Relaxed Phylogenetics and the Palaeoptera Problem: Resolving Deep Ancestral Splits in the Insect Phylogeny

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Received 25 February 2011; reviews returned and accepted 30 November 2012

Associate Editor: Thomas Buckley

Abstract.—The order in which the 3 groups of winged insects (the Pterygota) diverged from their common ancestor has important implications for understanding the origin of insect flight. But despite this importance, the split between the Odonata (dragonflies and damselflies), Ephemeroptera (mayflies), and Neoptera (the other winged orders) remains very unresolved. Indeed, previous studies have obtained strong apparent support for each of the 3 possible branching patterns. Here, we present a systematic reinvestigation of the basal pterygote split. Our results suggest that outgroup choice and limited taxon sampling have been major sources of systematic error, even for data sets with a large number of characters (e.g., in phylogenomic data sets). In particular, a data set of 113 taxa provides consistent support for the Palaeoptera hypothesis (the grouping of Odonata with Ephemeroptera), whereas results from data sets with lower taxa give inconsistent results and are highly sensitive to minor changes in data and methods. We also focus on recent methods that exploit temporal information using fossil calibrations, combined with additional assumptions about the evolutionary process, and so reduce the influence of outgroup choice. These methods are shown to provide more consistent results, for example, for supporting Palaeoptera, even for data sets that previously supported other hypotheses. Together, these results have implications for understanding insect origins and for resolving other problematic splits in the tree of life. [Bayesian phylogenetics; BEAST; Insect Phylogeny; Metapterygota; Palaeoptera; Pterygota.]

The evolution of flight allowed the winged insects, the Pterygota, to become one of the most diverse and successful groups on the planet (Grimaldi and Engel 2005). In 1924, Martynov divided the Pterygota into 2 parts: defining the Neoptera, or “new winged” insects, on the presence of complex structural elements that enable the wings to be folded back over the abdomen (Martynov 1924), and by elimination, the Palaeoptera, or “old winged” insects, which lack these structures. There are 3 supraordinal divisions of the Palaeoptera, namely, the dragonflies and damselflies (order Odonata), the mayflies (order Ephemeroptera), and the extinct (Carboniferous–Permian) superorder Palaeodictyopteroidea. Since then, while the monophyly of the Neoptera has been almost universally accepted (Martynov 1924; Hennig 1953, 1969; Kristensen 1991; Grimaldi and Engel 2005), the monophyly of the Palaeoptera and its extant taxonomic range (Odonata + Ephemeroptera) has been the subject of much debate. Indeed, different researchers have argued for all 3 possible branching patterns between the Odonata, Ephemeroptera, and Neoptera (Fig. 1). A clear resolution of these relationships is necessary for inferring the characteristics of the ancestral pterygotan insect and is thus crucial for understanding the origin of winged insect flight (Kingsolver and Koehler 1994).

Unfortunately, the application of cladistic methodology to large morphological data sets has been unable to resolve the Palaeoptera problem, and different authors have identified multiple synapomorphies that support the monophyly of the Palaeoptera (Fig. 1a; Martynov 1924; Hennig 1969; Kukalová-Peck 1983, 1991, 2008; Bechy 1996; Haas and Kukalová-Peck 2001), the Chiasiomyaria (Fig. 1b; Boudreaux 1979; Carle 1982a, 1982b), and the Metapterygota (Fig. 1c; Hennig 1953; Kristensen 1991; Staniczek 2000; Wheeler et al. 2001; Grimaldi and Engel 2005; Beutel and Gorb 2006; Willkommen and Hörnschemeyer 2007). In some respects, the disagreements among these studies are unsurprising because of the lack of a suitable outgroup for many characters. This is particularly true of wing venation characters, which are a major source of characters for proponents of all 3 hypotheses.

Other similar cases have been resolved by the introduction of molecular data. For example, the monophyly of the Ecdyssozoa (Aguinaldo et al. 1997); the close relationship between Crustacea and Hexapoda (Friedrich and Tautz 1995; Boore et al. 1998; Mallatt et al. 2004, Regier et al. 2005); or the position of Isoptera within Dictyoptera (Inward et al. 2007). However, concerning the basal pterygote relationships, molecular studies have shown no more agreement than have morphological approaches. Significant molecular support has been offered for the Palaeoptera (Giribet and Riberia 2000; Wheeler et al. 2001; Horváth et al. 2002; Kjer et al. 2006; Regier et al. 2010), Chiasiomyaria (Kjer 2004; Mallatt and Giribet 2006; Misof et al. 2007; Simon et al. 2009), and Metapterygota (Wheeler 1989; Ogden and Whiting 2003; Zhang et al. 2008) hypotheses. Even recent studies with large “phylogenomic” data sets (Zhang et al. 2008; Simon...
et al. 2009; Meusemann et al. 2010; Regier et al. 2010) have failed to resolve the issue.

