

A supermatrix-based molecular phylogeny of the family Drosophilidae

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Summary

The genus *Drosophila* is diverse and heterogeneous and contains a large number of easy-to-rear species, so it is an attractive subject for comparative studies. The ability to perform such studies is currently compromised by the lack of a comprehensive phylogeny for *Drosophila* and related genera. The genus *Drosophila* as currently defined is known to be paraphyletic with respect to several other genera, but considerable uncertainty remains about other aspects of the phylogeny. Here, we estimate a phylogeny for 176 drosophilid (12 genera) and four non-drosophilid species, using gene sequences for up to 13 different genes per species (average: 4333 bp, five genes per species). This is the most extensive set of molecular data on drosophilids yet analysed. Phylogenetic analyses were conducted with maximum-likelihood (ML) and Bayesian approaches. Our analysis confirms that the genus *Drosophila* is paraphyletic with 100% support in the Bayesian analysis and 90% bootstrap support in the ML analysis. The subgenus *Sophophora*, which includes *Drosophila melanogaster*, is the sister clade of all the other subgenera as well as of most species of six other genera. This sister clade contains two large, well-supported subclades. The first subclade contains the Hawaiian *Drosophila*, the genus *Scaptomyza*, and the *virilis-repleta* radiation. The second contains the *immigrans-tripunctata* radiation as well as the genera *Hirtodrosophila* (except *Hirtodrosophila duncani*), *Mycodrosophila*, *Zaprionus* and *Liodrosophila*. We argue that these results support a taxonomic revision of the genus *Drosophila*.

1. Introduction

Model organisms offer us our deepest understanding of many biological phenomena. Scientists are now capitalizing on the knowledge of these model systems to perform comparative studies of the phylogenetic relatives of many model organisms, such as *Arabidopsis thaliana* (Mitchell-Olds, 2001), *Caenorhabditis elegans* (Harris *et al.*, 2004), *Danio rerio* (Quigley *et al.*, 2005) and *Drosophila melanogaster* (Singh *et al.*, 2009). Such studies promise to unravel the genetic basis of phenotypic evolution and strongly implicate the evolutionary forces responsible for species divergence. Clearly, comparative studies of phenotypic differences

between species must be based on a good understanding of the phylogenetic relationships among the taxa involved (Felsenstein, 1985).

If the phylogeny is poorly known, the quality of the conclusions from comparative analyses will be poor. Unfortunately, the research traditions of those working on model organisms have not emphasized a phylogenetic framework, leaving us with an inadequate understanding of the relationships of model organisms to some of their close relatives (Al-Shehbaz & Kane, 2002; Kiontke *et al.*, 2004; Quigley *et al.*, 2004). The unfortunate result is that our phylogenetic information on clades containing model organisms is often fairly weak, even though these are precisely the clades best suited to comparative studies.

A prime example of this paradox is the genus *Drosophila* and closely related genera. Over the past 20 years, many studies dealing with parts of the

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Table 1. *ML estimates of parameter values for each data partition under the GTR+ Γ model*

Partition	Parameter										
	A	C	G	T	A \leftrightarrow C	A \leftrightarrow G	A \leftrightarrow T	C \leftrightarrow G	C \leftrightarrow T	G \leftrightarrow T	α
nuc 1st	0.268	0.207	0.347	0.177	1.401	1.634	1.254	0.665	4.033	1	0.364
nuc 2nd	0.283	0.244	0.205	0.268	1.766	2.917	0.973	2.284	3.542	1	0.299
nuc 3rd	0.132	0.368	0.275	0.225	4.979	13.403	7.225	2.077	12.609	1	0.964
mt 1st	0.272	0.164	0.256	0.309	0.416	3.232	1.539	0.493	77.898	1	0.173
mt 2nd	0.227	0.223	0.151	0.399	1.661	2.587	0.819	1.527	1.029	1	0.125
mt 3rd	0.436	0.068	0.029	0.466	1.638	277.252	6.260	29.226	344.918	1	0.388
16S	0.363	0.161	0.126	0.351	0.153	0.929	1.880	0.657	1.835	1	0.195
28S	0.317	0.164	0.204	0.315	0.854	2.448	2.726	0.315	2.401	1	0.192
tRNA	0.314	0.188	0.180	0.319	0.914	5.416	3.429	0.602	2.087	1	0.494

Parameter values include the base frequencies and the instantaneous substitution rates between nucleotides. The G \leftrightarrow T is set to 1.0 by default. α is the value of the shape parameter for the Γ distribution describing among-site rate variation. Data partitions include the codon positions for protein coding regions of each genome (nuclear, ‘nuc’; mitochondrial, ‘mt’). Values were calculated by RAxML as described in the text. Particular values of note include the very strong AT bias in mt 3rd positions in contrast to the GC bias in nuc 3rd positions, much less even substitution rates at 3rd positions of both genomes, and the weak transition/transversion ratio in 16S.

Drosophila phylogeny have been published (for an overview, see van der Linde & Houle, 2008), but surprisingly few have adequately addressed the phylogenetic relationships among the subgenera of *Drosophila* in the context of the various closely related genera. Consequently, even a cursory examination of the literature reveals that many aspects of drosophilid phylogeny are controversial or poorly studied (Ashburner *et al.*, 2005; Markow & O’Grady, 2006).

Grimaldi’s (1990) phylogeny based on morphological characters is the most recent comprehensive family wide treatment. An important competing phylogenetic hypothesis is that of Throckmorton (1975), which differs from it in many respects. Throckmorton’s work was clearly based on many sources of evidence (e.g. Throckmorton, 1962, 1965, 1966); unfortunately, he did not use explicit and reproducible methods. More recently, many phylogenetic hypotheses based on molecular data have been published (see Table 1, van der Linde & Houle, 2008, for the most important studies). The best of these have emphasized clades well below the genus level or have been based on small numbers of genes. Figure 1 shows the combination of gene numbers and species numbers in other phylogenetic studies using molecular data. Some aspects of the phylogeny, such as relationships within the *melanogaster* species subgroup (see Coyne *et al.*, 2004), now seem robustly supported by analysis of large sets of molecular data. At the same time, the results from other studies show that various clades within the phylogeny differ in many key respects.

