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# Title

## Assessing support for Blaberoidea phylogeny suggests optimal locus quality

### SHORT TITLE

Optimal locus quality

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## **KEYWORDS**

Character sampling, targeted sequencing, hybrid enrichment, phylogenetic experimental design, Blattodea, Isoptera

## **ABSTRACT**

Phylogenomics seeks to use next-generation data to robustly infer an organism's evolutionary history. Yet, the practical caveats of phylogenomics motivates investigation of improved efficiency, particularly when quality of phylogenies are questionable. To achieve improvements, one goal is to maintain or enhance the quality of phylogenetic inference while severely reducing dataset size. We approach this by assessing which kinds of loci in phylogenomic alignments provide the majority of support for a phylogenetic inference of cockroaches in Blaberoidea. We examine locus substitution rate, saturation, evolutionary divergence, rate heterogeneity, stabilizing selection, and *a priori* information content as traits that may determine optimality.

Our controlled experimental design is based on 265 loci for 102 blaberoidean taxa and 22 outgroup species. Loci with high substitution rate, low saturation, low sequence distance, low rate heterogeneity, and strong stabilizing selection derive more support for phylogenetic relationships. We found that some phylogenetic information content estimators may not be meaningful for assessing information content *a priori*. We use these findings to design concatenated datasets with an optimized subsample of 100 loci. The tree inferred from the optimized subsample alignment was largely identical to that inferred from all 265 loci but with less evidence of long branch attraction, improved statistical support, and potential 4-6x improvements to computation time. Supported by phylogenetic and morphological evidence, we erect three newly named clades (Anallactinae Evangelista & Wipfler *subfam. nov.*, Orkrasomeria *tax. nov.* Evangelista, Wipfler, & Béthoux, and Hemithyrsoicerini Evangelista *tribe nov.*) and propose other taxonomic modifications. The diagnosis of Pseudophyllodromiidae Grandcolas, 1996 is modified to accommodate Anallactinae and Pseudophyllodromiinae Vickery & Kevan, 1983. The diagnosis of Ectobiidae Brunner von Wattenwyl, 1865 is modified to add novel morphological characters.

## INTRODUCTION

The current “postgenomic” era of phylogenetics is characterized by large datasets and increased efforts to maximize their usage (Bravo *et al.*, 2019). Yet, while more data increase potential phylogenetic information (Simon *et al.*, 2018), they can also increase data artefacts and bias (Breinholt and Kawahara, 2013; Brown and Thomson, 2017; Dell'Ampio *et al.*, 2014; Platt *et al.*, 2018; Shen *et al.*, 2017). In this study, we target genomic loci and assess their contribution to phylogenetic inference and topological support through phylogenetic subsampling. There are known features of loci that are thought to be more informative than others for inferring phylogenetic relationships (e.g., optimal evolutionary rate, saturation, long branch score, heterogeneity, entropy; Borowiec *et al.*, 2015; Brown and Thomson, 2017; Gilbert *et al.*, 2015; Klopstein *et al.*, 2017; Molloy and Warnow, 2018; Reddy *et al.*, 2017; Tan *et al.*, 2015; Townsend, 2007). Phylogenetic subsampling allows assessment of the presence of confounding signal (Edwards, 2016; Simon *et al.*, 2018). This approach has been used to test how topologies change with taxon sampling (Evangelista *et al.*, 2018; Simon *et al.*, 2018), the utility of loci with different evolutionary rates (Narechania *et al.*, 2012), the stability of nodes of biological interest (Simon *et al.*, 2012), the effect of missing data (Xi *et al.*, 2016), and other phenomena (Edwards, 2016).

Determining the optimality of loci (Reddy *et al.*, 2017; Townsend, 2007), as opposed to characters, must be a practical priority given that DNA sequencing technologies read contiguous regions of genomes. This is especially true when deciding which loci to target using popular genome capture strategies (e.g., Brandley *et al.*, 2015; Gilbert *et al.*, 2015; Lemmon *et al.*, 2012). Although the features of individual characters are directly relevant to phylogenetic

reconstruction (Dornburg *et al.*, 2018), removing characters in alignments may fail to improve phylogenetic accuracy (Tan *et al.*, 2015). Here, we use the term “locus” to refer to some contiguous segment of a genome more than a few nucleotides long.

The relationship between the features and phylogenetic utility of molecular loci have long been studied (e.g., see Blaxter, 2004). Perhaps the prime suspect in investigating a locus’ quality for phylogenetic inference is its evolutionary rate (Klopfstein *et al.*, 2017). The optimal mean rate of a locus for resolving difficult tree shapes (Dornburg *et al.*, 2018; Steel and Leuenberger, 2017) is very conservative (Klopfstein *et al.*, 2017; Steel and Leuenberger, 2017). Yet, targeting optimal evolutionary rates does not necessarily improve phylogenetic inference (Chen *et al.*, 2015; Doyle *et al.*, 2015; Narechania *et al.*, 2012). High evolutionary rate can hinder phylogenomic studies when it leads to substitution saturation (Breinholt and Kawahara, 2013; Fong *et al.*, 2012). A locus’ evolutionary divergence among a set of taxa may better indicate its phylogenetic utility. This measure loosely accounts for phylogeny and is related to other informative features such as: long branch score (Borowiec *et al.*, 2015; Struck, 2014), evolutionary rate (Chen *et al.*, 2015), saturation (Borowiec, 2019), and entropy (Bai *et al.*, 2013; Lewis *et al.*, 2016). Conforming to model assumptions is another feature that should improve phylogenetic trees (Doyle *et al.*, 2015; Reddy *et al.*, 2017; but see Dell’Ampio *et al.*, 2014). For instance, patterns of rate heterogeneity may be poorly estimated by the gamma distribution (Kjer and Honeycutt, 2007). Finally, stabilizing selective pressure is another desirable trait. Positive selection pressure may mislead phylogenetic inference through convergent evolution, which may further induce compositional bias (Cox *et al.*, 2014).

The most direct approach might be to measure phylogenetic information content of loci. Information content can be assessed several ways, including: (i) with reference to a phylogenetic tree (Townsend, 2007) or (ii) without one (Misof *et al.*, 2014b); (iii) in a Bayesian framework (Dornburg *et al.*, 2016; Lewis *et al.*, 2016); or (iv) in an empirical approach (Kück *et al.*, 2012; Misof *et al.*, 2014b). Using only high information content markers has sometimes improved tree congruence (Chen *et al.*, 2015) and given greater agreement with favored morphological hypotheses (Borowiec *et al.*, 2015). Yet, assessing information content before all data is collected (*a priori*) is challenging because new taxa can influence how character information is interpreted (Hugall and Lee, 2007; Venditti *et al.*, 2006).

We examine node support for an empirical phylogeny derived from sets of loci of varying quality. We utilize data subsampling (Edwards *et al.*, 2017; Narechania *et al.*, 2012) to assess rate of convergence on reasonable tree topologies and certainty of nodes under various data subsamples (e.g., Edwards, 2016; Evangelista *et al.*, 2018; Simmons *et al.*, 2018; Simon *et al.*, 2018; Simon *et al.*, 2012; Soltis and Soltis, 2003). We test six features suspected to affect the accuracy of phylogenetic inference, including: substitution rate, substitution saturation, pairwise sequence distance, among site rate heterogeneity, selective pressure, and *a priori* phylogenetic information content.