These striking disagreements may reflect a real biological phenomenon: the rapid divergence of all 3 groups from their common ancestor in the distant past. The possibility of a rapid radiation in the evolution of the early winged insects is supported by the almost simultaneous appearance in the lowermost Upper Carboniferous of fossils identified as stem members of the 3 extant pterygotan lineages, and a complete lack of fossils assignable to any common stem (Carpenter 1992; Rasnitsyn and Quicke 2002; Grimaldi and Engel 2005). There are also well-characterized examples from other taxa, where phylogenetic disagreement and simultaneous appearance in the fossil record are combined with the signature of incomplete lineage sorting, strongly implying that 3 groups diverged in rapid succession (e.g., the 3 mammalian orders that comprise the Paenungulata [Nishihara et al. 2005]).

Whether or not it leads to genuinely conflicting signal among characters, ancient rapid radiation can also lead to weak phylogenetic signal, which may make analyses more susceptible to systematic error (i.e., more sensitive to small inadequacies in the data or methods employed [Felsenstein 1978; Hedtke et al. 2006]). Nevertheless, many studies of deep pterygote relationships have included only single members of Odonata and Ephemeroptera. Problems of limited taxonomic sampling are particularly acute when it comes to the choice of outgroup (Bergsten 2005; Shavit et al. 2007; Rota-Stabelli and Telford 2008), especially because many apterygotes have very fast rates of molecular evolution (Whiffin and Kjer 2008).

Second, systematic bias may arise from the choice of phylogenetic methods and their models. The use of parsimony has been prevalent in studies of the pterygotan splits (Giribet and Ribera 2000; Wheeler et al. 2001; Hovmöller et al. 2002; Ogden and Whiting 2005), but this method is particularly susceptible to long-branch-attraction problems (Felsenstein 1978; Hendy and Penny 1989). Even with explicitly model-based methods, model misspecification can lead to error. For example, artifactual groupings can arise from a failure to account for nonstationary base composition (Delsuc et al. 2003; Phillips and Penny 2003). The same problems can apply to algorithms such as POY, which performs alignment and topological estimation simultaneously (Kjer et al. 2007; Yoshizawa 2010).

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This study investigates the Palaeoptera problem, making a particular attempt to address potential sources of error discussed above. First, we use wide taxonomic sampling across the Palaeoptera, targeting as many genes for as many taxa as possible, with a supermatrix approach. Second, we use explicit tests and corrections for base compositional bias, employing RY recoding to remove any Guanine-Cytosine (GC) heterogeneity and
METHODS

DNA Sequence Data

For our core data sets, sequence data from species of Odonata, Ephemeroptera, Neoptera, and outgroup taxa were collected from Genbank (www.ncbi.nlm.nih.gov) (see Supplementary Table S1 for details: http://datadryad.org, doi: 10.5061/dryad.7d2g2). We aimed to target a representative species sample from each order for genes with wide taxonomic coverage. A supermatrix approach to gene alignment was used; there

to mitigate the loss of phylogenetic signal over time (Phillips and Penny 2003). Third, in addition to the standard phylogenetic methods employed in previous studies, this study uses the relaxed-clock method implemented in BEAST (Drummond et al. 2006), along with temporal information about arthropod divergences derived from the fossil record (Table 1). By exploiting temporal information to inform topological inference, this method removes the need to include outgroup taxa in the analysis; this allows us to assess the influence of outgroup choice on the results obtained.