The underlying source of this lack of consensus is that the available data are fragmentary. Taxon sampling of this very large group has been haphazard, and a few studies sequence more than a small number of genes. The result is that the sequence available for a pair of closely related species is likely to come from

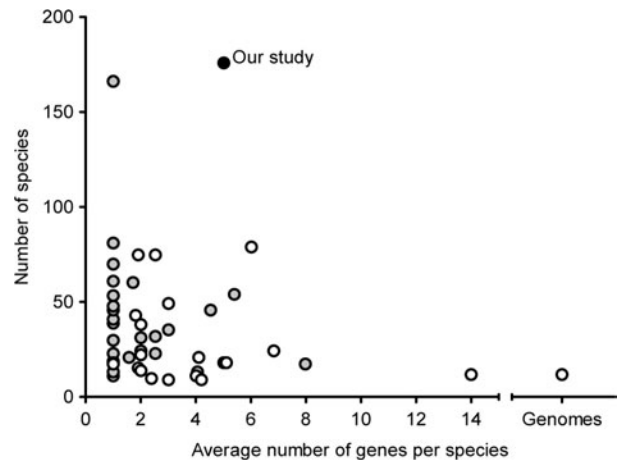


Fig. 1. Overview of average number of genes per species and number of species included in previous studies compared with those in our study. Black dot: our study; grey dots: studies limited to a single genus or *Drosophila* subgenus or major clade within the subgenus *Drosophila* (e.g. *immigrans-tripunctata* radiation, *virilis-repleta* radiation and Hawaiian *Drosophila*); white dots: studies covering at least two genera and/or *Drosophila* subgenera and/or major clades of the subgenus *Drosophila*.

different genes, making meaningful phylogenetic analyses difficult. We refer to this situation as a lack of overlap.

In this situation, phylogenetic hypotheses can be generated through a supertree analysis of published results (see, e.g. Bininda-Emonds *et al.*, 2002; Bininda-Emonds, 2004). Our supertree analysis and review covering *Drosophila* and its closely related genera (van der Linde & Houle, 2008) resulted in a generally well-resolved tree and clearly showed that the genus *Drosophila* as currently defined is paraphyletic with respect to various genera (e.g. *Scaptomyza*, *Hirtodrosophila*, *Samoia* and *Zaprionus*) placed within it

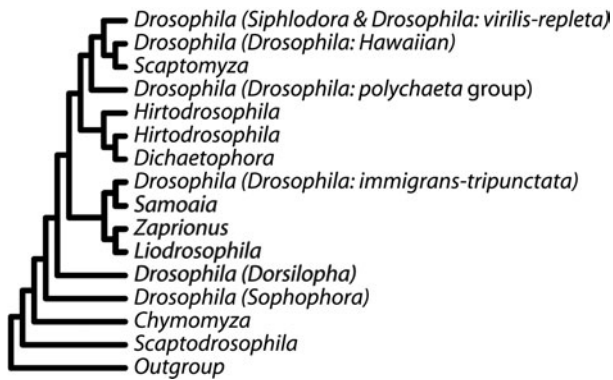


Fig. 2. The phylogenetic relationships as understood on the basis of the available literature before the study reported here.

(Fig. 2). Supertree methods have been criticized on various grounds, including that they give too much weight to weakly supported or erroneous nodes, difficulty in dealing with biased data, failure to use the original data, inapplicability of model-based methods of analysis and failure to use all the data efficiently (Kluge, 1989; Gatesy *et al.*, 2004; but see also Bininda-Emonds *et al.*, 2003; Bininda-Emonds, 2004). Some of these issues are apparent in our own supertree analysis (van der Linde & Houle, 2008).

Here, we report the results of a supermatrix analysis in which we used publicly available sequence data, plus a limited amount of new sequence chosen to increase overlap. Our data stand out in the number of species included (180; Fig. 1) and in the variety of taxa included. We note that, although ours is the most comprehensive study to date, overlap of the sequence data for many species remains limited. The focus of the study is to resolve the basal nodes within the genus *Drosophila sensu lato*. The major issue is the topology of the three main clades of the subgenus *Drosophila* and the various genera that are positioned among them (e.g. *Hirtodrosophila*, *Zaprionus* and *Scaptomyza*). In addition, the order of the two genera placed sister to the genus *D. sensu lato* (*Scaptodrosophila* and *Chymomyza*) is still insufficiently resolved (Tarrio *et al.*, 2001). The phylogenetic relationships between the various species groups in both the *immigrans-tripunctata* clade and the *virilis-repleta* clade are not yet fully resolved. Finally, the monophyletic nature of many groups is questioned.

2. Materials and methods

(i) Species and data

We compiled data for 541 species: 535 species in family Drosophilidae and six outgroup species in the families Tephritidae (one species), Ephydriidae (four) and Lauxaniidae (one). We screened loci in GenBank for which multiple drosophilids had been sequenced and selected 13 to maximize taxonomic overlap

among gene sequences. These include nine nuclear loci (*Adh*, *AmyRel*, *per*, *Ddc*, *Sod*, *yp1*, *28Sd1*, *28Sd2* and *28Sd8*) and four mitochondrial loci (*COI*, *COII*, *COIII* and *16S*). Most sequences were obtained from GenBank, supplemented with new sequences for *COI*, *COII*, *COIII*, *28Sd1* and *28Sd8*. Only protein-coding regions of the non-ribosomal genes were used. The aligned sequences for *AmyRel* were kindly provided by J.-L. Da Lage. After generating the full set of data, we selected species on the basis of number of genes available, number of base pairs and our need for a distance matrix covering a large number of species for which we have wing-shape data. On the basis of these criteria, we selected 180 species (see Supplementary Table 1). The total number of base pairs per species ranged from 339 to 13 539 bp (mean: 4333 bp); only seven taxa had fewer than 1000 bp. Accession codes can be found in Supplementary Table 1; new sequences are available from GenBank under accession codes GU597372 to GU597535. Collection locations of the 39 species for which we collected new sequences can be found in Supplementary Table 2.