Our empirical aims are to recover a robust phylogeny of blaberoidean cockroaches. Blaberoidea is a clade ~170 Myr-old (Evangelista *et al.*, 2019) or older (Djernæs *et al.*, 2015; Legendre *et al.*, 2015) comprising ~3600 of the ~7500 species of Blattodea (Beccaloni and Eggleton, 2013). The major relationships of Blaberoidea were recently investigated in a phylogenomic study (Evangelista *et al.*, 2019) but taxonomic sampling was limited. The major

lineages of Blaberidae and many other splits occurring in the last 100 Myr were not sampled (Evangelista *et al.*, 2019). Studies that included denser taxon sampling recovered unstable topologies (Bourguignon *et al.*, 2018; Evangelista *et al.*, 2018; Legendre *et al.*, 2017; Legendre *et al.*, 2015). We combine previously published phylogenomic datasets with 265 genomic loci for 90 newly sequenced species of blaberoidean cockroaches. From the 265 loci dataset we compose two optimized subsamples of 100 loci each. By comparing the full data tree and the two subsample trees, we derive conclusions about tree plausibility and the phylogeny of Blaberoidea.



## MATERIALS AND METHODS

### *Taxon Sampling*

We added 90 newly sequenced Blaberoidea to the Blattodea sampled in Evangelista *et al.* (2019) and Wipfler *et al.* (2019). Accession numbers and sample details are listed in supplemental data. These were chosen to cover biogeographical regions and known “tribal-level” groupings as widely as possible (supplemental data). Live samples were obtained from breeders and remaining samples were museum specimens (see NCBI accession SRP155429 for full specimen information). Tissue was taken from the middle leg of all samples. Polyneopteran outgroups were chosen among published transcriptomes (Misof *et al.*, 2014a; Wipfler *et al.*, 2019).

### *Loci Capture and Probe Design*

Using alignments of orthologous loci from Misof *et al.* (2014a) we extracted sequences for *Blaberus atropos* and then used BLAST+ (Camacho *et al.*, 2009) to identify homologous sequences in transcriptomes of 17 cockroach species (*Anallacta methanoides*, *Asiablatta kyotensis*, *Blattella germanica*, *Cryptocercus wrighti*, *Diploptera punctata*, *Ectobius sylvestris*, *Ellipsoidion sp.*, *Gyna lurida*, *Ischnoptera deropeltiformis*, *Lamproblatta albipalpus*, *Lobopterella dimidiatipes*, *Nauphoeta cinerea*, *Panchlora nivea*, *Paratemnopteryx coulouiana*, *Princisia vanwaerebecki*, *Sundablatta sexpunctata*, and *Symploce sp.*). These were added to the *B. atropos* sequences and aligned with MAFFT v. 7.3 (Katoh and Standley, 2013; –localpair –maxiterate 1000 –adjustdirection). Of the resulting 599 alignments, we chose 100 at random, 92 which demonstrated high *a priori* information content, and 90 which demonstrated tree likeness but not high information content. We define loci having high *a priori* phylogenetic information content

as being able to recover a resolved topology (tree-likeness) and having high character support for non-conflicting bipartitions (see Supplement S1 for details). Probes for targeted enrichment were designed to target the final set of ~280 alignments (untrimmed, nucleotide versions) using Baitfisher v. 1.2.5 (Mayer *et al.*, 2016). The resulting probe sequences were further quality-filtered and subsequently produced by Arbor Biosciences (formerly, MYcroarray).

### *Library Preparation and Sequencing*

Genomic DNA was extracted from specimens belonging to 90 species (supplementary data) using the DNEasy kit (Qiagen USA), sheared using a timed Fragmentase (New England BioLabs Inc.) protocol and assessed using a Bioanalyzer (Agilent, Santa Clara, CA). Index-multiplexing strategies were planned and specimens were arranged on the plate to minimize the probability of cross-contaminating closely related samples. After NEBNext Ultra library preparation, indexed library pools were enriched with respect to targeted loci (MYbaits v.3.01) and then sequenced by GeneWiz USA using Illumina HiSeq's rapid-run paired-end-250 protocol.

### *Bioinformatics and Phylogenetic Inference*

Demultiplexed FASTQ files had adapters removed and low-quality bases trimmed (Krueger, 2017; Trimalore v. 0.4.3 options: -q 20; -stringency 3; -e 0.1; -length 30). Reads were assembled with Trinity v.2.0.6 (Grabherr *et al.*, 2011; Haas *et al.*, 2013). Orthologs from OrthoDB v. 7 (Waterhouse *et al.*, 2013) were identified in the 90 sequenced libraries and 37 additional Blattodea and Polyneoptera sequences (Evangelista *et al.*, 2019) using Orthograph v. 0.6 (Petersen *et al.*, 2017) with *Drosophila melanogaster*, *Pediculus humanus*, *Tribolium*

*castaneum*, and *Zootermopsis nevadensis* as reference genomes [default options except --anysymbol option called in MAFFT (Katoh and Standley, 2013), and blast-max-hits = 50]. 265 targeted loci were extracted from the ortholog set. Quality filtered reads are available on NCBI GenBank (SRP155429).

Each locus was aligned in MAFFT v. 7.3 (Katoh and Standley, 2013; options: -retree 4 -maxiterate 10 -adjustdirection) and then trimmed from the edges to eliminate leading or trailing sites missing >80% of data. A second, alignment was conducted in MAFFT v. 7.3 (-localpair -maxiterate 1000), which was then adjusted to maintain consistent reading-frame. Alignments were finalized with manual adjustment in AliView v. 1.18 (Larsson, 2014) to remove poor quality reads and correct misaligned sections. Custom scripts in Mathematica 10 (Wolfram Research, 2012) available in the package Phyloinformatics v. 0.9 (Evangelista, 2019) were used to manage sequence files, translate sequences, trim and concatenate alignments. We refer to the final concatenated alignment (127 taxa) as the "265\_Full" alignment.

We ran PartitionFinder 2 (Lanfear *et al.*, 2016) with the 265\_Full alignment with blocks defined as codon positions per locus, possible models as GTR and GTR+G, branch lengths considered as unlinked, best model chosen with AICc, and recluster search scheme (percent = 10; max = 1000). Using the resulting codon partitioning scheme, we ran a preliminary tree search with 10 independent runs in RAxML v. 8.2 (Stamatakis, 2014), implemented on the CIPRES portal (Miller *et al.*, 2010). Assessment of the best preliminary tree showed that a few taxa (*Amazonina platystylata*, *Doradoblatta* sp., *Ischnoptera galibi*, *Lanxoblatta* sp., *Panchlora stolata*, *Pycnoscelus femapterus*, *Pycnoscelus striata*) had exceptionally long branches. The same taxa were among those with the largest proportion of missing data (supplementary data). After

reassessing the alignments in which these species were present, we removed *Pycnoscelus striata*, *P. femapterous*, *Ischnoptera galibi*, *Amazonina platystylata*, and *Doradoblatta* sp. from the analysis under the grounds that (i) their data was low quality (short reads ambiguously aligned and with many nucleotide differences) and (ii) the pattern of data presence would not allow for testing of their hypothesized taxonomic assignment (see supplementary data). When running the tree searches there were no exceedingly long branch lengths, and Blaberidae was monophyletic.

