**SUPPLEMENTARY INFORMATION**

The following information is provided in reply to comments by one of the referees, to whom we express our thanks. This additional information supports our approach and it is therefore useful to make it available, without necessarily being included in the paper itself.

*S1. On the validity of morphological characters used for Thyrsophorini systematics*

*S2. Testing morphological datasets*

*S3. Morphological datasets and extend of biogeographical conclusions*

*S4. Historical evidence on the systematic evidence of Thyrsophorini*

*S5. Molecular and Morphological evidences on Thyrsophorini systematics*

*S6. Constraining morphological topology with molecular backbone*

*S7. Supplementary tables*

*S8. Supplementary figures*

**S1. On the validity of morphological characters used for Thyrsophorini systematics.**

For several reasons, *c.* 10 characters were suggested as not optimal for morphological phylogenetics. Extreme variability (eg. Female Egg guide) or even unreliable support for homology were indicated by the reviewer for these characters. To deal with the first situation (intra-generic variability) we used the type species of the genus as representative of species in the genus. This approach has several problems because it does not consider the variability of species-rich genera (eg. *Psococerastis*), but in spite of this, it allows an initial hypothesis about phylogenetic positions. On the other hand, the establishment of *a priori* homology for other characters is both (*i*) impossible to discuss within an objective scheme and (*ii*) circular in its definition. Despite the importance of an expert opinion in morphological phylogenetics, the foundations of science are not justified by personal considerations. The validity of phylogenetic hypothesis is merged within the analytical scheme: any character is bad for formulating phylogenetic hypotheses but still debatable with more evidence.

Any of the characters that we have selected for our analyses has been used to hypothesize phylogenetic relationships amongst Thysophorini psocids, and thus our results represent a hypothesis of these relationships. This is obviously not the final truth, but is valid when considering every effort that has been made on the systematics of tribe. The validity of our results should be discussed by other

authors who publish about the same topic using other lines of evidence or different methods. Our results are based on a model and therefore depend on the characters and methods that we choose. The topology that we have obtained is a hypothesis that is open to discussion.

Finally, we have indicated a circular tendency during the selection of homologous characters because there is a subsequent phylogenetic analysis that corroborates the *a priori* suggestion (Homologous or non-homologous). Parsimony analyses also indicate which characters are non-homologous, and this is also a criteria for discussing their validity in a phylogenetic hypothesis. Therefore, we can establish character states for several features and evaluate their validity when reviewing the topology.

**S2. Testing morphological datasets.**

With the aim of promoting an interesting discussion we have taken into account two combinations of the suggestions of the referee regarding the character matrix (Table S1). We have (i) an **original** dataset (the original submitted matrix), (ii) a second matrix excluding variable characters (egg Guide; **DS1**) and (iii) a small matrix excluding both hyper-variable characters and those with homology problems (**DS2**). Parsimony analyses suggest no differences between DS1 and the original dataset. Hyper-variable character do not imply changes in the topology, and thus, excluding or including will not affect our hypothesis. When we consider the exclusion of both hyper-variable characters and other with homology problems (as is strictly suggested by the referee) we obtained congruent relations in one clade *(Cycetini, (Thyrsopsocus, (Thyrsophorus, (Dictyopsocus, (Poecilopsocus, Thyrsopsocopsis)))))* that includes both Cycetini and *Thyrsopsocopsis*, which are our main focus in the manuscript. Both datasets support this clade and thus, the suggestions of the refee do not change the hypothesized phylogenetic relations that we discuss in our manuscript. These different datasets give more strength to our first results. We suggest that the characters, which were suspected to have homology problems only resolve the relations amongst clade B (see Figure S2) depicting the relations within clade A. The polytomy obtained using DS2 cause remarkable problems during the biogeographical analyses (see below).

**S3. Morphological datasets and extend of biogeographical conclusions.**

Our historical biogeographical analysis was based on the phylogenetic hypothesis. As the referee criticized our phylogeny, the biogeographical analyses were also criticized. As we have explained above, the foundations of our initial analysis were well-established and support the subsequent and derived biogeographical conclusions. Despite this, we used the same approach as for phylogenetic analysis: we compared the original dataset with the topology obtained using the suggestions of the referee on the character matrix (Table S2).