(ii) Alignment

Nucleotide sequences were aligned with Clustal X (Thompson *et al.*, 1997) and manually inspected in MacClade (Maddison & Maddison, 2005) for resolution of regions of ambiguity or disagreement and consolidated indels. Alignment of all protein-coding regions was trivial because amino acid indels were rare and readily interpreted. Sequences for the genes were concatenated for each taxon. The alignment and trees [maximum parsimony (MP), partitioned maximum-likelihood (ML) and Bayesian] are available from TreeBase under accession code SN4940.

(iii) Phylogenetic analysis

Heterogeneity of nucleotide composition among informative sites was estimated with PAUP* version 4.0b10 (Swofford, 2002). Only two of the 13 genes, *AmyRel* and *Adh*, showed heterogeneity. Phylogenetic analyses were conducted under MP, neighbour-joining (NJ), ML and Bayesian approaches. Because of the number of species without overlapping data, we did not test for congruence using, for example, a partition-homogeneity test (Farris *et al.*, 1994, 1995). All MP analyses were conducted with PAUP* version 4.0b10 (Swofford, 2002) with heuristic searches with tree bisection-reconnection (TBR) branch swapping and 20 random-addition starting trees; the first 2000 trees found were retained. All substitutions were weighted equally; gaps were treated as missing data. To determine whether changes in base composition in *AmyRel* and *Adh* might mislead phylogenetic reconstruction, we analysed these genes separately using NJ with LogDet distances in PAUP* and

compared the results to the ML and Bayesian trees for well-supported conflicts. LogDet is less sensitive to base-composition heterogeneity (Swofford *et al.*, 1996). Although the LogDet NJ tree and the ML/Bayesian trees differed, the differences were not well supported, and the ML gene tree was not appreciably more similar to the concatenated tree than was the LogDet NJ tree, suggesting that convergence on nucleotide frequencies was not misleading the combined-data analyses.

We conducted ML analyses in several ways to account for the complexity of the data. First, a series of analyses on unpartitioned data was conducted with PAUP*. ML parameter values were estimated under a nested array of substitution models for a random MP tree as implemented in Modeltest 3.04 (Posada & Crandall, 1998); likelihood-ratio tests (Yang *et al.*, 1995) and the Akaike Information Criterion (Akaike, 1973) were used to identify the simplest models of sequence evolution that adequately fit the data and phylogeny. The most complex model was selected by both criteria: GTR + I + Γ . Parameters were fixed for the values estimated on the initial MP tree. Heuristic searches were then conducted with two alternatives for generating starting trees. In the first search, the first 20 trees were saved from each of 10 random-addition replicates from MP analyses (200 maxtrees total), and these 200 trees became the starting trees for the ML search, providing some initial sampling of tree space. MP trees were used rather than a single NJ tree because non-overlapping data among sets of taxa resulted in undefined distances and anomalous placement of some taxa in the NJ tree. Parsimony appeared less affected by non-overlapping data, in that recovered trees were consistent with published studies. In addition, five parallel random-sequence-addition runs were conducted, each of which required approximately 200 h to build the starting trees. The search starting with the MP trees yielded a more likely tree ($\ln L = -178603$ as opposed to -178606), and that tree is reported here.

Our data include protein-coding and RNA genes from mitochondrial and nuclear genomes, so a single model may be insufficient to account for the data. We therefore conducted partitioned ML analyses using RAxML (Stamatakis *et al.*, 2008) using the Cipres Portal 1.15 to access the San Diego Supercomputer Center. Conditions followed the default settings, including a GTR + Γ model, and no per-gene branch length optimization (branch lengths were proportional across partitions). We partitioned the data by codon position separately for the three nuclear codon positions and the three mitochondrial codon positions, as well as by genome for the ribosomal genes and for the tRNAs, producing nine partitions (1st, 2nd and 3rd nuclear; 1st, 2nd and 3rd mitochondrial; mt rRNA, nu rRNA and tRNA). We repeated the analyses

unpartitioned for comparison with the PAUP* results to distinguish the effects of partitioning from software-specific tree-search strategies. Parameter values as estimated by RAxML for each partition are reported in Table 1.

Non-parametric bootstrapping (Felsenstein, 1985) was performed under ML with two approaches, one using the genetic algorithm approach in GARLI version 0.951 (Zwickl, 2006) with the data unpartitioned and the other using RAxML to allow partitioned data. Garli analyses used 200 replicates and the GTR + I + Γ model with parameters estimated by GARLI. The search was conducted with a random starting tree and an automatic run termination after a minimum of 5000 generations that did not improve topology, a $\ln L$ improvement of less than 0.02 due to topological changes, a 0.05 score improvement threshold, and default genetic algorithm settings. The second bootstrapping approach used RAxML with both unpartitioned and partitioned data sets. Bootstrapping was run for 250 replicates (RAxML selected 150 as sufficient), representing the combined output of two independent runs (100 and 150 replicates) with different starting seeds, with default settings. Partitioning was the same as in the ML searches. MP bootstrapping was conducted with 500 replicates, and 50 trees were saved in each random-addition replicate.

Bayesian analyses used the mpi (multiple processors) version of MrBayes 3.2 (Ronquist & Huelsenbeck, 2003) distributed over eight processors. We partitioned the data as with RAxML. Two independent analyses of four heated chains each were run for 80 million generations. Parameters were estimated for each partition separately ('unlinked'); trees and parameters were recorded every 1000 generations. Convergence was estimated by means of cumulative and sliding plots from "Are We There Yet?" (AWTY) (Wilgenbusch *et al.*, 2004) as well as by examination of likelihood plots and posterior probabilities of individual clades for subsets of the runs. The chains converged slowly on the basis of the AWTY and likelihood plot diagnostics, possibly because large blocks of data were missing and overlap among several taxa was limited, yielding a burn-in of 50%. Split-frequency standard deviations never indicated full convergence, plateauing around 0.1 by 20 million generations. We calculated a majority-rule consensus tree of the post-burn-in trees from both runs to summarize posterior probabilities.