Trees were inferred for three alignments: 1) the full alignment (“265\_Full”), 2) using only the 2<sup>nd</sup> codon positions (correcting for noise; “265\_2nd”), 3) low missing data alignment (correcting for relationships inferred from missing data patterns; “265\_Reduced”). The latter alignment was created by only retaining nucleotide positions having data for 51 or more taxa (Phyloinformatics function trimAlign2 missingProportion = 0.60; Evangelista, 2019)). The same partitioning, modelling and RAxML parameters as used above were applied to each analysis but with 100 independent tree runs (GTRGAMMA, -f d, -N 100). We inferred one more tree using the 265\_Full alignment in IQTree (Nguyen *et al.*, 2015) using partitions determined by PartitionFinder2, models determined by IQTree (Kalyaanamoorthy *et al.*, 2017) and the options: -ninit 200 -nbest 10 -allnni -ntop 40 -wbt -wsl -wsr. These four trees (265\_Full, 265\_2nd, 265\_Reduced, 265\_Full\_IQ) were later used as a baseline for establishing subsample convergence on a reasonable topology. We assessed support for the three RAxML trees by bootstrap resampling using the auto-MRE stopping criteria (60, 300 and 108 for the first three trees respectively) and calculating bootstrap frequencies and node certainty scores (Kobert *et al.*, 2016).

### *Designing locus subsample sets*

We designed experimental samples of loci based on calculations of the following six features for each of the 265 individual alignments: substitution rate, substitution saturation, mean pairwise sequence distance, substitution rate heterogeneity, level of selection, and *a priori* information content. We additionally calculated data completeness, and nucleotide compositional bias.

Details on how each feature was calculated are given in Supplement S1. Each subsample was designed to be non-overlapping in one of our six features (e.g., all loci with high substitution rate or all loci with low substitution rate) (Fig. 1, Table S1.2), while independent to all other features (Fig. S1.1). The saturation and selection test subsamples could not be made sufficiently independent (Table S1.2), so additional controlling tests were done (see below and Fig. S4.1). A few selected loci were then added to ensure all taxa were represented in each set. *Panchlora stolata*, and *Lanxoblatta* sp., were too poorly represented among loci to include in all sets, so they were removed from all alignments and trees in our tests.

### *Random addition concatenation subsampling*

We utilized the random addition concatenation of loci (RADICAL) described in Narechania *et al.* (2012) to infer phylogenies from each subsample set. This was implemented using the “radicalRun” function in Phyloinformatica v. 0.93. Within RADICAL the fast tree reconstruction method (options -fast, -ntop 10) in IQ-TREE (Nguyen *et al.*, 2015) was utilized. To overcome the low data completeness for some taxa, the first step of this implementation chose the three alignments with the most taxa represented and concatenate them with nine randomly drawn alignments. Subsequently, five loci were added at random for each additional step until all loci

were sampled. A starting BIONJ tree was used in the first step (option -t BIONJ) and subsequent steps use the final tree from the previous step as an initial tree. The GTR+G model was used in an unpartitioned analysis parallelized over two cores. This was repeated for ~100 iterations for each treatment.

To assess convergence of each subsample set we measured the mean of all Robinson-Foulds (RF) distances (Robinson and Foulds, 1981) from the RADICAL tree from each step at each iteration to the four full-data trees (265\_Full, 265\_2nd, 265\_Reduced, 265\_Full\_IQ). We plotted the means and fit with exponential models, which Narechania *et al.* (2012) showed was the shape of typical RADICAL curves.

To assess stability of topologies recovered from each set, a measure of phylogenetic precision, we plotted RF comparisons among all trees within a RADICAL step. We used a linear best-fit model for this data, as opposed to the exponential model, to accommodate the expectations that some RF values could equal 0.

We compared distributions of RF distances among the test subsampling treatments to assess the differences among subsamples. We compare each of the RADICAL tests at the 14<sup>th</sup> step (the latest step that is not the last step for any treatment) and the last step, which showed identical patterns of statistical significance. All statistical comparisons were done with a Z-Test, which is not sensitive to slight deviations from normality with sample size greater than 40 (Ghasemi and Zahediasl, 2012).

We also used each RADICAL tree set to assess their certainty (Kobert *et al.*, 2016) of relationships in the 265\_Full tree. We calculated relative tree certainty (rTC) and relative tree certainty-all (rTCA) using the stochastic bipartition adjustment.

### *Final Tree Searches*

The results from RADICAL identified five locus features that supported relationships more than others. To test the effect of applying this concept of phylogenetic information content to an analysis *a priori*, we selected one set of 100 loci demonstrating the optimal combination of these features (65,798 total nucleotides; “100\_Full” alignment) and a second set of 100 that also considered taxon completeness (83,822 nucleotides long; “C100\_Full” alignment; see Supplement S1 and Table S1.3 for details).

Final tree searches and bootstrapping were performed on the 100\_Full and C100\_Full alignments in RAxML v. 8.2 using the same protocol, partitioning and node support strategy discussed above with 100 independent tree searches. Searches were again performed on three conformations of each alignment: 1) all 100 loci (“Full”), 2) only 2<sup>nd</sup> codon positions (“2nd”), 3) only positions present for more than 50% of taxa (“Reduced”).

## **RESULTS**

The 265\_Full phylogenetic inference (Fig. 2) yields a number of deep relationships with strong node support: Ectobiinae (Ectobiidae) is recovered as sister to all other Blaberoidea; Anallactinae (*subfam. nov.*; Supplement S2) is recovered as sister to Pseudophyllodromiinae (together Pseudophyllodromiidae Supplemental Section 2); Blattellidae + Nyctiboridae (see Supplemental Section 2) inferred as sister to Blaberidae (together Orkrasomeria *tax. nov.* Supplemental Section 2); and Blaberidae is recovered as monophyletic. There is strong node support throughout Blattellidae + Nyctiboridae except for within Nyctiboridae, Pseudomopini

and Hemithyrsocerini *tribe nov.* There is also strong support in most of Pseudophyllodromiidae with the exception being Plectopterini *s.l.* Node support is lacking throughout most of Blaberidae but two moderately well supported clades (the “Peri-Atlantic” and “Peri-Indian” clades) sort most taxa. *Rhabdoblatta stipata* as sister to the remaining Blaberidae, and Neotropical Epilamprinae as sister to (Peri-Atlantic + Peri-Indian Blaberidae) are strongly supported by our data.

Node support for the 265\_Full tree (Fig. 2) was highest among bootstrap replicates inferred from the 265\_Reduced alignment (mean bootstrap = 0.94; mean IC = 0.85), moderately high among bootstrap replicates from the 265\_Full alignment (mean bootstrap = 0.93; mean IC = 0.83), and lowest among bootstrap replicates from the 265\_2nd alignment (mean bootstrap = 0.85; mean IC = 0.66). Numerous relationships in the 265\_Full and 265\_Reduced trees were not recovered in the best tree inference with only 2<sup>nd</sup> codon positions (Fig. 2).

Experimental comparisons of six features (Fig. 1) using the random-addition concatenation (RADICAL) process (Fig. 3) showed that fast substitution rate, low saturation, low mean pairwise sequence distance, low rate heterogeneity, and strong stabilizing selection all contribute to faster convergence to the full data tree topologies (P-values all  $\ll .005$ ; Fig. 4A; also see, Fig. S4.2). Loci with high rate heterogeneity, which tend to be longer, improved tree recovery but only when not corrected for locus length (Fig. S4.4). Fast substitution rate, low mean pairwise sequence distance, low rate heterogeneity, strong stabilizing selection, and low information content all result in more precise estimation of trees (P-values all  $\ll 0.005$ ; Fig. 4B; also see, Fig. S4.3). Saturation had no statistically significant effect on tree precision.