Table 1. Dating information for BEAST analyses

<table>
<thead>
<tr>
<th>Node</th>
<th>Fossil and deposit locality</th>
<th>Age (Ma)</th>
<th>Reference</th>
<th>Prior distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Root</td>
<td>Crustacea–Hexapoda split</td>
<td>Lower Cambrian, 543–550</td>
<td>Benton et al. (2009) and Siveter et al. (2003)</td>
<td>Exponential, mean = 8, offset = 500</td>
</tr>
<tr>
<td>1 Collembola</td>
<td>Rhynieza praecursor (springtail) from Rhynie chert, Scotland</td>
<td>Devonian: (Pragian–Emsian), 412.3–391.9</td>
<td>Grimaldi and Engel (2005) and refs therein; Palaeobiology database: <a href="http://paleodb.org/">http://paleodb.org/</a></td>
<td>Lognormal, mean = 30, log(SD) = 0.6, offset = 391.9</td>
</tr>
<tr>
<td>2 Pterygota</td>
<td>Gr滋nflies (Protodonata) and Protorthopterans (ancestral Neoptera) from Commentry and Montceau-les-Mines deposits, France; Lithoncera lamersii (Protoephemeroptera) from Mazon Creek, Illinois</td>
<td>Members of all groups present by Late Carboniferous, 318–299</td>
<td>Grimaldi and Engel (2005) and references therein</td>
<td>Normal, mean = 369.0, SD = 22.5</td>
</tr>
<tr>
<td>3 Orthoptera</td>
<td>Raphidula rubra (oldest representative of modern Ensifera), Ledoe Basin, France</td>
<td>Late Permian, 260–251</td>
<td>Bethoux et al. (2002), in Grimaldi and Engel (2005)</td>
<td>Gamma, shape = 2.0, scale = 13.45, offset = 251.0</td>
</tr>
<tr>
<td>4 Dictyoptera</td>
<td>Bazcisuterines lapidus (Isoptera) from Zaza formation of Baissa, Siberia, Russia</td>
<td>Early Cretaceous, 145–99.6</td>
<td>Engel et al. (2007) and Gratshev and Zherikhin (1994)</td>
<td>Gamma, shape = 2.0, scale = 33.4, offset = 99.6</td>
</tr>
<tr>
<td>6 Hemiptera</td>
<td>Panaxonius magnifica (Heteroptera) from Newcastle Coal Measure, Australia</td>
<td>Late Permian, 260–251</td>
<td>Percival (1985)</td>
<td>Gamma, shape = 2.0, scale = 13.5, offset = 251.0</td>
</tr>
<tr>
<td>7 Hymenoptera</td>
<td>Cretotrigona prisca (Hymenoptera: Apidae) from Maastrichtian amber from New Jersey</td>
<td>Late Cretaceous, 65–80</td>
<td>Michener and Grimaldi (1989a, 1989b) and Engel (2000)</td>
<td>Gamma, shape = 2.0, scale = 65.0, offset = 145.0</td>
</tr>
<tr>
<td>8 Ephemeroptera</td>
<td>Paragynura gregaria and Shantius lacustris (Ephemeropoda) from Coahuila amber, extinct mayflies from the Daohugou formation of China</td>
<td>Early Jurassic, 201.6–197</td>
<td>Grimaldi and Engel (2005) and Nel et al. (1993)</td>
<td>Gamma, shape = 2.0, scale = 23.2, offset = 197.0</td>
</tr>
<tr>
<td>9 Anisozygoptera</td>
<td>Liassogomphus brodieri, from Liassic outcrops in Europe, including Switzerland, Germany, England, and Luxembourg</td>
<td>Early Jurassic, 201.6–197</td>
<td>Grimaldi and Engel (2005) and Nel et al. (1993)</td>
<td>Gamma, shape = 2.0, scale = 23.2, offset = 197.0</td>
</tr>
<tr>
<td>10 Aeshnidae/ Petaluridae/ Gomphidae</td>
<td>Aeshnidae/Petaluridae/Gomphidae taxa</td>
<td>Middle to Late Jurassic, 161–145</td>
<td>Fleck et al. (2008)</td>
<td>Gamma, shape = 2.0, scale = 32.5, offset = 145.0</td>
</tr>
<tr>
<td>11 Zygoptera</td>
<td>Triassosolidae taxa from Triassic deposits of South America, Australia and Central Asia</td>
<td>Triassic, 251–201.6</td>
<td>Carpenter (1992)</td>
<td>Gamma, shape = 2.0, scale = 22.4, offset = 201.6</td>
</tr>
<tr>
<td>12 Archaeogrylidae</td>
<td>Triassomachilus urtensis, Triassic deposits in Russia</td>
<td>Triassic, 251–201.6</td>
<td>Shatov (1948) in Grimaldi and Engel (2005)</td>
<td>Gamma, shape = 2.0, scale = 22.4, offset = 201.6</td>
</tr>
</tbody>
</table>

Note: All geological ages are in accordance with Walker and Geissman (2009).
is evidence that missing data are not a serious problem for topological reconstruction, if most taxa have data for most bases in the sequence (Wiens and Morrill 2011, but see also Lemmon et al. 2009). Nevertheless, we avoided genes for which there were only a few representative species. In some cases, when not all of the sequence data were available for a single species, chimerical taxonomic units were assembled from 2 members of the same genus, or in a few cases from 2 members of the same family.

For our primary data set, “data set 1,” we compiled sequence data from 113 species; 35 from each of the Odonata, Ephemeroptera, and Neoptera, plus 8 outgroup taxa from Thysanura, Archaeognatha, Collembola, and Diptera (Crustacea). This sampling scheme represents near-complete family-level coverage for the Odonata (26/32 families recognized in the World Odonata List; Schorr et al. 2010), a large proportion of Ephemeroptera families (28/42 families recognized by Barber-James et al. 2008), and near-complete ordinal-level coverage for the more diverse Neoptera (25/28 recognized orders) (see Supplementary Table S1 for more information). The sequences for data set 1 comprised four ribosomal genes: mitochondrial 12S and 16S (788 bp), nuclear 18S and 28S (3595 bp), as well as one nuclear protein-coding gene: histone 3 (313 bp) (342 bp of coding region); total sequence length was 4725 bp.

We also compiled a second data set, “data set 2,” with a greatly reduced taxon sample of 10 species per order, together with outgroups (38 species in total). For these taxa, 2 additional gene sequences were available: mitochondrial COII (684 bp), and nuclear EF1a (1077 bp of coding region) (total sequence length = 6365 bp).