3. Results and discussion

At the level of the previously recognized genera, the results of the ML and Bayesian analyses were strongly concordant with each other (Fig. 3). The main differences between the analyses are in the placement of the *immigrans-tripuncata*, *Zaprionus* and

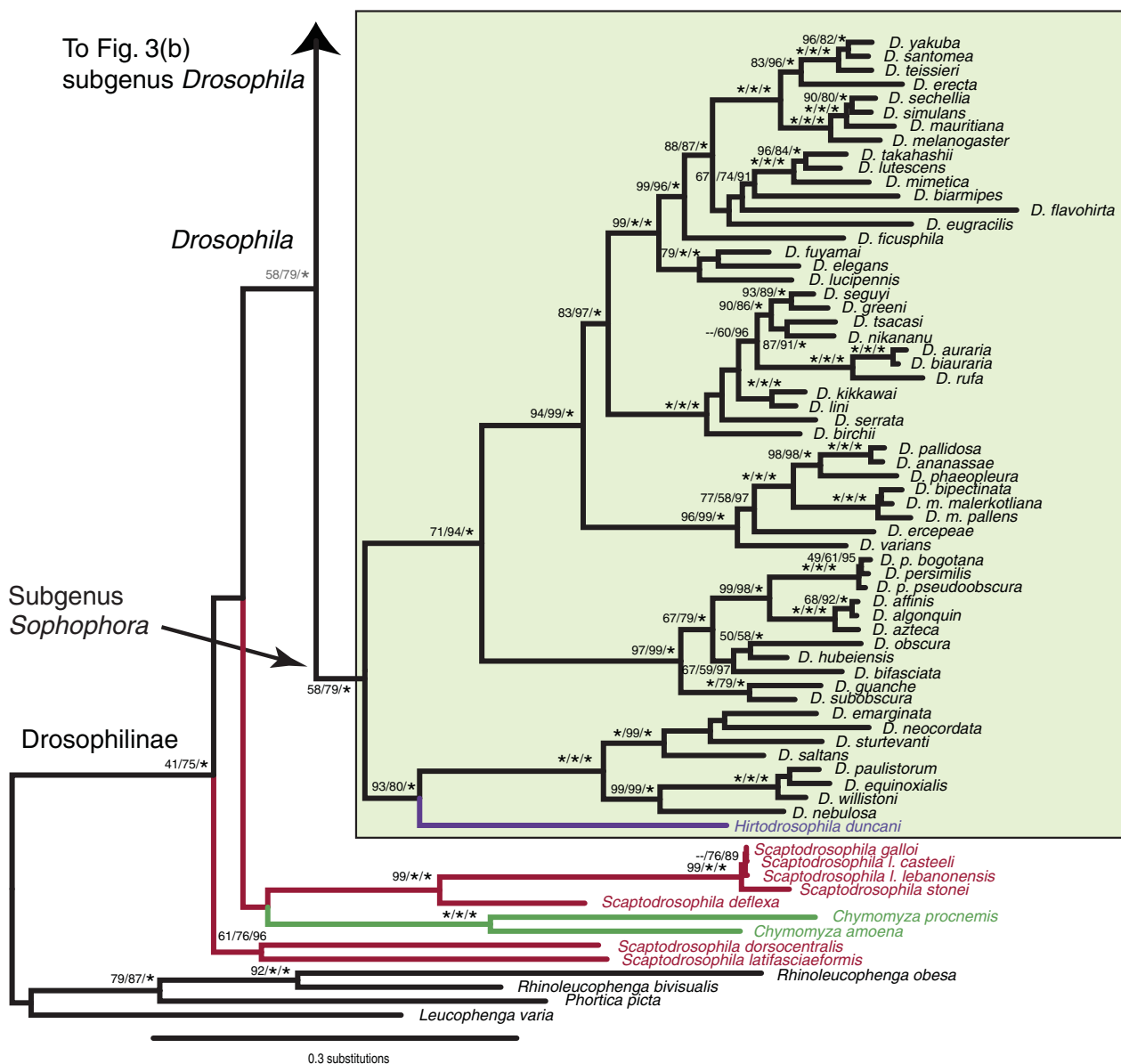


Fig. 3. Partitioned ML phylogram of the Drosophilidae. Taxon names along branches are the traditional classification, whereas names within the coloured boxes are the proposed genus names for species currently assigned to *Drosophila*. Branches coloured by current genus; *Drosophila* appears in black. Support values above branches are unpartitioned ML bootstrap (bs; PAUP), partitioned ML bs (RAXML) and Bayesian posterior probabilities (pp), respectively, expressed as percentages. Only bs > 70 or pp > 85 are shown. Symbols: ‘*’ indicates 100; ‘—’ indicates the node is below 50% in the bootstrap majority tree and not present in the Bayesian majority rule tree.

Hirtodrosophila/*Mycodrosophila* clades and among the poorly supported nodes near the root of *immigrans-tripunctata* clade. The concordance between the ML and Bayesian analyses within genera differed dramatically for different genera. The MP results were also largely concordant, lacking any significant conflict (MP bs > 80%); the strict-consensus MP tree and the ML tree had 140 nodes in common. All but three differences (all in subgenus *Drosophila*, discussed individually below) were confined to regions poorly supported in all analyses and with < 42% MP bootstrap support. MP bootstrap values were strongly correlated with the other support values and were

nearly always the lowest of the four values. Because MP bootstrap values do not provide a strong independent signal, only the model-based values are reported on Fig. 3.

(i) *Steganinae* and *Drosophilinae*

Traditionally, the family Drosophilidae is split into two subfamilies, the Drosophilinae and the Steganinae (Hendel, 1917; Duda, 1924; Throckmorton, 1962, 1965, 1975; Okada, 1989; Grimaldi, 1990; Sidorenko, 2002). Our small sample of subfamily Steganinae (four taxa) suggests that it may be paraphyletic with

[ML unpartitioned bootstrap (MLu bs): 42; Bayesian posterior probability (pp), reported as a percentage: 81] relative to the nodes for the family Drosophilidae (MLu bs: 95; pp: 100) and subfamily Drosophilinae (MLu bs: 58; pp: 100).