Relative tree certainty (rTC) of the 265\_Full topology as calculated from RADICAL subsample trees (Table 1) was highest among the subsamples for fast substitution rate (rTC = 0.58), high *a priori* information content (rTC = 0.58), and low mean pairwise sequence distance (rTC = 0.56). The lowest support is demonstrated by loci that are highly unsaturated (rTC = 0.462), high mean pairwise sequence distance (rTC = 0.49) and low rate heterogeneity (rTC = 0.49). These values can be interpreted as the sum of all internode certainties (IC) normalized by the number of non-tip edges. IC scores are the relative frequency of the recovered bipartition in relation to the two most frequently recovered bipartitions (Kobert *et al.*, 2016; Salichos *et al.*, 2014).

The two trees inferred from the optimized subsamples of 100 loci were 48 (100\_Full) and 20 (C100\_Full) RF distance away from the 265\_Full tree (Table 2). For context, the 265\_2nd and 265\_Reduced trees were 60 and 56 RFs different, respectively. C100\_Full tree had the lowest distance to 265\_Full tree (Table S5.1) and is in the 99.95<sup>th</sup> percentile of all the 23,740 comparisons to the baseline trees done in RADICAL (100\_Full tree's distance was in the 88<sup>th</sup> percentile). The 100\_Full and C100\_Full trees also had slightly longer internal branch lengths compared to external branch lengths (i.e., decreased leafiness; Table 2). The mean bootstrap support and internode certainty of 100\_Full and C100\_Full were slightly lower than those in 265\_Full (Table 2). The only trees deemed plausible given an alignment were 265\_Full, 100\_Full, C100\_Full, and C100\_Reduced (Table 2). The C100\_Full phylogeny was the only tree deemed plausible considering more than one alignment.

The C100\_Full and 100\_Full locus sets are composed of loci that demonstrated improved convergence (Fig. 3, 4). Trees inferred from these sets display a lower ratio of total external

branch length to internal branch length compared to the 265\_Full phylogeny (Table 2). Among all the trees inferred, the C100\_Full tree was estimated to be the most plausible given AU tests (Table 2). All the other trees were acceptable as plausible given their own alignment but not under any other alignment. C100\_Full was the only tree accepted by more than one AU test (Table 2; also, see Table S5.2, S5.3).

## DISCUSSION

### *Phylogeny of Blaberoidea*

The relationships among the four monophyletic clades of Blaberoidea (Fig. 2) largely conform to previous phylogenomic analysis (Evangelista *et al.*, 2019) but conflict with pre-genomic, morphological and combined-data phylogenetic studies. One of the earliest cladistic analyses recovered ((Pseudophyllodromiinae + Blaberidae) + (Nyctiborinae + Ectobiinae + Blattellinae)) (Grandcolas, 1996; but see Klass, 2001). Evangelista *et al.* (2017) summarized topologies from phylogenetic studies published between 2003 and 2015 (Djernæs *et al.*, 2012; Djernæs *et al.*, 2015; Inward *et al.*, 2007; Klass and Meier, 2006; Legendre *et al.*, 2015; Maekawa *et al.*, 2003; Murienne, 2009; Pellens *et al.*, 2007) and underlined that there was little consensus about the backbone relationships of Blaberoidea. The most common topology was (Blattellinae + Nyctiborinae) + (Ectobiinae + (Pseudophyllodromiinae + Blaberidae)) but the poor support for these relationships with molecular data was highlighted in Evangelista *et al.* (2018). A recent mitogenomic study recovered ((Anallactinae + Ectobiinae) + Pseudophyllodromiinae) + (Nyctiborinae + (Blattellinae + Blaberidae)) but with <0.5 posterior probability (or <50% bootstrap) on all but one node (Bourguignon *et al.*, 2018).

Our analysis included multiple terminal taxa that are important for clarifying some systematic issues. Robust placement of *Saltoblattella* within Baltini (Fig. 2) clarifies ambiguous prior affinities (Bohn *et al.*, 2010; Djernæs *et al.*, 2012; Djernæs *et al.*, 2020). The sister-group relationship of *Lobopteromorpha* with *Anallacta* also helps clarify morphological synapomorphies for the Anallactinae *subfam. nov.* (Supplement S2). Our results support *Anisopygia* in Pseudophyllodromiinae (Djernæs *et al.*, 2020; see also Legendre *et al.*, 2015). Previous phylogenetic studies have recovered *Nahublattella* as outside of Pseudophyllodromiidae (Djernæs *et al.*, 2020; Klass and Meier, 2006; Ware *et al.*, 2008). The most recent analysis (Djernæs *et al.*, 2020) included two species of *Nahublattella* but had low genetic coverage and unstable placement. With coverage on 81 nuclear genomic loci (30% completeness) we recover *Nahublattella incompta* deep within Pseudophyllodromiinae with strong support, which agrees with its original morphology-based classification (Anisyutkin, 2009). *Calhyphnorna* is listed as Blattellinae on the Cockroach Species File online database (Beccaloni, 2018) but this may be an error since Princis (1965) listed it in Anaplectidae and near *Plectoptera*. The latter agrees with our placement of *Calhyphnorna* in Plectopterini *s.l.* Previous genetic barcode analyses indicated a close relationship of *Calhyphnorna* with *Chorisoneura* (Evangelista *et al.*, 2014) also found here in Plectopterini *s.l.* Support for *Mediastinia* and *Ectoneura* in Ectobiinae clarifies the position of the former taxa. *Mediastinia* was previously classified as Pseudophyllodromiinae, but only based on a superficial morphological description (Hebard, 1943). *Ectoneura* has already been recovered in Ectobiinae by Bourguignon *et al.* (2018) as expected from its morphology-based classification (Bohn *et al.*, 2010). The

phylogenetic affinity of these two genera with *Ectobius* will assist in improved morphological revision of Ectobiinae (see Supplement S2).

The relationships among Blaberidae were highly volatile in our analyses, but some novel conclusions can be drawn (Fig. 2). Some recent studies have had strong taxon sampling of “Peri-Atlantic Blaberidae” but had low support for the placement of most of the constituent lineages (Djernæs *et al.*, 2020; Legendre *et al.*, 2017). Contrary to these prior studies, we recover these taxa as monophyletic with strong support. Within the “Peri-Atlantic Blaberidae” we find strong support for a monophyletic Panchlorinae. Panchlorinae is poorly defined, due to a simplification in morphology (Gurney and Roth, 1972). Before the present, no phylogenetic study had sampled African members of this predominantly neotropical genus. Dense sampling of Peri-Indian Blaberidae shows a greater extent of the rapid radiation that previous studies have only hinted at (Bourguignon *et al.*, 2018; Evangelista *et al.*, 2019; Legendre *et al.*, 2017). In agreement with Legendre *et al.* (2017), we recover *Thanatophyllum akinetum* in Neotropical Epilamprinae, whereas it was previously considered to be a “Zetoborinae” (Djernæs *et al.*, 2020; Grandcolas, 1990). The recovered topology of Blaberinae differs from that recovered by Djernæs *et al.* (2020), which also had a strongly supported topology. The position of the unusual genus *Aptera* is not strongly resolved, which was the case in other studies as well (Djernæs *et al.*, 2020; Legendre *et al.*, 2017; Legendre *et al.*, 2015). Novel approaches addressing the relationships among other lineages will be needed, as our inference gives little resolution.