The main problem is that the topology obtained constraints the extend of the biogeographical conclusions (compare figures S3 and S4). Non-resolved phylogenies are not accepted in RASP software, and thus, several statistical analyses could not be done. One of the advantages of using statistics is the estimated uncertainty that could be derived by the different methods. Parsimony does not reflect uncertainty, but allows the use of ambiguous distributions and non-resolved phylogenies (See figure S4). The results obtained with the corrected character (**DS2**) matrix are poor, because they do not resolve the relationships among clade B, but they do resolve clade A as does the original dataset. A non-fully resolved phylogeny implies that the conclusions about the historical biogeography of the lineages will not be as good, based on non-objective criticism on the character matrix.

We here discussed the suggestions by the referee, and we hope that we demonstrated the problems that occur by accepting such corrections. Especially the suggested corrections of the character matrix are here shown to be less useful, because they would not change the parsimony topology but they would limit the conclusions about the biogeography of the lineage.

## S4. Historical evidence

The systematic position of the former Thyrsophorinae and Cerastipsocini has been problematic, but until Yoshizawa & Johnson's (2008) proposal, a general consensus among psocidologists accepted each lineage as reciprocally monophyletic. Brief discussions regarding the position of Thyrsophorinae and Cerastipsocini were presented by several experts (see Table S3). None of the previous analyses tested the monophyly of Thyrsophorinae+Cerastipsocini using formal analytical methods on morphological datasets, but all of them concluded the straightforward distinction between them.

It's clear that the distinction of the two lineages has depended on the applied lines of evidence. Morphological examinations have suggested the existence of two distinct lineages, but the examination of 6 genes merged the evolutionary history in a single lineage. Our phylogenetic hypothesis is the only one based on quantitative methods that formally tests the position and validity of Cerastipsocinae and Thyrsophorinae.

**S5. Molecular and Morphological evidence on Thyrsophorini systematics.**

There are sampling differences among our analyses and those based on a molecular dataset. These differences are the consequence of methodological issues that generate biases in sampling, but should be taken into account by statistical methods (ML or BI) or corrected using several strategies in parsimony analyses (e.g. Including genus types). Our sampling includes all 15 genera of Thyrsophorini, but the molecular evidence resolves the relations of only 5 genera (*Thyrsophorus, Cerastipsocus, Psococerastis, Longivalvus* and *Clematoscenea*). The monophyly of Ceratipsocini + Thyrsophorinae was supported by molecular analyses and also by our results using morphological data.

In our morphological phylogeny, the topology suggested the monophyly of Thyrsophorinae + Cerastipsocini, with the former merged into the latter. Our results support the nomenclatural act made by Yoshizawa & Johnson (2008) when they proposed Cerastipsocini as a synonym of Thyrsophorini. In this sense, the position of *Eremopsocus* and *Ghesquierella* eliminates the reciprocal monophyly of each lineage, and thus, our results are in accordance with the molecular dataset. We also tested the monophyly of this clade using several outgroups in accordance to the phylogenetic proposal of Yoshizawa & Johnson (2008) (see Fig. 5).

## S6. Constraining morphological topology with molecular backbone

As suggested by the referee, we constrained the Thyrsophorini phylogeny following Yoshizawa & Johnson (2008) topology. Constraining the topology has important consequences on the derived relationships and we are therefore generally not in favour of this methodological artifact. When testing phylogenetic relationships, why should *a priori* relationships be established? Therefore, we opted to test the relationships by recurring to different lines of evidence. Despite this, we found differences between our results and results from the suggested analyses:

1. **Resolution**. Using the same parameters (K=3, TBR 1000 replicates, etc.) we obtained two polytomies in the ingroup using the new analyses, that would yield poor results from the biogeographical analyses.
2. **Thyrsophorini monophyly**. Both phylogenetic reconstructions support the tribal monophyly (Table S4), but unconstrained topology yields higher supports for all nodes. On the other hand, the constrained topology is less parsimonious than the unconstrained one.
3. **Thyrsophorus+Cerastipsocus**. Morphological evidence does not support the Thyrsophorus+Cerastipsocus clade, which was recovered by molecular evidence. Constrained topology with highly supported clades in molecular analyses (e. g. Thyrsophorus+Cerastipsocus) does not make morphological phylogeny compatible when considering the consensus tree (See Fig. S6).