Previous analyses of these subfamilies suggest that no single character distinguishes the two subfamilies (see Ashburner *et al.*, 2005, for discussion). The only molecular study that has included species of both subfamilies (Remsen & O'Grady, 2002) confirmed this basal subdivision, although one of the unrooted molecular trees (16S) also suggests that this subfamily is paraphyletic. Our results stress the need for additional sampling of species from both subfamilies before any conclusions regarding the basal nodes within the family Drosophilidae can be drawn.

(ii) *Scaptodrosophila* and *Chymomyza*

Our analyses are equivocal with respect to the positions of *Chymomyza* and *Scaptodrosophila*, and the two alternative arrangements are both poorly supported. *Chymomyza* appears monophyletic [two species, MLu bs, ML partitioned bootstrap (MLp bs) and pp support all 100], whereas *Scaptodrosophila* is paraphyletic with respect to two moderately to well-supported clades (*Scaptodrosophila deflexa* plus *Scaptodrosophila lebanonensis* group, 99–100 for all analyses; *Scaptodrosophila dorsocentralis/latifasciiformis* only moderate). Examination of the underlying data reveals a very limited overlap in sequences between species of the two *Scaptodrosophila* clades, which could explain the lack of support for monophyly of the genus.

Scaptodrosophila and *Chymomyza* appear to be the closest relatives to *Drosophila* for which sequences are available. Most morphological (Okada, 1963; Hu & Toda, 2001) and molecular (DeSalle, 1992a; Kwiatowski *et al.*, 1994, 1997) studies do not contradict Tarrío *et al.* (2001), who suggested that *Scaptodrosophila* diverged from other drosophilids before *Chymomyza* did, on the basis of almost 5000 bp of sequence from five nuclear genes. Remsen & O'Grady (2002) found that *Scaptodrosophila* and *Chymomyza* formed a sister clade to the *Sophophora* but with low support. Other studies have been unable to resolve this node (Throckmorton, 1975; Grimaldi, 1990; Remsen & DeSalle, 1998; Kwiatowski & Ayala, 1999; Tatarenkov *et al.*, 1999; Da Lage *et al.*, 2007). Our results do not provide clear support for any of the topologies and raise questions about the monophyly of the genus *Scaptodrosophila*. These issues can only be resolved with further data.

(iii) Genus *Drosophila* and included genera

The genus *Drosophila*, together with the included genera, forms a moderately supported clade (MLu bs:

58; MLp bs: 79; pp: 100), and most species are placed in two major clades. One is the monophyletic subgenus *Sophophora* (MLu bs: 58; MLp bs: 79; pp: 100; Fig. 3a). The remaining genera and subgenera form a separate well-supported clade (MLu bs: 93; MLp bs: 95; pp: 100; Fig. 3b), within which most species are distributed over two major clades. The first major clade contains the Hawaiian drosophilids – Hawaiian *Drosophila* clade and *Scaptomyza* – and the *virilis-repleta* radiation and is well supported (MLu bs: 88; MLp bs: 96; pp: 87). The two Hawaiian clades are each monophyletic and sister to each other (98–100 for all analyses). The sister taxon to the Hawaiian drosophilids is the *virilis-repleta* radiation, which is monophyletic in all analyses with strong support (MLu bs: 94; MLp bs: 100; pp: 87).

The second major clade contains three groups (Fig. 3b), the *immigrans-tripunctata* radiation, *Zaprionus* and *Hirtodrosophila*/*Mycodrosophila*. Together with some of the smaller genera, they form a weakly supported clade (MLu bs: 51; MLp bs: 68; pp: 87). Unfortunately, the analyses failed to resolve the topology among the three basal lineages consistently. The *immigrans-tripunctata* radiation was monophyletic in all analyses (MLu bs: 81; MLp bs: 100; pp: 100), as was the genus *Zaprionus* (MLu bs: 89; MLp bs: 90; pp: 98). The *Hirtodrosophila* and *Mycodrosophila* species, except *H. duncani*, form a clade (MLu bs: 89; MLp bs: 94; pp: 99). The genus *Liodrosophila* was placed in the sister clade of the genus *Zaprionus* in all analyses, although with weak support.

The subgenus *Dorsilopha* and the genus *Dettopsomyia* were placed basal to these two major clades. In the unpartitioned ML analysis, the two genera form a clade with weak bootstrap support (61%), whereas in the Bayesian analysis, they are successive outgroups to the major lineage, but the pp for the relevant node is only 62%.

The largest *Drosophila* phylogeny to date with respect to number of genes used is based on the genomes of the 12 sequenced species (*Drosophila* 12 Genomes Consortium, 2007). The topology of the 12-genome study is identical with our topology for the same species, underlining the robustness of our analysis. The subgenus *Sophophora* is the sister clade of the remaining subgenera, as well as of the regularly included genera (Beverley & Wilson, 1984; DeSalle, 1992b; Wojtas *et al.*, 1992; Pélandakis & Solignac, 1993; Thomas & Hunt, 1993; Kwiatowski *et al.*, 1994, 1997; Russo *et al.*, 1995; Remsen & DeSalle, 1998; Kwiatowski & Ayala, 1999; Tatarenkov *et al.*, 1999; Tarrío *et al.*, 2001; Remsen & O'Grady, 2002; Robe *et al.*, 2005; Da Lage *et al.*, 2007). The position of the major clades in the subgenus *Drosophila* combined with the included genera is not recovered consistently, but our results support the grouping of the Hawaiian

Drosophila clade with *Scaptomyza* (Throckmorton, 1975; DeSalle, 1992a; Thomas & Hunt, 1993; Kambysellis et al., 1995; Russo et al., 1995; Remsen & DeSalle, 1998; Kwiatowski & Ayala, 1999; Tatarenkov et al., 1999, 2001; Davis, 2000; Davis et al., 2000b; Remsen & O'Grady, 2002; Da Lage et al., 2007; O'Grady & DeSalle, 2008), which together form the sister clade of the *virilis-repleta* radiation (Kambysellis et al., 1995; Russo et al., 1995; Remsen & DeSalle, 1998; Kwiatowski & Ayala, 1999; Tatarenkov et al., 1999, 2001; Gailey et al., 2000; Tarrío et al., 2001; Tatarenkov & Ayala, 2001; Remsen & O'Grady, 2002; Da Lage et al., 2007). Most studies recover the remaining three major clades – *Zaprionus*, the *immigrans-tripunctata* radiation and *Hirtodrosophila*/*Mycodrosophila* – as sister taxa to each other, but no consensus has emerged about their branching order (Kwiatowski & Ayala, 1999; Tatarenkov et al., 1999; Davis et al., 2000a; Gailey et al., 2000; Robe et al., 2005; Da Lage et al., 2007).