There are also several systematic issues that can be clarified within Blattellidae + Nyctiboridae. The genus *Megaloblatta* has traditionally been recognized as Nyctiborinae but

morphologically distinct from all others (Salazar and Malaver, 2012). Djernæs *et al.* (2020) listed this genus as *incertae sedis* due to the lack of evidence demonstrating relationship to other Nyctiboridae. Our best tree (Fig. 2) recovers *Megaloblatta* within Nyctiboridae with moderate support. The genera we recover in Paracoblattini (*Paratemnopteryx*, *Paracoblatta* and *Asiablatta*) were also recovered with strong support in Bourguignon *et al.* (2018). Earlier, Roth (1990) proposed this clade on morphological grounds, although he did not examine *Asiablatta*. *Theganopteryx* falls strongly in Blattellinae. This genus was previously thought to be in Ectobiinae but Bohn *et al.* (2010) discussed why this was not supported. While we recover *Chorisoblatta* as sister to *Chromatonotus* we also doubt the accuracy of this relationship (see Supplement S3). *Beybienkoa* is recovered as sister to *Xestoblatta*. At various times these genera have been thought of as close relatives of *Ischnoptera* (Bourguignon *et al.*, 2018; Hebard, 1916; Legendre *et al.*, 2015), but this is the first time all three have been studied together. Further discussion of morphological support, and novelties in our phylogenetic inference are discussed in Supplement S3.

While strong support for Blattellidae + Nyctiboridae + Blaberidae has been demonstrated with both morphological and genomic data (Bourguignon *et al.*, 2018; Evangelista *et al.*, 2019; Klass and Meier, 2006) we have now extensively sampled taxa within the principal lineages of each clade. Given the unambiguous support for this relationship, we newly define it as Orkrasomeria *tax. nov.* (Supplement S2). Dense taxon sampling within Pseudophyllodromiidae and Orkrasomeria both imply a complex biogeographical history that should be given future study (but see Djernæs *et al.*, 2020). Recovery of an African “Epilamprinae” as sister to the remaining Blaberidae (Fig. 2) implies that further sampling of these species are needed. The

backbone topology of Blaberidae also suggests a complex biogeographical history (Djernæs *et al.*, 2020), likely due to dispersal given the age of this clade (Bourguignon *et al.*, 2018; Evangelista *et al.*, 2019).

### *Relationship between locus quality and phylogenetic support*

We compared rate of phylogenetic convergence among loci of varying quality in a random concatenation test. In this context, *a priori* information content was not a predictor of convergence on the tree topology (Fig. 4A). Locus features that did result in improvements to convergence were high substitution rate, low saturation, low rate heterogeneity, strong stabilizing selection, and low mean pairwise sequence distance (Fig. 4A).

We also compared support of the 265\_Full topology with the RADICAL subsample trees from each of these respective sets. In agreement with the test of convergence, loci with a high substitution rate and low mean pairwise sequence distance resulted in high tree certainty. However, there were conflicting results as well. Loci with *a priori* high information content demonstrated the highest tree certainty. High saturation, high rate heterogeneity both outperformed low saturation and low rate heterogeneity respectively. We discuss these results below.

The lack of superior convergence of loci with *a priori* high information content is perhaps surprising but not unprecedented (Chen *et al.*, 2015). This may not be a failure of the methods (i.e., MARE and SAMS) to infer information content but rather an inappropriate application of the methods. For instance, the subset of taxa we applied these methods to have

been insufficient since taxon sampling impacts inferred character evolution (Hugall and Lee, 2007; Venditti *et al.*, 2006). Additionally, MARE intentionally scores a locus as being uninformative if there is a high proportion of missing data, and missing data patterns change after new sequences are added. Thirdly, single genes may not contain enough characters to inform phylogenetic information estimators. Assignment of character state changes as autapomorphies, synapomorphies or symplesiomorphies depends on the number of available characters. Finally, the methods could be confounded by long branch attraction (LBA), mistaking saturated loci for highly tree-like loci and wrongly attributing homoplasy to split support. While we do not see exceedingly long branches, all the reconstructed trees do exhibit features typical of long branch effects [e.g., abundant short internodes (Fig. 2 and Fig. S3.1) and a high leafiness (Table 2); Kück *et al.*, 2012; Wägele and Mayer, 2007].

Yet, the high support for the 265\_Full tree among the trees inferred from the *a priori* high information content loci might suggest that there is a more signal in these data. Filtering of loci with SAMS to determine information content resulted in discarding loci with strong signal for conflicting relationships. This relates directly to tree certainty, which is higher when the abundance of alternative topologies is low. We would note though, that the set of loci used for comparison (i.e., *a priori* non-high information content) also lent moderately high support for the 265\_Full tree. Both analyses indicate that the relationships in the tree can be reliably inferred from either set of loci and thus true information content may be well distributed in either set of loci.

Fast evolving and low saturation loci converged rapidly towards the expected topology. This result contradicts the idea that saturation is a consequence of high evolutionary rate of a locus, two features that were not highly correlated ( $R = -0.11$ ; Table S1.1, S1.2) in our dataset. This seemingly contradictory finding results from how we calculated these values and how we framed our study on whole loci. First, we used tree-independent methods for approximating evolutionary rates and saturation, which were most appropriate for designing our experiment but do not provide the most sensitive estimates (see Supplement S1). Second, since we used the mean rate of the entire locus we are losing information about the distribution of rates within that locus. Evolutionary rate of an individual nucleotide position would correlate highly with true substitution saturation. However, when considering the mean rate of all positions in a locus, loci with a low or high mean rate can be equally saturated. For instance, consider two loci of equal length. All third codon positions may be saturated in both loci but in one the other codon positions may be informative and fast evolving while in the other they may be invariant. This suggests that a more informative value would be the distribution of site-specific rates for a given locus. This also contrasts with the assumption that slow evolutionary rates are assumed to be superior (Chen *et al.*, 2015). Although the superiority of slow rates are only supported when fast evolutionary rate result in saturation and the optimal rate changes depending upon the phylogenies' shape (Dornburg *et al.*, 2018). Unsaturated but fast evolving loci should have a higher density of phylogenetic information than slow loci.

Despite the overall low convergence of highly saturated loci, they lent relatively higher node support to the 265\_Full tree. Convergence was calculated as the mean RF distance to four plausible species trees, and thus these tests are not directly analogous, but the comparison is



interesting none-the-less. The wide variance in RF values among trees from low saturation loci (Fig. 4A) suggests a diverse sample of trees, many of which are very different from the four baseline trees. Another potential reason for the high node support demonstrated by high saturation loci could be that some relationships in the 265\_Full tree are falsely informed by highly saturated sites (i.e., long branch attraction).

Low rate-heterogeneity among loci also improved convergence in tree topology (Figs. 3, 4). This is consistent with studies showing that rate heterogeneity confounds the assumptions of phylogenetic models (Frandsen *et al.*, 2015; Galtier *et al.*, 2006) and better adherence to those models improves phylogenetic inference (Doyle *et al.*, 2015; Kjer and Honeycutt, 2007; Reddy *et al.*, 2017). However, this effect is only seen if locus rate heterogeneity is corrected for locus length. Uncorrected high rate heterogeneity is not problematic (Fig. S4.4) since a higher variance in rates can be a result of loci being longer (Table S1.1). In reference to support of the 265\_Full topology, while more heterogeneous loci resulted in higher tree certainty, the difference in certainty from low heterogeneity loci was negligible.

Strong stabilizing selection (Figs. 3, 4), as defined by low mean dN/dS, also improved tree convergence. This agrees with higher mean locus dN/dS corresponding to: more non-synonymous sites under positive selection, which are difficult to model (discussed in Beaulieu *et al.*, 2019); and purifying selection of synonymous substitution (Spielman and Wilke, 2015), which yield compositional bias and phylogenetic errors (Cox *et al.*, 2014).