Ribosomal sequences were aligned manually in Se-Al (Rambaut 1996). Where RNA alignment was unclear, RNA secondary structures were referred to from the Gutell Lab database (Cannone et al. 2002). Any highly variable regions that could not be aligned confidently were excluded from phylogenetic analysis and the remaining sequences were concatenated. For further analyses, data were partitioned by gene because our markers differed in genomic location, base composition, and, perhaps, in levels of selective constraint. In addition, for protein-coding genes, an additional partition applied to the third codon positions, which are primarily synonymous and so subject to very different levels of constraint (see also Shapiro et al. 2006 who argue for this partition choice on empirical grounds).

Base Composition Bias

Base composition heterogeneity across taxa can add systematic error to analyses (Conant and Lewis 2001). Accordingly, all partitions in all data sets were assessed with the basefreq command in PAUP*4.0b10 (Swofford 2003), which uses a chi-squared test for base frequency differences among taxa. When significant heterogeneity was found in a partition, we compiled new versions of our alignment, using RY recoding (Phillips and Penny 2003). In practice, this involved coding all purines as G and all pyrimidines as C for further analysis. Data were then retested for heterogeneity. In cases where RY recoding did not remove composition bias, biased partitions were excluded from the alignment. Details of all sequences recoded and excluded can be found in Supplementary Table S2.

Additional problems can arise with the use of mitochondrial markers which are rapidly evolving, subject to strand inversion bias (Hassanin et al. 2005) and have given anomalous results elsewhere in the arthropod tree (Delsuc et al. 2003; Nardi et al. 2003; Cameron et al. 2004; Hassanin 2006; Carapelli et al. 2007; Rota-Stabelli and Telford 2008; Timmermans et al. 2008; Masta et al. 2009; Rota-Stabelli et al. 2010a). Accordingly, we also repeated all analyses with these markers excluded.

Phylogenetic Analyses

Maximum-likelihood (ML) analyses were conducted in RAxML, v.70.4 (Stamatakis 2006; Stamatakis et al. 2008), applying the general time-reversible (GTR) model of sequence evolution with across site rate variation modeled to a Gamma distribution, (GTR+Γ)—corresponding to the GTRGAMMA model in RAxML for each partition (Rodriguez et al. 1990). Twenty separate ML analyses were performed (using the “-d” command in RAxML), and the tree with the highest likelihood was chosen from this set. A separate thorough bootstrap analysis with 100 replicates was also executed to examine the relative support for each clade.

For Bayesian analyses, topology and divergence dates were estimated simultaneously in BEAST v1.7 (Drummond and Rambaut 2007). Data were partitioned and for the four-nucleotide-encoded regions, a GTR+Γ model was applied, for comparison with the ML results. For the RY-recoded regions only 2 substitution types were possible, and so we used the F81+Γ model (Felsenstein 1981) (implemented in BEAST by fixing the transition/transversion ratio, to 0.5 in an HKY+Γ model). The birth–death model of speciation and an uncorrelated lognormal-relaxed molecular clock model were employed, with all parameters estimated from the data. Clock and tree parameters were linked across partitions, but a separate substitution rate parameter “mu” was estimated for each. Prior distributions on the root and 11 other nodes were applied based on an interpretation of the arthropod fossil record. BEAST requires that these dated nodes be monophyletically constrained. We consequently placed date distributions and constraints only on nodes that were highly supported in the ML analysis. Full details of all prior distributions for divergence times are found in Table 1. All other priors were left as the default values in BEAUri (Drummond and Rambaut 2007).

Supplementary Table S3 summarizes the distributions for the marginal priors specified for each calibrated node and compares these to the values obtained from running the complete prior (see below for details). This suggests
that, in this case, interaction between the different elements of our prior did not substantially distort our actual prior knowledge (Heled and Drummond 2012).

All BEAST analyses in this study were run for a total of 200 million generations and sampled every 20,000 generations. Convergence and the resultant proportion of burn-in were assessed using the diagnostic plots in the programs “Are We There Yet” (AWTY; Wilgenbusch et al. 2004) and Tracer v1.5 (available from http://beast.bio.ed.ac.uk/). The effective sample sizes (ESSs) of parameters of interest (species tree, relaxed-clock parameters) were greater than 1000, and all ESS values were above 100. Most analyses had a burn-in of 50 million generations resulting in 15,000 trees in the posterior distribution, and all had at least 10,000 sampled trees.

To test the strength of support for the 3 hypotheses using Bayesian methods, Bayes factors were calculated. To establish the prior probabilities of the 3 possible groupings, analyses were rerun with nucleotide bases recoded as N for 10,000,000 generations with 1,000,000 discarded as burn-in. Because both “models” (taxon branching orders) appear in the same Markov chain Monte Carlo (MCMC), the Bayes factor (i.e., the ratio of marginal likelihoods) can be calculated simply as: B(data) = \( \frac{\pi(M_1|data)/p(M_1)}{\pi(M_2|data)/p(M_2)} \), where \( \pi(M_1|data) \) is the posterior probability of hypothesis \( M_1 \), and \( p(M) \), its prior probability.