**S7. Supplementary tables.**

**Table S1.** Three datasets used for parsimony analyses. We found congruent results and support for our initial analyses.

| Name | Excluded characters | Character numbers | Similar clades |
|---|---|---|---|
| **Original** | None | | All |
| **DS1** | Hyper-Variable | | All |
| **DS2** | Hyper-Variable<br>Homology problems | | (Cycetini, (Thyrsopsocus, (Thyrsophorus, (Dictyopsocus, (Poecilopsocus, Thyrsopsocopsis))))) |

**Table S2.** Extend of conclusions and analysis available for different datasets.

| Name | Available analyses | Topology type | Conclusions |
|---|---|---|---|
| **Original** | -Parsimony Ancestral reconstruction<br>-BBM<br>-S-Diva | Fully resolved phylogeny (Binary) | Thyrsopsocopsis Dispersal and Cycetini Vicariance. Several other biogeographic scenarios |
| **New suggestions** | -Parsimony | Partly-resolved phylogeny | Vicariance or Dispersal for Cycetini. |

**Table S3.** Classification of Psocidae (=Psocinae) by several authors. Cerastipsocini & Thyrsophorinae are in bold and in italics.

| Evidence | Author | Family | Subfamily | Tribe |
|---|---|---|---|---|
| Morphology | Roesler (1944) | | Psocinae | Amphigerontiini<br>Psocini<br>***Cerastipsocini***<br>***Thyrsophorini*** |
| Morphology | Badonnel (1951), Lienhard (1998) | Psocidae<br>***Thyrsophoridae*** | Amphigerontinae<br>***Cerastipsocinae***<br>Psocinae | Cerastipsocini<br>Metylophorini<br>Cycetini |
| Morphology | Mockford (1993) | Psocidae | Amphigerontinae<br>Psocinae<br>***Thyrsophorinae*** | ***Cerastipsocini***<br>Cycetini<br>Metylophorini<br>Psocini<br>Ptyctini |
| Morphology | Li (2002) | Psocidae | Amphigerontinae<br>Psocinae<br>***Cerastipsocinae***<br>Sigmatoneurinae<br>***Thyrsophorinae*** | Amphigerontiini<br>Blastini<br>Stylatopsocini<br>Oreopsocini<br>Psocini<br>Ptyctini<br>Trichadenoctenini<br>Metylophorini |
| Molecular | Yoshizawa & Johnson (2008) | Psocidae | Amphigerontinae<br>Psocinae<br>Kaindipsocinae | Amphigerontiini<br>Blastini<br>Stylatopsocini<br>Psocini<br>Ptyctini<br>Trichadenoctenini<br>Atrichadenoctenini<br>***Thyrsophorini***<br>Metylophorini |

**Table S4.** Summary statistics for the constrained (Referee suggestions) and unconstrained (Author's) topologies.

| Topology | Length | Ci | Ri | Tribal monophyly (GC values) | | |
|---|---|---|---|---|---|---|
| | | | | Bst | Bremmer | Jackknife |
| **Referee** | 134 | 38 | 55 | 7 | 0.07 | 9 |
| **Author's** | 127 | 40 | 59 | 95 | 0.33 | 60 |