Minimizing mean pairwise sequence distance among loci yielded the greatest improvement to tree convergence (Figs. 3, 4) and increased node support (Table 1). Sequence distance is correlated to a suite of other features also related to phylogenetic utility (Bai *et al.*,

2013; Borowiec, 2019; Borowiec *et al.*, 2015; Chen *et al.*, 2015; Lewis *et al.*, 2016; Struck, 2014). In particular, decreasing mean pairwise sequence distance may be similar to minimizing saturated loci because they both reduce the probability of LBA (Struck, 2014). LBA can lead to rogue taxon placement, which our analysis is particularly sensitive to due to usage of the RF metric (Kuhner and Yamato, 2015).

Our experimental design specifically attempts to control for extraneous features (see Figs. S1.1, S4.2, S4.4). We paid particularly close attention to locus length which was moderately correlated with rate heterogeneity, mean pairwise sequence distance, and saturation (Table S1.2). Yet, these treatments with longer loci did not perform better (i.e., Fig. S4.4). Thus, more effectively controlling for locus length may yield a stronger effect-size.

### *Phylogenomic Improvements*

Our analyses demonstrate some clear relationships between features of genetic loci and the quality of downstream phylogenetic inference. These relationships could be used to improve future analyses. As a test of this, we inferred two additional phylogenetic trees, 100\_Full and C100\_Full, using collections of loci deemed to improve convergence on the species tree. Both of these trees demonstrate patterns consistent with higher phylogenetic signal (Table 2) (Dornburg *et al.*, 2018) and the C100\_Full tree demonstrated the most plausibility given an alignment (Table 2). Regardless of if these represent true topological improvements, we have remarkably inferred two exceptionally similar trees (Table 2) with comparable node support after discarding a majority of the data (Fig. 5).

Reducing dataset size has practical implications for phylogenetic projects. Computation time for alignment estimation and topology testing (AU test) is reduced proportionally to the reduction in dataset size (Table 3). Gains in efficiency of phylogenetic inferences are 4-6 fold improvements (Table 3). These are significant in practice. For instance, the C100\_Full tree only took 275 CPU hours to reach the optimization stop criteria, over a month faster than 265\_Full (1025 CPU hours). Reducing heterogeneous loci provides the ability to simplify the evolutionary mode – avoiding over-parameterization (Sullivan and Joyce, 2005) and further improving computation time. We did not re-estimate optimal partition and model schemes for our dataset so we could consistently compare our results with the 265\_Full phylogeny. Yet, doing so would be a qualitative improvement (e.g., Philippe and Roure, 2011).

Reducing computational effort of tree inference is important considering that phylogenetic studies rarely do such analyses only once. For instance, we conducted two preliminary tree inferences and two quality checking inferences, each of which involved analyzing the 265\_Full alignment. When adding together main tree searches, those of different alignment conformations and assessing support through resampling methods, computation time becomes a limiting resource even when having access to multiple world-class supercomputing clusters (e.g., Shen *et al.*, 2017 and this study). Improving the practicality of inferring trees and their support makes the application of downstream analyses (e.g., divergence date inference, diversification analyses, inferring trait evolution) more feasible as well. The important caveat, though, is one must have a large preliminary dataset from which to select the most optimal loci.

## *Conclusions*

We inferred a robust phylogeny of Blaberoidea using 265 genomic loci and 126 taxa. This phylogeny provides congruence for previously hypothesized relationships and some novel classifications that can now be defined with advanced genomic and taxon sampling. When subsampling loci by quality, we find that the relationships in the tree are primarily supported by loci with high evolutionary rate, low saturation, low mean pairwise sequence distance, low rate heterogeneity, and strong stabilizing selection. Calculating *a priori* phylogenetic information content, as defined by split signal and tree-likeness, did not meaningfully provide additional support for relationships. These findings are consistent with past studies and phylogenetic theory (Cox *et al.*, 2014; Dornburg *et al.*, 2018; Doyle *et al.*, 2015; Townsend, 2007), and provide the opportunity to potentially target increasingly informative loci with locus capture methods (Brandley *et al.*, 2015; Gilbert *et al.*, 2015; Lemmon *et al.*, 2012). Subsamples reduced by two thirds of total data length and optimized under the above specifications exhibited recovery of a phylogeny exceptionally similar to the tree inferred from all the data. Thus, targeting maximally phylogenetically useful loci can potentially reduce the monetary cost and computational resources of projects drastically while maintaining the quality of the results.

## *Availability of data and material*

Transcriptome datasets were taken from Evangelista *et al.* (2019) and newly sequenced data is deposited on the NCBI Sequence Read Archive (SRP155429). Other analyzed files are available on the Dryad digital repository (doi:10.5061/dryad.9mf1pr7).

Dryad link for reviewers: <https://datadryad.org/review?doi=doi:10.5061/dryad.9mf1pr7>

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## *Authors' contributions*

DAE, FL and AYK obtained funding for the study. DAE and FL conceived the study and organized the taxon sampling design. DAE ran preliminary analyses and designed genomic sampling with assistance from SSi and BW. DAE, MMW and JLW designed the molecular baits. DAE extracted and enriched genomic DNA, with MMW, JLW, and MKK providing guidance. DAE did all bioinformatics, wrote custom software, executed all analyses, with guidance from FL. DAE, OB and FL revised taxonomic descriptions of taxa with assistance from BW. DAE and FL wrote the paper with assistance from SSi, AYK and BW. DAE and BW composed the figures. SSi, BW, JLW, MKK, and OB, provided early access to transcriptome datasets and contributed in analyses and curation of those datasets as well as feedback to the manuscript.

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## Conflict of Interest statement

The authors declare no conflicting interests.



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## TABLES AND FIGURES

### *Figure legends*

Figure 1 - Distributions of feature values tested for phylogenetic utility. Box-plots show the distribution of values (rescaled between 0 and 1) for both treatments of eight factors tested: substitution rate, substitution saturation, mean pairwise sequence distance, among site rate heterogeneity corrected for locus length, selection (dN/dS), *a priori* information content, locus length, and total among site rate heterogeneity. Boxes represent middle 75% quantiles; whiskers represent the remaining quantiles with points being outliers. White lines are the median and black lines are the mean. N indicates how many loci are in each treatment.

Figure 2 - Phylogeny of Blaberoidea (265\_Full tree) as inferred from a partitioned RAxML tree inference from 265 loci. Support values in color-coded Navajo rugs are internode certainty and bootstrap frequency scores calculated from three trees, as described in the legend. “NA”/pink indicates the bipartition does not appear in the specified tree. Branch lengths are proportional to substitutions. Numbers correspond to tip taxa depicted in photographs. Photographs by Dominic A. Evangelista.

Figure 3 - RADICAL curves for six tests of phylogenetic utility. Dots represent the mean Robinson-Foulds distance to four baseline trees. Lines show best fit exponential curves.

Figure 4 - Distribution plots showing (A) mean similarity (RF distance) to baseline trees and (B) similarity among tree inferences of two treatments for six factors. Each comparison is from the 14<sup>th</sup> concatenation step of each RADICAL run. Asterisks indicate a statistically significant difference, as determined by a Z-Test of mean comparisons ( $\alpha < 0.005$ ).

Figure 5 - Heat map of support for selected backbone relationships in Blaberoidea. Support for relationships are given for the nine trees indicated in column labels. Alternative proposed relationships are indicated by cell coloration. Only relationships with more than 70% support are consider unambiguous and colored solidly [see Evangelista *et al.* (2018) for the method of calculating support for relationships from bipartition support values]. Nucleotide length of each alignment is shown in the bottom row, and the cell is colored proportional to the values.

## Tables

Table 1

Table 1 - Comparison of support for the 265\_Full tree among RADICAL tree sets.