(iv) Subgenus *Sophophora*

Our analyses recover the previously identified Neotropical and Old World clades within the subgenus *Sophophora*. The Neotropical clade contains the *willistoni* and *saltans* species groups (all support values: 100), whereas the 'Old World' clade contains the *obscura*, *ananassae*, *montium* and *melanogaster* species groups (MLu bs: 71; MLp bs: 94; pp: 100). The *obscura* and *ananassae* species groups form sequential sister groups to the *montium* and *melanogaster* species groups (cf. Da Lage et al., 2007). Each of the six species groups was monophyletic (MLbs: 96–100; pp: 100), and the topology was well supported in both the ML and Bayesian analyses.

The subgenus *Sophophora* has been traditionally split into eight species groups, of which the four largest – *melanogaster*, *obscura*, *saltans* and *willistoni* – are generally included in phylogenetic studies (Pitnick et al., 1999; Tatarenkov et al., 1999; Bächli, 1999–2009; O'Grady & Kidwell, 2002; Remsen & O'Grady, 2002; Ashburner et al., 2005; Da Lage et al., 2007). Recently, Da Lage et al. (2007) proposed to elevate the *montium* and *ananassae* species subgroups to the level of species groups, bringing the total number to 10. The 10 groups are distributed among the two major clades, one containing the *melanogaster*, *montium*, *ananassae* and *obscura* species groups and the other containing the *willistoni* and *saltans* species groups (Pélandakis et al., 1991; Pélandakis & Solignac, 1993; Russo et al., 1995; Kwiatowski & Ayala, 1999; Pitnick et al., 1999; O'Grady & Kidwell, 2002; Remsen & O'Grady, 2002; Da Lage et al., 2007).

Our study confirms the generally accepted topology of the subgenus *Sophophora*, as well as the validity of

the proposal by Da Lage et al. (2007) to split the *melanogaster* species group into three: *ananassae*, *montium* and *melanogaster*. Among these three species groups, the *montium* and *melanogaster* groups are sister to each other (MLu bs: 83; MLp bs: 97; pp: 100). This topology has been observed in many studies (cf. Hsu, 1949; Inomata et al., 1997; Goto & Kimura, 2001; O'Grady & Kidwell, 2002; Kastanis et al., 2003; Lewis et al., 2005b; Kopp, 2006; Prud'homme et al., 2006; Da Lage et al., 2007). In this context, the placement of the *fima* species group as the sister clade of the *ananassae* species subgroup (Pélandakis & Solignac, 1993) provides an additional argument for accepting the proposed split of the *melanogaster* species group.

The subgenus *Sophophora* as currently defined is already recognized as paraphyletic; the genus *Lordiphosa* (not included in our study) is the sister clade of the *willistoni-saltans* clade (Katoh et al., 2000; Hu & Toda, 2001). In our study, the only member of the *duncani* species group, *H. duncani* (Wheeler, 1949), was also placed in this subgenus as the sister to the *willistoni-saltans* clade.

(v) *Virilis-repleta* radiation

Most studies suggest division of the *virilis-repleta* radiation into *repleta* and *virilis* clades (Pitnick et al., 1999; Katoh et al., 2000; Carrasco et al., 2003; Robe et al., 2005; Wang et al., 2006). In our analyses, the *virilis* species group was placed sister to the *repleta* clade with high support in the Bayesian analysis (pp=100) but not in the ML analyses (MLu bs: 48; MLp bs: 67). The *repleta* clade, which includes one of the two species of the subgenus *Siphlodora* (*Drosophila flexa*), was reasonably well supported (MLbs: 82; MLp bs: 88; pp: 79), but the topology of the species groups within the clade differed slightly in the MP, ML and Bayesian analyses, primarily in the position of the *dreyfusi* species group (*Drosophila camargoi*). Generally, the support for the nodes dealing with the placement of the various species groups is low. Monophyly for most of the species groups is strongly supported, except for the *robusta* species group, which is paraphyletic, in line with a previous study including this group (Wang et al., 2006).

The topology within the *virilis-repleta* radiation is poorly resolved, although some consensus on aspects of the tree has emerged. The *robusta*, *melanica*, *angor* and *quadrisetata* species groups generally form a clade (MLu bs: 94; MLp bs: 100; pp: 90) (Watabe & Peng, 1991; Pitnick et al., 1999; Remsen & O'Grady, 2002; Wang et al., 2006), whereas the *repleta* clade consists of the *repleta*, *mesophragmatica*, *bromeliae*, *dreyfusi*, *annulimana*, *flavopilosa* and *canalina* species groups (Pitnick et al., 1999; Tatarenkov & Ayala, 2001; Remsen & O'Grady, 2002; Carrasco et al., 2003;

Robe *et al.*, 2005; Wang *et al.*, 2006; Da Lage *et al.*, 2007) with moderate support (MLu bs: 82; MLp bs: 88; pp: 79). The studies differ in the position of the *virilis* species group; Pitnick *et al.* (1999) and Wang *et al.* (2006) place it sister to the *robusta-melanica* clade, whereas others place it sister to the *repleta* clade (Pélandakis & Solignac, 1993; Tatarenkov & Ayala, 2001; Remsen & O'Grady, 2002). Our results favour its placement sister to the *repleta* clade (MLu bs: 48; MLp bs: 67; pp: 100), but further study is clearly needed to resolve this issue. The *nannopectera* species group is generally placed within the *repleta* clade (Pitnick *et al.*, 1999; Tatarenkov & Ayala, 2001; Carrasco *et al.*, 2003; Wang *et al.*, 2006), whereas Robe *et al.* (2005) place it outside the whole genus on the basis of a Bayesian analysis of the *amd* gene, while Remsen & O'Grady (2002) place it sister to the *melanica-robusta* clade.