## S8. Supplementary figures

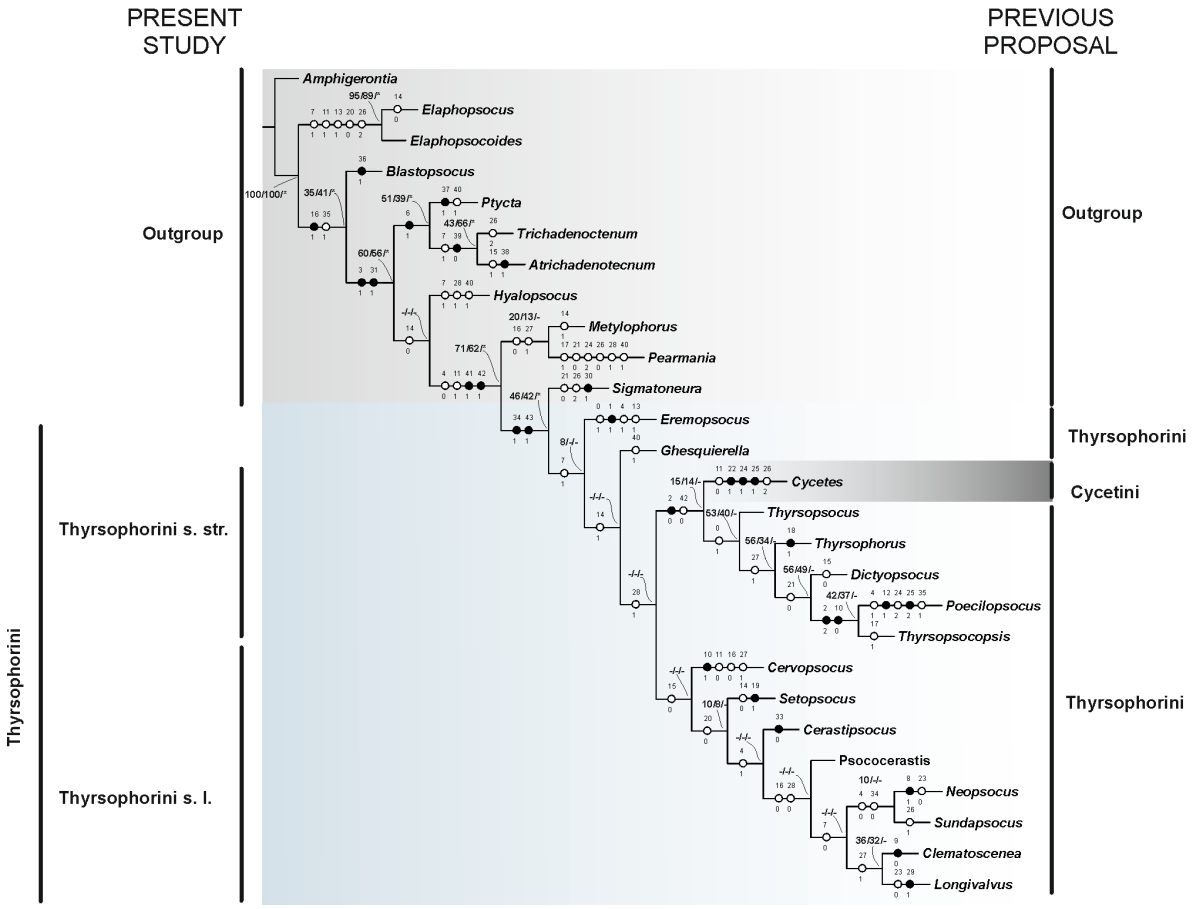


**Figure S1.** Parsimony analysis derived from the original dataset. The same topology was obtained for DS1.

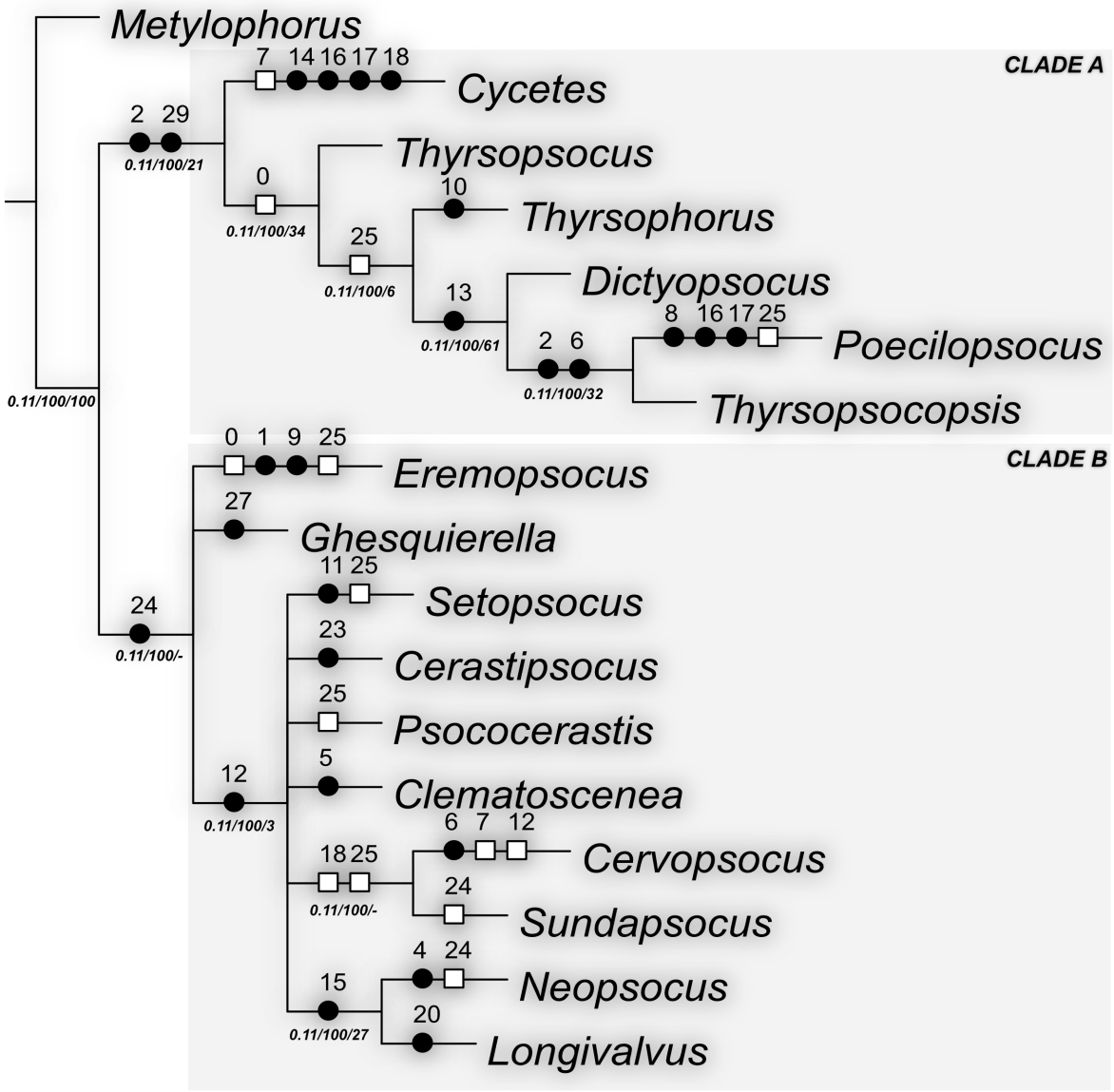


**Figure S2.** Parsimony analysis derived from the DS2 dataset.