Feature	Value	Relative tree certainty <sup>a</sup>	Relative-Tree Certainty-All <sup>b</sup>	Tree Certainty / Alignment Length	Tree Certainty / # of loci
Substitution rate	Fast	0.581	0.599	5.65E-06	0.00599
	Slow	0.546	0.577	5.90E-06	0.00563
Substitution saturation	High	0.538	0.569	7.13E-06	0.00657
	Low	0.462	0.489	7.02E-06	0.00563
Pairwise sequence distance	High	0.491	0.523	5.83E-06	0.00564
	Low	0.562	0.567	7.75E-06	0.00646
Rate heterogeneity (corrected)	High	0.516	0.550	7.91E-06	0.00670
	Low	0.492	0.521	7.09E-06	0.00639
Stabilizing selection	Strong	0.540	0.570	6.15E-06	0.00587
	Weak	0.517	0.531	5.77E-06	0.00562
Aprior information content	High	0.578	0.598	6.89E-06	0.00628
	Low	0.538	0.547	6.45E-06	0.00584
Locus Length	Long	0.557	0.592	4.30E-06	0.00680
	Short	0.405	0.434	9.43E-06	0.00494

<sup>a</sup> Relative tree certainty (rTC) is the sum of all internode certainties (IC) normalized by the number of non-tip edges (Kobert *et al.*, 2016; Salichos *et al.*, 2014). IC scores are the relative frequency of the recovered bipartition in relation to the two most frequently recovered bipartitions.

<sup>b</sup> Relative tree certainty-All is the same as rTC but calculated with IC-All. IC-All scores are the relative frequency of the recovered bipartition in relation to the all the other most frequently recovered bipartitions (Kobert *et al.*, 2016; Salichos *et al.*, 2014).





Table 2

Table 2 - Comparison of tree quality and support among nine trees.

<b>Tree</b>	<b>Leafiness<sup>a</sup></b>	<b>RF<sup>b</sup></b>	<b>ln L<sup>c</sup></b>	<b>Mean tree bootstrap support</b>	<b>Relative tree certainty</b>	<b># of AU tests passed<sup>d</sup></b>
265_Full	0.171	0	-3038176.6	92.1	0.81	1
265_2nd	0.214	60	-433293.3	73.7	0.51	0
265_Reduced	0.151	56	-793673.2	87.4	0.75	0
100_Full	0.154	48	-919296.0	87.9	0.72	1
100_2nd	0.179	98	-117967.0	60.9	0.34	0
100_Reduced	0.151	66	-444162.8	85.9	0.70	0
C100_Full	0.164	20	-1207800.6	89.7	0.74	2
C100_2nd	0.198	96	-159517.2	65.4	0.41	0
C100_Reduced	0.157	44	-501350.8	87.8	0.74	1

<sup>a</sup> The ratio of total tip branch lengths to internal branch lengths.

<sup>b</sup> Robinson-Foulds distance to the 265\_Full tree.

<sup>c</sup> Log-likelihood of the tree given its alignment.

<sup>d</sup> how many times the tree was accepted ( $p > 0.05$ ) by an AU test (maximum of three).

Table 3

Table 3 - Comparison of various activities derived from three alignment conformations of 265 loci and two sets of 100 loci.).

<b>Alignment</b>	<b>Alignment length</b>	<b>CPU time for best tree (Hrs)<sup>a</sup></b>	<b>Bootstrap replicates to meet stop criteria</b>	<b>AU test CPU time (min)<sup>b</sup></b>	<b>Time to align (min)<sup>c</sup></b>
265_Full	268,202	1025.4	60	96	132.5
265_2nd	89,411	175.6	300	-	NA
265_Reduced	39,808	109.8	108	-	NA
100_Full	65,798	166.0	156	37	40
100_2nd	21,937	27.2	408	-	NA
100_Reduced	21,449	37.6	108	-	NA
C100_Full	83,822	275.0	60	36	53
C100_2nd	27,946	38.4	360	-	NA
C100_Reduced	23,982	38.6	108	-	NA

<sup>a</sup> 100 starting trees in RAxML.

<sup>b</sup> 10,000 RELI bootstraps, unpartitioned analysis for nine trees

<sup>c</sup> Extrapolated from alignment of 10 unaligned FASTA files of varying lengths using MAFFT (options: -localpair -maxiterate 1000 -adjustdirection)