Reanalyses of Published Data Sets
For the reanalysis of Simon et al. (2009), amino acid sequence alignments of their “maxgene” data set were obtained from treebase (Morell 1996). We analyzed this data set as specified by Simon et al. (2009). For the ML analysis in RAxML, this corresponded to an approximate algorithm (PROTMIXWAG) to optimize tree topology before estimating parameters using the WAG + \( \Gamma \) model (Whelan and Goldman 2001). For our BEAST analysis, we also used the WAG + \( \Gamma \) model for comparison and placed a prior for the origin of the Pterygota on the root height (Table 1, Node 2), with all other prior parameters left as default.

For the reanalyses of Zhang et al. (2008) and Lin et al. (2010), nucleotide sequence data were obtained from Genbank or kindly provided by the authors. Two versions of this data set were analyzed using both ML in RAxML and Bayesian methods in BEAST. First, we analyzed the original data set as described by Lin et al. (2010). This data set included only the first and second coding positions of each mitochondrial protein sequence. For the RAxML analysis, following Lin et al. (2010), 2 partitions were allocated per gene and the GTR + \( \Gamma \) model of sequence evolution was applied to each partition. For comparison, a GTR + \( I + \Gamma \) model was also estimated for each partition in the BEAST analysis. Prior distributions were placed on the root age (the split between the Collembola and the Insecta: corresponding to Node 1 in Table 1) and on 5 other nodes: Pterygota, Isoptera, Ephemeroptera and Odonata (corresponding, respectively, to Nodes 2, 6, 8 and 10 in Table 1) and an additional prior on the Archaeognatha (Node 12 in Table 1). All other BEAST priors were left as default (Drummond and Rambaut 2007).

In addition to the original data set of Lin et al., we analyzed an edited data set in which base composition bias was also addressed. For this edited data set, mitochondrial protein-coding genes were first obtained from Genbank, aligned by eye, partitioned and then tested for base composition heterogeneity, as described above. The third codon positions of all genes except ATP8 showed heterogeneity even after recoding and so were excluded from further analysis. The first and second codon positions of 3 genes (ND2, ND4, and ND5) were also RY-recoded. For this data set, each full-coding partition was assigned the GTR + \( \Gamma \) model, and in BEAST, each RV-coded partition was assigned the F81 + \( \Gamma \) model.

RESULTS

Analysis of 113-Taxon Data Set 1
Figure 2 shows the maximum clade credibility tree for our primary data set 1, and Table 2 shows the corresponding results from both ML and Bayesian approaches. All analyses of this data set show support for a Palaeopteran clade. Tests for heterogeneity in base composition showed significant heterogeneity in 3 regions of our alignment (third codon positions of histone H3, and the mitochondrial \( rRNA_{12S} \) and 16S—see Supplementary Table S2), but recoding- or excluding-affected sequences had little effect on the results (Table 2); neither did repeating analyses with substitution models chosen by jModelTest (Posada 2008) (not shown) or excluding mitochondrial markers altogether (Table 2). Finally, results were consistent when the outgroup taxa were removed, and the tree rooted using temporal information alone in BEAST (Table 2).

Although results for data set 1 are consistent, the Bayesian results are far more statistically precise: ML analyses show moderate differences in the bootstrap support for Palaeoptera and Chiastomorpha, whereas BEAST showed very strong posterior support for the Palaeoptera. One key reason for this must be that our ML analysis was a free-rate method (which indirectly allows substitution rates to be unique for each branch in the tree), whereas our BEAST analysis drew each rate from a lognormal distribution, whose mean and variance were estimated concurrently with the tree (Drummond et al. 2006). This procedure reduces the number of rate parameters estimated from \( 2n−3 \) for a tree of \( n \) tips, to \( n+1 \) (the dates of the \( n−1 \) nodes plus a mean and variance of the lognormal), and this reduction in the number of parameters will increase the precision of the results. However, it will also tend to favor branching patterns that lead to more clock-like patterns.
of molecular evolution insofar as they are compatible with the temporal calibrations placed on the tree.

Additional analyses showed that our BEAST results were not sensitive to the particular form of the relaxed-clock model nor to the particular form of the prior placed on the uncalibrated node ages (results using an exponential model of rate change or a Yule process model of cladogenesis were qualitatively unchanged; see Supplementary Table S4). In contrast, removal of the fossil information on the internal nodes (Table 1) decreased support for the Palaeoptera—although it remained the favored hypothesis (see Supplementary Table S4). Investigation of our prior (i.e., without the molecular data) showed that Palaeoptera was indeed favored a priori when the fossil data were included (prior probabilities: Palaeoptera 51%, Chiastomaria 22%, and Metapterygota 27%). However, Bayes factors, which factor out the priors, indicate that there is strong evidence for the Palaeoptera over either of the alternative hypotheses, Chiastomaria, or Metapterygota (Table 2).