D. flexa belongs to the small subgenus *Siphlodora*, which has only been included in a single analysis before ours (Remsen & O'Grady, 2002), where it was placed as the sister species of the *nannopectera* species group. Our results show it to be a basal member of the *repleta* lineage, which includes the *nannopectera* species group.

Parsimony differs from the model-based results, showing moderate conflict in two respects. MP places *Drosophila hydei* sister to *Drosophila hamatofila* (MP bs: 63%) and *Drosophila buzzatii* sister to the *Drosophila mulleri/mojaviensis* clade (MP bs: 54%).

(vi) Immigrans-tripunctata radiation

Our results place the *immigrans* clade (bs and pp: 100) as the sister group to the *tripunctata/funebris* groups (MLu bs: 62; MLp bs: 89; pp: 100), but relationships within the *tripunctata/funebris* clade are unstable, and many nodes are poorly supported. In agreement with previous studies, the *tripunctata* and *guarani* clades are not monophyletic (Frota-Pessoa, 1954; Throckmorton, 1975; Carrasco *et al.*, 2003; Yotoko *et al.*, 2003; Robe *et al.*, 2005; Da Lage *et al.*, 2007; Hatadani *et al.*, 2009). The broad coverage of species in this study also suggests that the *testacea* and *funebris* species groups are not monophyletic. *Drosophila bizonata* (*bizonata* species group) is placed within the *testacea* species group, whereas the two species of the *funebris* species group are placed at different locations in the tree. Additional work is needed in this group.

Previous studies are generally consistent regarding the major splits in the *immigrans-tripunctata* radiation. All but two (Da Lage *et al.*, 2007; Katoh *et al.*, 2007) have concluded that the *immigrans-tripunctata* group is monophyletic. Most authors place the *immigrans* species group sister to the remaining members of the *immigrans-tripunctata* radiation

(Pélandakis & Solignac, 1993; Remsen & O'Grady, 2002; Carrasco *et al.*, 2003; Perlman *et al.*, 2003; Yotoko *et al.*, 2003; Robe *et al.*, 2005), but mirroring our results, previous studies are equivocal about relationships within the *tripunctata/funebris* clade (Pélandakis & Solignac, 1993; Remsen & O'Grady, 2002; Carrasco *et al.*, 2003; Yotoko *et al.*, 2003; Robe *et al.*, 2005; Da Lage *et al.*, 2007; Hatadani *et al.*, 2009). Additional studies with a better coverage of species will be required before the relationships between the various groups can be resolved.

(vii) *Drosophila repletoidea*

Yassin and co-workers (Yassin, 2007; Yassin *et al.*, 2008, 2010) have shown that the *tumiditarsus* species group, which contains *D. repletoidea*, is positioned close to the genus *Zaprionus* and that several species of the *Zaprionus* subgenus *Anaprionus* actually belong to the *tumiditarsus* species group. Our only representative of the subgenus *Anaprionus* has not been affected by this taxonomic change, and is closely related to the remaining species of the genus (cf. Yassin *et al.*, 2010; Amir Yassin, personal communication). Our model-based analyses indicate that *D. repletoidea* is most probably in a clade with the genera *Zaprionus* and *Liodrosophila* (MLu bs: 71; MLp bs: 52; pp: 83), together sister to the *immigrans-tripunctata* radiation. In contrast, the MP analysis weakly places it sister to the Hawaiian *Drosophila/Scaptomyza/Dettopsomyia* clade, with no intervening node with greater than 27% MP bs. The ML and Bayesian results are more decisive; several intervening clades are well supported (e.g. the *virilis-repleta* radiation/Hawaiian *Drosophila/Scaptomyza* clade).

(viii) Paraphyly of taxa

Our results confirmed that several species groups, e.g. *tripunctata*, *guarani*, *testacea*, *robusta* and *funebris*, as well as genera, e.g. *Drosophila* and *Hirtodrosophila*, were paraphyletic or even polyphyletic. Our results indicated that *Hirtodrosophila* is not monophyletic, as suggested by Bächli *et al.* (2004), whereas the monophyly of *Scaptodrosophila* is unclear. For *Scaptodrosophila*, the paraphyly might just be an artefact of the underlying data (see above), in that the overlap in sequences between the two clades is relatively small. The situation for *Hirtodrosophila* is clearly different. In our analysis, the overlap in the sequences between *H. duncani* and *Hirtodrosophila thoracis* spans four different genes. *H. duncani* is placed within the subgenus *Sophophora* sister to the *willistoni* and *saltans* species groups, whereas *H. thoracis* is grouped with the other *Hirtodrosophila* species, nested within *Mycodrosophila*. Previous work

has suggested this placement of *H. duncani*. It was placed in its own unique species group on the basis of its unique male genitalia (Wheeler, 1949). Nater (1950, 1953) concluded that the male genitalia are most similar to those of the *obscura* subgroup. Burla (1956) noted that, among *Hirtodrosophila*, this species is closest to *Drosophila* in several internal and external morphological characteristics, whereas Throckmorton (1962) placed it close to or in *Sophophora*. Finally, Grimaldi (1990) concluded that apart from ‘the presence of the long sensilla trichodea on the first flagellomere ... *Drosophila duncani* has no other *Hirtodrosophila* features’.

Several species groups were paraphyletic or polyphyletic as well. The most striking is the *tripunctata* species group, whose members were scattered within the *immigrans-tripunctata* radiation. This result is in agreement with previous studies (Frota-Pessoa, 1954; Throckmorton, 1975; Carrasco et al., 2003; Yotoko et al., 2003; Robe et al., 2005; Da Lage et al., 2007; Hatadani et al., 2009). Additional studies are needed on this group.

The *guarani* species group is paraphyletic with two major species subgroups – *guarani* (including *Drosophila ornatifrons* and *guaru*) and *guaramun* (*Drosophila maculifrons*) – positioned in different locations of the *immigrans-tripunctata* radiation. The support for splitting this group was especially strong in the Bayesian analysis (two intervening nodes with $pp > 95$), but weak in the ML analyses (largest intervening MLp bs = 50%). This result agrees with previous studies (Kastritsis, 1969; Clayton & Wheeler, 1975; Throckmorton, 1975; Yotoko et al., 2003; Robe et al., 2005; Hatadani et al., 2009); treating both subgroups as species groups seems to be fully justified.