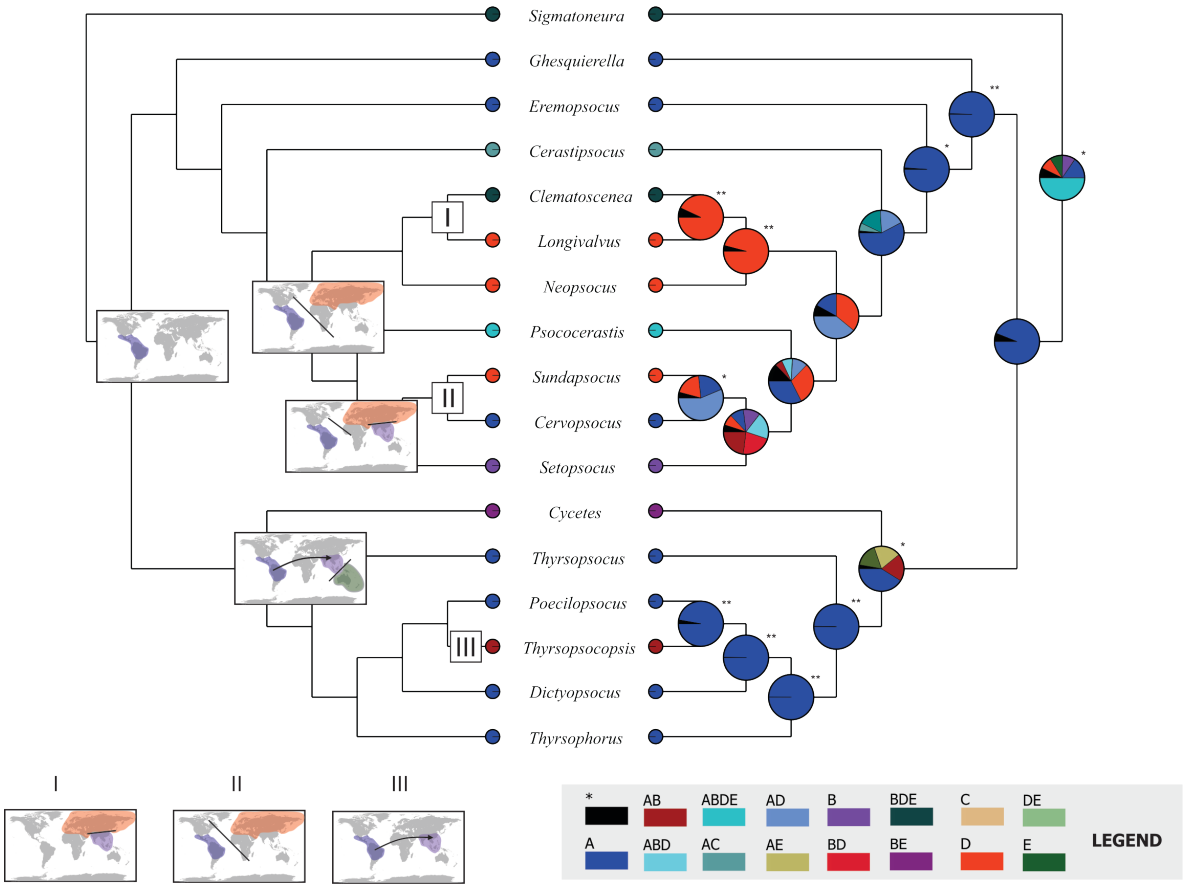


**Figure S3.** Biogeographic reconstruction of the Thyrsophorini evolution based on BBM and S-Diva analyses.

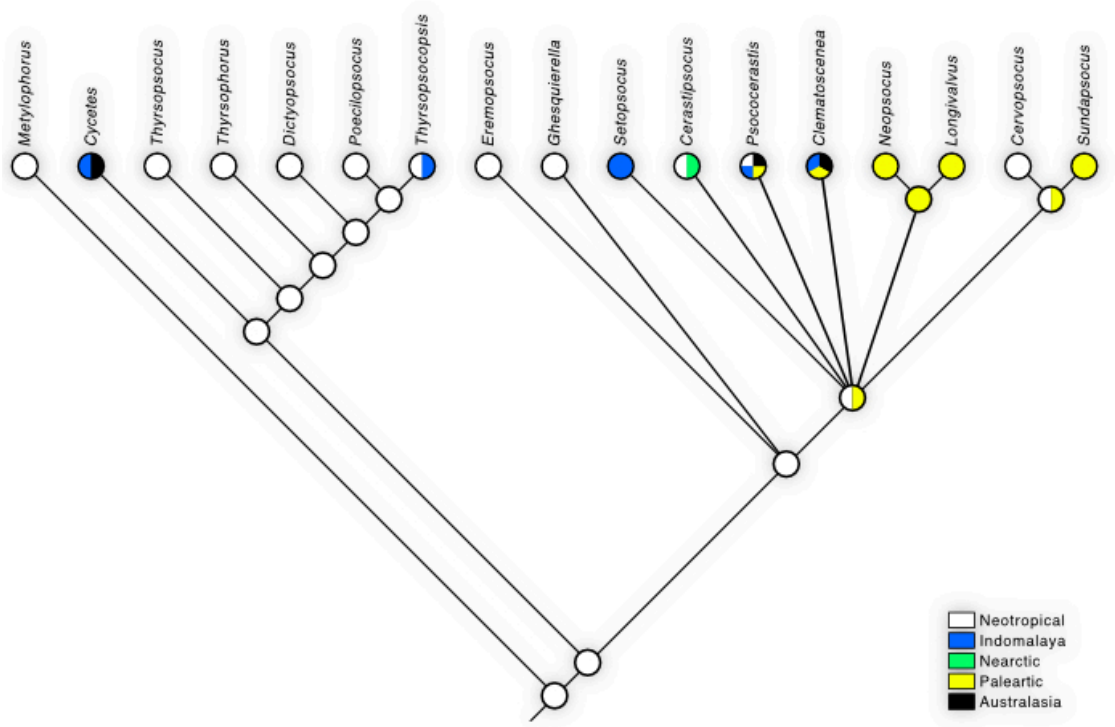


**Figure S4.