Because the use of a relaxed-clock model increases support for the Palaeoptera hypothesis over the Chiastomaria hypothesis, we next asked whether the pattern of rate change implied by the Chiastomaria hypothesis was particularly extreme (Drummond et al. 2006; Smith et al. 2006). To investigate this possibility, we repeated our BEAST analysis, but with a constrained chiastomarian topology. Figure 3 shows the estimated rates for the basal branches of the tree under the unconstrained Palaeoptera and the constrained chiastomarian phylogenies. This plot indicates that the rates are very similar in the 2 cases. The branch representing the stem Neoptera is fast under both groupings, while that leading to the Palaeoptera is particularly slow (Figs. 2 and 3), but neither are outlying compared with the lognormal distribution of rates estimated for the whole tree (i.e., the point estimates for these branches fall well within the best-fit lognormal distribution for the tree as a whole; Fig. 3), and this distribution differs little in the 2 cases.

Finally, our time tree (Fig. 2) provides no evidence that the radiation of the basal pterygotes was particularly rapid. We estimate that around 30 million years (myr) separated the divergence of the Palaeoptera from the Odonata–Ephemeroptera split (Fig. 2; posterior median 31.7 myr [95% CI 2.7–78.2]; prior median 30.1
### Table 2. Results of phylogenetic analyses

<table>
<thead>
<tr>
<th>Data set (no. taxa)</th>
<th># Genes</th>
<th>Length (bp)</th>
<th>Grouping</th>
<th>ML Bootstrap</th>
<th>Posterior</th>
<th>Bayes factor</th>
<th>BEAST</th>
<th>Posterior</th>
<th>Bayes factor</th>
<th>BEAST (no OG)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. (113 sp) Full</td>
<td>5</td>
<td>4732</td>
<td>Palaeoptera</td>
<td>0.61</td>
<td>0.99</td>
<td>—</td>
<td>0.95</td>
<td>—</td>
<td>13.291</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Chiastomyaria</td>
<td>0.36</td>
<td>0.01</td>
<td>29.881</td>
<td>0.02</td>
<td>11.76</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Metapterygota</td>
<td>0.00</td>
<td>0.00</td>
<td>≥1000</td>
<td>0.03</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Composition</td>
<td></td>
<td></td>
<td>—</td>
<td></td>
<td></td>
<td></td>
<td>0.95</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td>bias corrected</td>
<td>4</td>
<td>4372</td>
<td>Palaeoptera</td>
<td>0.54</td>
<td>0.96</td>
<td>—</td>
<td>0.95</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Chiastomyaria</td>
<td>0.44</td>
<td>0.04</td>
<td>8.342</td>
<td>0.03</td>
<td>13.044</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Metapterygota</td>
<td>0.00</td>
<td>&lt;0.01</td>
<td>247.998</td>
<td>0.03</td>
<td>13.842</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nuclear only;</td>
<td></td>
<td></td>
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<td>—</td>
<td>0.95</td>
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<td>15.951</td>
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<td>7</td>
<td>6381</td>
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<td>—</td>
<td>0.62</td>
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Notes: Values indicate bootstrap support (ML) or posterior probability (BEAST) for the specified clade. ML or maximum posterior groupings are shown in bold. Bayes factors in bold indicate substantial support for the preferred model.

![Figure 3](https://academic.oup.com/sysbio/article-abstract/62/2/285/1670647/Relaxed-Phylogenetics-and-the-Palaeoptera-Problem/13:32)  
Figure 3. Rate measurements for the unconstrained Palaeoptera (black) and constrained Chiastomyaria (dashed gray) BEAST trees for data set 1. Median posterior rate estimates (in substitutions per site per million years) are shown with 95% Credibility Intervals. Estimates are shown for stem lineages including the Pterygota (branch in Fig. 2), and Palaeoptera (branch in Fig. 2). Similar statistics for the whole tree were calculated using the maximum posterior estimates of the parameters of the lognormal distribution (which modeled rate variation across the tree).

...myr [95% CI 0.0–89.1]. If we conservatively assume that the ancestral Palaeoptera had annual generations (as is typical of many extant Palaeoptera), and an effective population size of order 10⁶ (typical of cosmopolitan insect species for which we have good estimates: Lehmann et al. 1998; Michel et al. 2006; Shapiro et al. 2007), then this implies a mean neutral coalescence time of 4 myr (=4Nₑ generations), which is rapid compared with the ~30 myr of the branch. Furthermore, we place the origin of the crown-group Pterygota well before the near-simultaneous appearance of the Odonata, Ephemeroptera, and Neoptera in the lowermost Upper Carboniferous (Carpenter 1992; Rasnitsyn and Quicke 2002; Grimaldi and Engel 2005); estimated branching of the Pterygota: median 385.3 myr [95% CI 353.3–418.0] and Palaeoptera: median 351.4 myr [95% CI 298.2–396.4]. Of course, these dates are for coalescence times rather than the appearance of morphological synapomorphies, but the estimates are nonetheless consistent with a substantial period of hidden divergence (see “Discussion” section).

