds mtDNA analysis at deep branches (Xia et al. 2003). The superior resolution of the concatenated phylogeny highlights the value of integrated taxonomy over single data type approaches.

Molecular data are currently available for only 10 of the 17 potential *Phlaeopterus* species, and only a single locus, COI, has been sequenced so far. In order to increase the resolution of our analyses, we plan to sequence COI as well the nuclear locus CAD for all 17 potential species.

Literature Cited

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Acknowledgments

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