** Historical biogeography of Thyrsophorini inferred from Parsimony analysis.

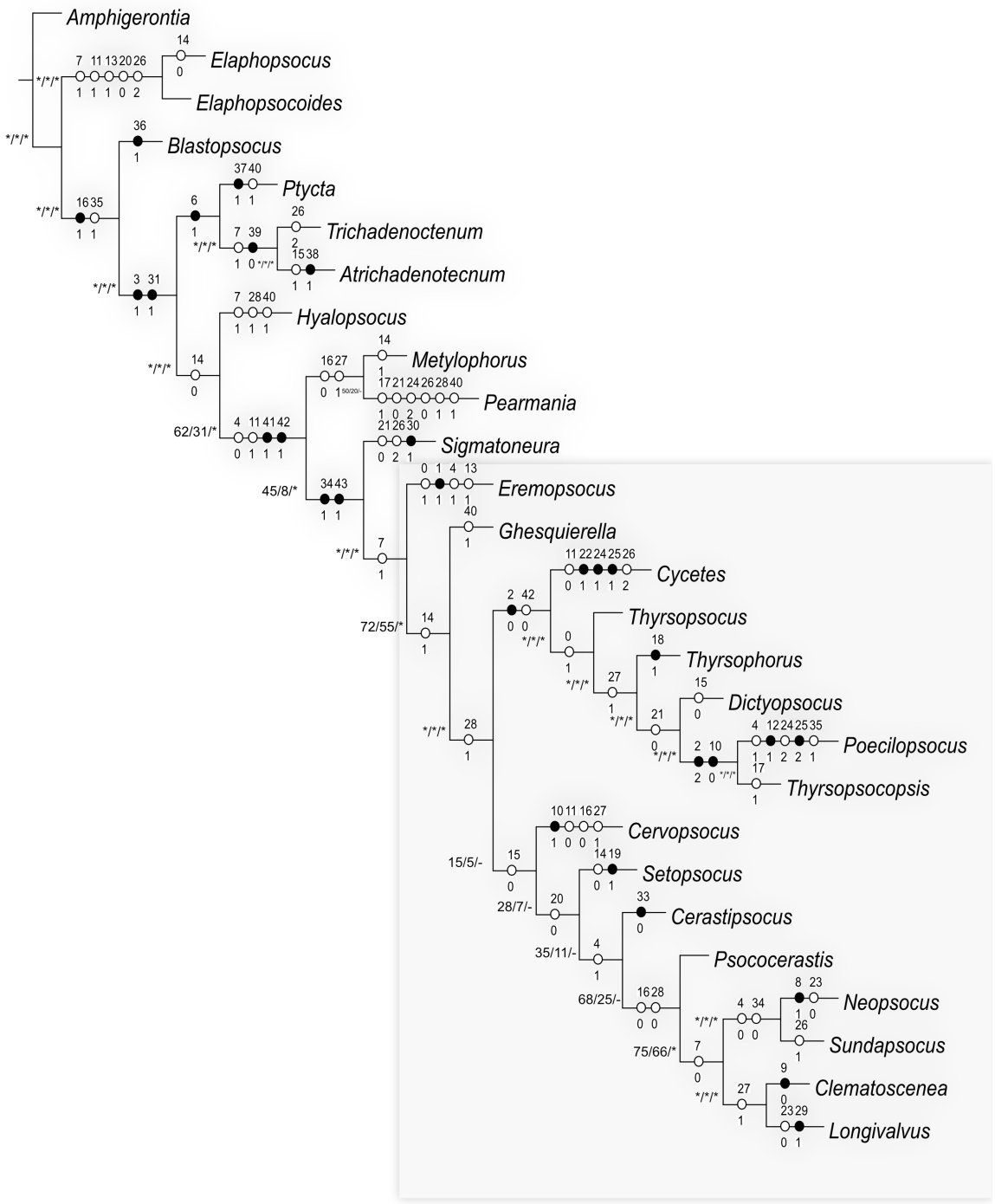


**Figure S5.** Morphological phylogeny of Thyrsophorini psocids. The monophyly of Thyrsophorini + Cerastipsocini was highly supported as suggested also by molecular evidence (Yoshizawa & Johnson 2008).


*Molecular* *Morphology*

**Figure S6.** Morphological phylogenies obtained using parsimony analyses with the same parameters. Molecular results indicate that a molecular backbone was used for constraining relations (Yoshizawa & Johnson 2008).