Analysis of 38-Taxon Data Set 2

Although our primary data set 1 gave consistent results, results for our data set 2 (which contain many fewer taxa, but 2 additional genes) are highly...
inconsistent. For the full data set, ML and Bayesian approaches both return a metapterygotan clade (albeit with low support), which was decisively rejected for data set 1. Furthermore, results changed qualitatively with relatively minor changes in the data: correction for base composition heterogeneity, with or without the removal of mitochondrial markers, led to support for Chiaostomyaria from both ML and Bayesian methods (Table 2 and Supplementary Table S5). To test whether this inconsistency was due to the taxon-poor nature of the data set, we reanalyzed a subset of our taxon-rich data set 1, which contained the same taxa as data set 1. Results were again inconsistent and sensitive to small changes in data, with ML analyses now favoring either Chiastomyaria or Palaeoptera (Supplementary Table S5). Despite this general pattern, however, the removal of the outgroup taxa, and the rooting of the tree with temporal information, again favored Palaeoptera under all conditions (as with data set 1), albeit without strong Bayes factor support in all cases (Table 2 and Supplementary Table S5).

Reanalyses of Published Data Sets

Analysis of our own data sets showed support for the Palaeoptera, but these results were consistent only when (i) taxon sampling was extensive (as for data set 1) or (ii) temporal information was used to root the tree. This suggests that inconsistency in the literature concerning the basal Pterygote node might reflect systematic error stemming from sparse taxon sampling and distant outgroups. Indeed, most published studies have used even fewer taxa than our data set 2 (although often using many more genes).

Some of these previous studies also found support for Palaeoptera as true clade. For example, Regier et al. (2010), used 60 genes from 10 pterygote taxa (2 Odonata, 2 Ephemeroptera, and 6 nonendopterygote Neoptera) and several closely related hexapod outgroups (including 2 Zygentoma, 2 Archaeognatha, 3 Collembola, and 1 Diplura), while Meusemann et al. (2010) used 129 genes (filtered from over 700) from 19 pterygotes (1 Odonata, 1 Ephemeroptera, and 17 nonendopterygote Neoptera) together with 3 Archaeognatha and 3 Collembola outgroups.

Although results of these 2 studies were consistent with each other, other multigene data sets have shown strong support for the alternative hypotheses (Zhang et al. 2008; Simon et al. 2009; Lin et al. 2010). For example, Simon et al. (2009, 2010) used a data set containing 125 genes from 8 taxa (1 Odonata, 1 Ephemeroptera; 4 Neoptera, and 1 Collembola [Onychirus arcticus] as outgroup) and obtained strong support for Chiaostomyaria. A difference between this study and the similar studies of Meusemann et al. (2010) and Regier et al. (2010)—which supported Palaeoptera—is the choice of outgroup. The latter studies used wingless insect groups (Archaeognatha and Zygentoma) while Simon et al. (2009) use the more distantly related Collembola. To assess the impact of outgroup choice, we reanalyzed the data set of Simon et al. (2009) in BEAST, with and without the outgroup taxa. When the outgroup was included, these data produced decisive evidence for Chiaostomyaria with both ML and Bayesian methods (100% bootstrap support and posterior probability). However, when the outgroup was excluded from the BEAST analyses, the supported topology was Palaeoptera, although posterior support (95%) was weak.

Results even more discordant with our own were obtained by Zhang et al. (2008). These authors obtained strong support for the Metapterygota using the complete mitochondrial genomes of 11 taxa (1 Odonata, 1 Ephemeroptera, 7 Neoptera, with 1 Thysanura, and 1 Archaeognatha as outgroup). The data set of Zhang et al. (2008) was extended by Lin et al. (2010), to include an additional 3 Neoptera, 2 Odonata, 1 Ephemeroptera, and 10 outgroup taxa. These authors found support for a modified Chiaostomyaria, but with the Plecoptera (stoneflies) grouping with Ephemeroptera; thus, this data set supported a paraphyletic Neoptera, which is at odds with most insect phylogenies (Zwick 2000; Kjer et al. 2006; von Reumont et al. 2009; Ishiwata et al. 2011).

To investigate the discrepancies between these results and our own, we reanalyzed the data set of Lin et al. (2010); the results of this reanalysis are in Table 3. ML analysis, as expected, favored the modified Chiaostomyaria found by Lin et al. (2010). However, the BEAST analysis of the same data suppor-
ted Metapterygota, consistent with the original findings of Zhang et al. (2008). Finally, a BEAST analysis without outgroups found most support for a nonstandard Palaeoptera, with Odonata as sister group to an Ephemeroptera+Plecoptera clade. The grouping of the Plecoptera outside of the Neoptera (Lin et al. 2010) is contradicted by many other studies, using both morphological and molecular characters (Zwick 2000; Kjer et al. 2006; von Reumont et al. 2009; Ishiwata et al. 2011), a situation that may be analogous to other anomalous results in the arthropods using mtDNA (Delsuc et al. 2013; Nardi et al. 2003; Cameron et al. 2004; Hassani et al. 2005; Hassani 2006; Carapelli et al. 2007; Rota-Stabelli et al. 2008; Timmermans et al. 2008; Masta et al. 2009; Rota-Stabelli et al. 2010b). Because of the nonstandard placement of the Plecoptera, we repeated all analyses with this sequence removed. In this case, each of the analyses with outgroups included, favored Metapterygota (Zhang et al. 2008)—that is a different basal branching to that supported by Lin et al. (2010)—while the BEAST analysis without outgroup again favored Palaeoptera.