A third species group suspected to be polyphyletic is the *robusta* group (Wang et al., 2006), and this conclusion was corroborated in our analysis as well. An unexpected find in the *immigrans-tripunctata* radiation was the placement of the single included species of the *bizonata* species group (*D. bizonata*) within the *testacea* species group. Before our study, no analysis has included members of the *bizonata* group together with multiple species of the *testacea* group. The support in both the ML (MLu bs: 90; MLp bs: 98) and the Bayesian analyses is strong (100). Finally, the *funebis* species group was not monophyletic. The two subgroups – *funebis* and *macrospina* – were positioned at different locations within the phylogeny, although the ML and Bayesian analyses differed in the exact position. Support was strong for a closer relationship of *Drosophila funebis* with *Drosophila pinicola* than with *Drosophila macrospina* (MLu bs: 85; MLp bs: 100; pp: 100).

The paraphyletic nature of the genus *Drosophila* has been reported before by various authors

(Throckmorton, 1962, 1965, 1975; Beverley & Wilson, 1984; Grimaldi, 1990; DeSalle, 1992a,b; Pélandakis & Solignac, 1993; Thomas & Hunt, 1993; Kwiatowski et al., 1994, 1997; Kambysellis et al., 1995; Russo et al., 1995; Remsen & DeSalle, 1998; Tatarenkov et al., 1999, 2001; Davis et al., 2000b; Gailey et al., 2000; Katoh et al., 2000; Hu & Toda, 2001; Tarrío et al., 2001; Remsen & O’Grady, 2002; Da Lage et al., 2007; O’Grady & DeSalle, 2008; van der Linde & Houle, 2008). Our results confirm that several genera – *Hirtodrosophila*, *Mycodrosophila*, *Zaprionus*, *Scaptomyza* and *Liodrosophila* – are placed between the three major clades of the subgenus *Drosophila*. The ML and Bayesian analyses differed slightly in the exact placement of the *Hirtodrosophila*/*Mycodrosophila*, *Zaprionus* and *immigrans-tripunctata* clades, but agreed on all other nodes.

A resolution to the paraphyletic nature of the genus *Drosophila* will be addressed separately. Three solutions are available: (1) do nothing (O’Grady & Markow, 2009); (2) sink the included genera into *Drosophila* and (3) split the genus along the major clades. Splitting the genus is clearly the most desirable from a purely taxonomic point of view but has the major practical disadvantage that the type specimen for the genus is *D. funebis* (Fabricius) which is not in the same clade as *D. melanogaster*. To avoid the widespread confusion that would result from renaming *D. melanogaster*, an application to preserve the name *D. melanogaster* has been submitted to the International Commission on Zoological Nomenclature and is currently under consideration (van der Linde et al., 2007). If the commission rules in favour of this application, proposals to split the genus are more likely to be entertained by the enormous *Drosophila* community.

(ix) Impact of analytical approach

Despite the limited character overlap for some species and uneven sampling, our results are remarkably robust across the methods of analysis. Results obtained with different methods show no strong conflict. Many clades are well supported in all of the analyses. In addition, partitioning under ML had little effect on the topology. The partitioned and unpartitioned results differ in only a small number of nodes, and none of these differences received strong support under either partitioning scheme. Partitioned bootstrap values were generally greater than unpartitioned. For example, 45 nodes had greater bootstrap values under partitioning (of four percentage points or more) than without, compared to 14 with the reverse, for those values reported on Fig. 3. Sixty-three (35.6%) nodes differed by no more than three points. The most noticeable differences were between Bayesian and ML support values. As has often been reported, posterior

probabilities can be much higher than bootstrap values, sometimes artefactually so (Lewis *et al.*, 2005a). The most striking examples in our analyses were in the *immigrans-tripunctata* radiation, where bootstrap values of less than 40, some as low as 18, were associated with near 100% posterior probabilities. We therefore interpret some of these high pp values with caution.

Considerable debate has surrounded the relative merits of the supermatrix approach as used here and the supertree approach, the latter synthesizing topological information across studies (Bininda-Emonds *et al.*, 2003; Bininda-Emonds, 2004; Gatesy *et al.*, 2004; de Queiroz & Gatesy, 2007). A particular concern about the supermatrix approach is the potential bias created by large numbers of missing data, an issue side-stepped by supertree approaches because the latter do not directly analyse characters. Most studies exploring missing data in large sets have concluded that the supermatrix approach is relatively robust to this problem and that the real question is how many informative data is present, not how many might be missing (Wiens, 2003; de Queiroz & Gatesy, 2007; Wiens & Moen, 2008). Reassuringly, the primary results we report here are well supported and consistent with those revealed by a supertree approach (van der Linde & Houle, 2008), a pattern that Baker *et al.* (2009) argued was evidence against a misleading bias in either method. We note, however, that the simulation studies have concentrated on the number of missing data, not their distribution within the matrix – in other words, on the behaviour of phylogenetic methods when overlap between some taxa is limited. This focus certainly reduces the effective phylogenetic information below the total number of characters for each taxon. In addition, Lemmon *et al.* (2009) have shown that ML and Bayesian methods can be positively misleading or provide inflated support values as a result of ambiguous (missing) data. We therefore look forward to future studies that are more complete.

4. Conclusions

Our study includes more drosophilid taxa than any previous molecular phylogenetic study. We obtained better taxon sampling of subfamily Drosophilinae than previous studies by focusing attention on species that are not traditionally assigned to the genus *Drosophila*, which have been omitted from most previous studies. We obtained this coverage by assembling a matrix of data with a great number of missing data. Despite the potential pitfalls of analyses of such data, results obtained by different methods produced similar results, adequately resolving many aspects of the overall phylogeny, including several long-standing issues. Our study confirms the general observation

that the genus *Drosophila* is paraphyletic and points toward issues that still need attention.

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