Figures

Figure 1

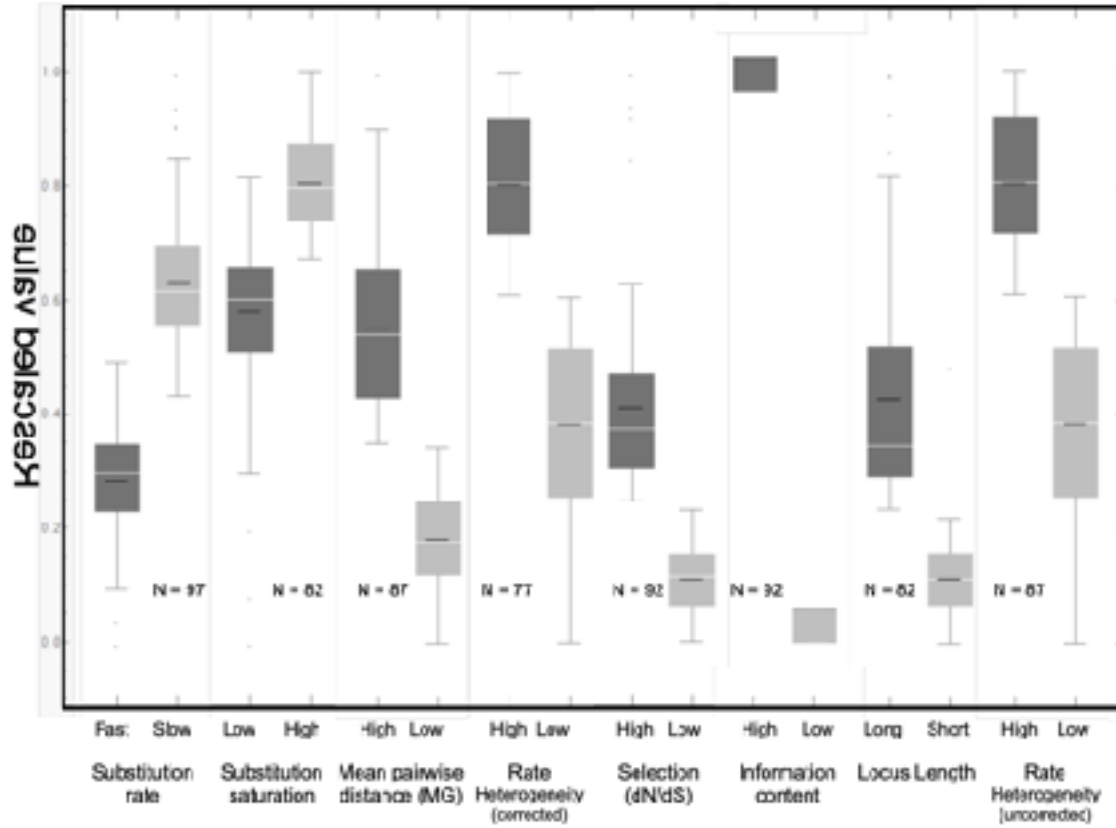




Figure 3

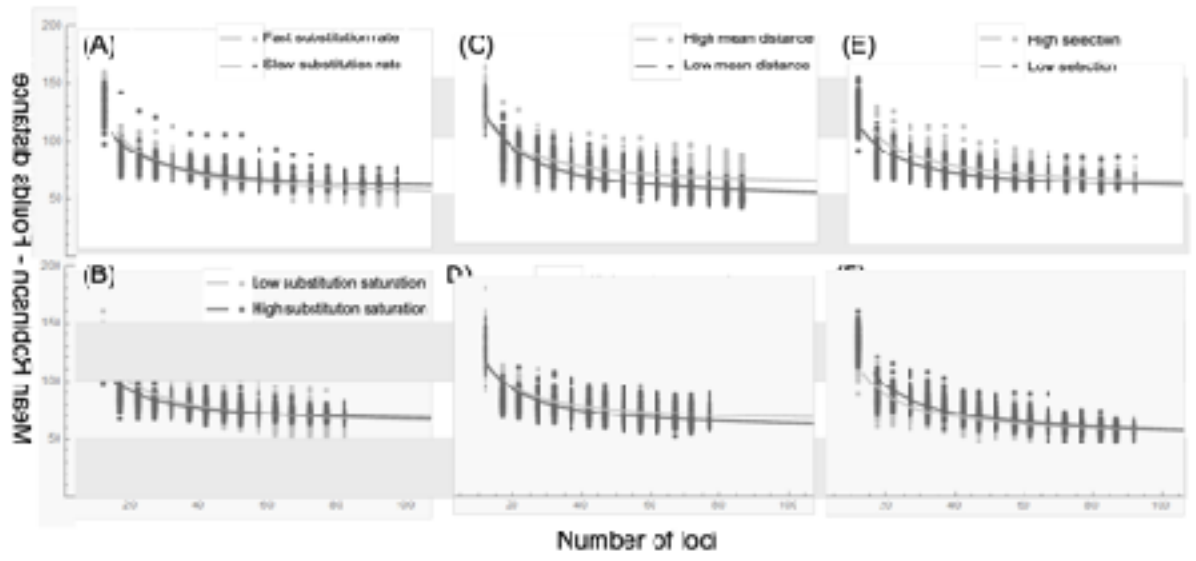


Figure 4

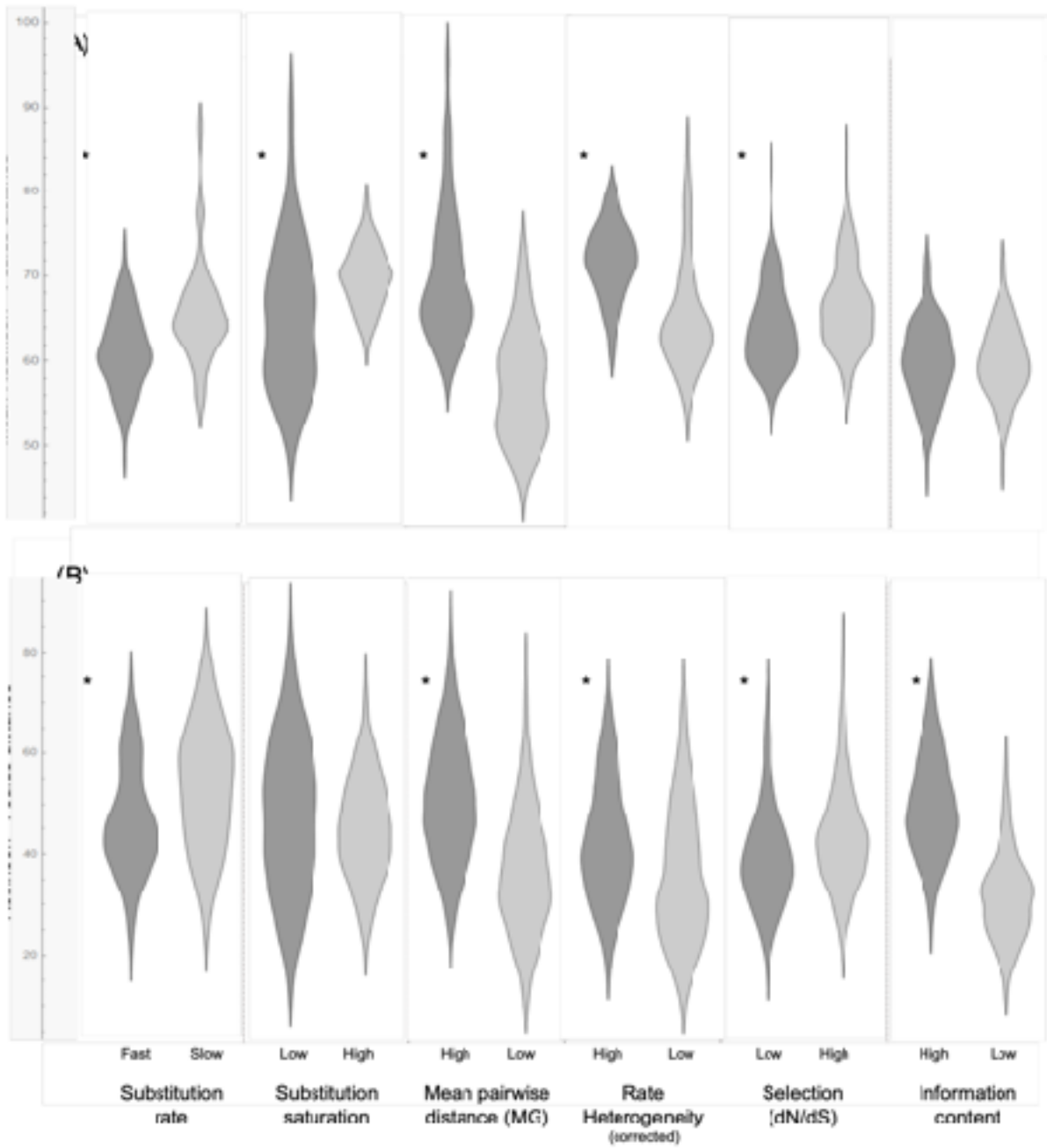


Figure 5

		265_Full	100_Full	C100_Full	265_Reduced	100_Reduced	C100_Reduced	265_2nd	100_2nd	C100_2nd
Sister to remaining Blaberoidea	Ectobiidae									
	<i>Mediastinia</i> sp.									
Sister to Pseudophyllodromiinae	Anallactinae									
Sister to remaining Pseudophyllodromiinae	Neoblattellini									
Sister to Blattellinae	Nyctiborinae <i>Nyctibora</i> sp.									
	Nyctiborinae [- <i>Paratropes</i> ( <i>Megaloblatta</i> sp. + <i>Nyctibora</i> sp.) + Blattellinae									
	( <i>Symplocini</i> + Blattellini)									
Sister to remaining Blattellinae	( <i>Symplocini</i> + Blattellini)									
Sister to Blaberidae	Blattellidae									
Sister to remaining Blaberidae	<i>Rhabdoblatta stipata</i>									
Sister to Peri-Atlantic Blaberidae	Peri-Indian Blaberidae									
Sister to Neotropical Epilamprinae	Remaining Blaberidae									
Ambiguous (<70%) relationship support		268,202	65,798	83,822	39,808	21,449	23,982	89,411	21,937	27,946
		Nucleotide length								



## SUPPORTING INFORMATION

**Supplementary text S1-S5.** Supplementary results and discussion. Supplemental methods (S1), Taxonomic changes (S2), supplemental discussion of the Blaberoidea phylogeny (S3), additional tests of locus quality (S4), and evaluation of data reduction for phylogenetics (S5).

**Supplementary data.** Supplementary data and results files. Data include alignments, PartitionFinder files, preliminary taxonomic hypotheses, loci features, and taxon list. Results include RADICAL output files and phylogenetic trees.