DISCUSSION

The branching of the basal pterygote lineages has proved a problem for biologists since it was first investigated in the early 20th century. Morphologists have argued for all 3 possible groupings, and so, later, have researchers using DNA sequence data. Even the
recent application of large phylogenomic data sets has produced support for all 3 branching patterns. In some cases, inconsistency among molecular phylogenies may result from incomplete lineage sorting (i.e., between-locus variation in gene lineages, which can arise when speciation events occur more rapidly than the coalescence of alleles [Pamilo and Nei 1988]). We have estimated that the basal radiation of the Pterygota was not particularly rapid (Fig. 2), but there is no way to convincingly reject incomplete lineage sorting with our data sets (containing, as they do, so few independent markers). However, we can show that other sources of systematic error are important. In particular, lineage sorting cannot explain the disagreements between studies using different mtDNA markers (e.g., Zhang et al. 2008; Lin et al. 2010), because all mitochondrial genes are inherited as a single unit (Moore 1995; Ballard and Whitlock 2004). Furthermore, with our data set 2, ML analyses of individual partitions gave quite inconsistent results, even when these are completely linked and so must have followed the same genealogy in reality; most notably, different groupings were supported by different codon positions of the EF1-α locus (Supplementary Table S6).

If incomplete lineage sorting is not the sole source of disagreement, then systematic error must also play a role (Baurain et al. 2007). Our results suggest that 2 factors are particularly important. First, we have shown that reduced taxon sampling can lead to results that are highly dependent on small changes in the data and assumptions of the analysis. Indeed, our 38-taxon data sets showed apparent support for all data and assumptions of the analysis. Indeed, our results suggest that reduced taxon sampling can lead to results that are highly dependent on small changes in the data and assumptions of the analysis. Indeed, our 38-taxon data sets showed apparent support for all data and assumptions of the analysis. Indeed, our results suggest that reduced taxon sampling can lead to results that are highly dependent on small changes in the data and assumptions of the analysis. Indeed, our 38-taxon data sets showed apparent support for all data and assumptions of the analysis.
the Palaeoptera hypothesis (Figs. 1a and 2) suggests that this state might be truly synapomorphic, rather than symplesiomorphic (a shared primitive state), as originally conjectured by Martynov (1924). As such, this grouping makes it far more probable that neopteran wing folding is the primitive state or at least evolved from a non-palaeopterous ancestor—and this would have important implications for the origins of insect flight (Kristensen 1991; Kingsolver and Koehl 1994; Woolfit 1994; Woolfit and Zuk 1994; Woolfit and Zuk 1997). However, drawing strong conclusions is complicated by the fact that different sets of wing vein fusions are likely to be responsible for the palaeopteran trait in Odonata and Ephemeroptera, and indeed in members of the extinct Palaeodictyopteroidea—although some parts of the complex of wing vein fusions that separately prevent wing folding may be common to all of these groups. Furthermore, we currently lack agreement among morphologists about which veins in the very highly derived odonate wing correspond to which veins in other insects (Tillyard 1926; Hamilton 1972; Carle 1982b; Riek and Kukalová-Peck 1984; Watson and O’Farrell 1991), and about where the Palaeodictyopteroidea should be placed on the phylogeny. These issues will have to be decided by further morphological examination of extant and Palaeozoic insects.

SUPPLEMENTARY MATERIAL

Supplementary material, including data files and/or online-only appendices, can be found at http://datadryad.org, doi: 10.5061/dryad.74d2g.

FUNDING

This work was supported by the John Maynard Smith Scholarship at the University of Sussex, awarded to JAT, and National Science Foundation (USA) grants DEB 0428334 and DEB 0816865 awarded to Karl Kjer, financially supporting JAT.

ACKNOWLEDGMENTS

The authors thank Chung-Ping Lin for providing the Euphas mitochondrial genome sequence, as well as Ian Barnes, Mark Blaxter, Lindell Bromham, Simon Ho, Alan Hodgkinson, Martin Jones, Karl Kjer, Rob Lanfear, Mike May, Jeremy Maris, Mark Miller, and CIPRES, Matt Phillips, Simon Phillips, Dana Price, David Smith, Alexis Stamatakis, Adrian Thomas, Jessica Ware, and Meg Woollfit for assistance. Finally, we are particularly grateful to the anonymous reviewer of a previous draft of this article, who spotted a major error in our earlier analysis.


