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Abstract

The fowls (Anseriformes and Galliformes) comprise one of the major lineages of birds and occupy almost all biogeographical regions of the world. The group contains the most economically important of all bird species, each with a long history of domestication, and is an ideal model for studying ecological and evolutionary patterns. Yet, despite the relatively large amount of systematic attention fowls have attracted because of their socio-economic and biological importance, the species-level relationships within this clade remain controversial. Here we used the supertree method matrix representation with parsimony to generate a robust estimate of species-level relationships of fowls. The supertree represents one of the most comprehensive estimates for the group to date, including 376 species (83.2% of all species; all 162 Anseriformes and 214 Galliformes) and all but one genera. The supertree was well-resolved (81.1%) and supported the monophyly of both Anseriformes and Galliformes. The supertree supported the partitioning of Anseriformes into the three traditional families Anhimidae, Anseranatidae, and Anatidae, although it provided relatively poor resolution within Anatidae. For Galliformes, the majority-rule supertree was largely consistent with the hypothesis of sequential sister-group relationships between Megapodiidae, Cracidae, and the remaining Galliformes. However, our species-level supertree indicated that more than 30% of the polytypic genera examined were not monophyletic, suggesting that results from genus-level comparative studies using the average of the constituent species' traits should be interpreted with caution until analogous species-level comparative studies are available. Poorly resolved areas of the supertree reflect gaps or outstanding conflict within the existing phylogenetic database, highlighting areas in need of more study in addition to those species not present on the tree at all due to insufficient information. Even so, our supertree will provide a valuable foundation for understanding the diverse biology of fowls in a robust phylogenetic framework.

Introduction

The fowls (Galloanserae; ducks, chicken, and allies) are generally regarded as a monophyletic group (Sorenson *et al.* 2003; Cracraft *et al.* 2004; but see Olson & Feuccia 1980; Ericson 1996, 1997) that, according to Dickinson (2003), consist of eight families with 452 species. Fowls, which are typically separated into duck-like (Anseriformes) and chicken like species (Galliformes), include the most economically important birds on earth. Many species in this group have a long history of domestication for socio-economic reasons (e.g. food, game, feather, or display, among others), including chicken (e.g. *Gallus Gallus*), quails (e.g. *Coturnix japonica* and *Colinus virginianus*), ring-necked pheasants (*Phasianus colchicus*), turkeys (e.g. *Meleagris gallopavo*), guinea fowls (e.g. *Numida meleagris*),peafowls (*Pavo cristatus*), ducks (e.g. *Anas platyrhynchos*), and geese (e.g. *Anser anser* and *A. cygnoides*). The global economic value of domesticated fowls is enormous. For example, more domestic chicken meat (over 68 million tons) than beef was produced worldwide in 2004 (FAO 2007). Income from eggs and poultry in the United States was approximately US $29 billion in 2004 (USDA 2007). Hunting of migratory birds (e.g. ducks and geese) in the United States generates US $1.3 billion annually for thousands of small businesses (USFWS 2007), and game shooting in the UK similarly supports some 70,000 full-time jobs (PACEC 2006).

Fowls are likewise of particular interest to many biologists. The group comprises the sister group of all remaining species of Neognathae [all living birds with the exception of tinamous (Tinamidae) and ratites (Struthionidae,

Rheidae, Casuariidae, Dromaiidae, and Apterygidae)], and occupies almost all major biogeographical regions of the world (Cracraft *et al.* 2004). Despite this deep divergence and worldwide distribution, Anseriformes and Galliformes together possess extremely restricted extant species richness relative to their sister group (Neoaves), which covers over 9000 species (Dickinson 2003). Even so, fowls display a remarkable life-history and behavioral diversity as well as morphological plasticity (del Hoyo *et al.* 1992; Dunning 1993; del Hoyo *et al.* 1994; Kear 2005). For example, species within Galliformes show more than a 100-fold difference in body mass (e.g. from < 100 g for *C. japonica* to approximately 10,000 g for *M. gallopavo*), and more than a 20-fold difference in clutch size (e.g. from one for Lophura bulweri to approximately 20 for *Aepypodius arfakianus*). Many galliform species tend to be sedentary, whereas most Anseriform species migrate long distances. Within Galliformes, some grouse are characterized by adaptations to open habitats, whereas megapodes and cracids are adapted to forest habitats. Anseriformes are adapted generally to an aquatic lifestyle (e.g. webbed feet), but their reliance on the aquatic habitat differs widely among species. Swans and geese often feed on land at some distance from water, whereas most ducks forage in or close to water. Some fowl species (e.g. *Crax alberti* and *A. laysanensis*) are recognized as being critically endangered (IUCN 2007), whereas others (e.g. *P. colchicus* and *A. platyrhynchos*) are exploited as overabundant game species. Such remarkable diversity in Galloanserae makes it an exceptional group for studying a wide range of questions in ecology, evolution, conservation and management.

Biologists often employ a comparative approach to recognize, test, and interpret adaptive patterns and processes in ecology and evolution. To do so properly, a phylogenetic framework is essential to account for the nonindependence among taxa that arises through the process of descent with modification (Felsenstein 1985b; Harvey & Pagel 1991). Thus, a large, well-resolved (species-level) phylogeny, in addition to its systematic value, represents an indispensable tool for testing broad-scale hypotheses in nature, greatly increasing the statistical power of the associated comparative analyses. Currently, however, it is generally not possible to build large, comprehensive trees from a direct, conventional analysis of true biological characters, such as DNA sequences, due to uneven distribution of research effort across taxa resulting in insufficient homologous data (Sanderson *et al.* 2003; Bininda-Emonds 2005). This state of affairs also holds for Galloanserae, with a general lack of large species-level trees from any single molecular, morphological, or combined data set. To date, the most comprehensive trees for each of Anseriformes and Galliformes are genus-level trees, with Livezey (1997) summarizing the findings of several partial phylogenies for Anseriformes based on morphology and Crowe *et al.* (2006) deriving a tree for Galliformes from an analysis

of morphological and molecular data from 158 out of the 292 extant species.

Instead, supertree analysis provides an alternative method to generate comprehensive and rigorous estimates of phylogeny (Sanderson *et al.* 1998; Bininda-Emonds *et al.* 2004a). Using formal algorithmic procedures, this method combines multiple existing and overlapping source trees, each ideally based on independent data sets (see Gatesy *et al.* 2002), and therefore is able to use more of the information present in the global systematic database. Supertree construction remains a controversial technique and has attracted repeated criticism because it uses only the topological information of the source trees and thus loses contact with the raw data (e.g. Springer & de Jong 2001; Gatesy *et al.* 2002). Biases in some methods have also been noted (e.g. Wilkinson *et al.* 2005, 2007). However, simulation studies have repeatedly shown that supertrees built with sufficiently large and numerous source trees represent the phylogenetic information provided by the source trees accurately (Bininda-Emonds & Sanderson 2001; Chen *et al.* 2003; Levasseur & Lapointe 2003; Piaggio-Talice *et al.* 2004). With these advantages, comprehensive supertrees have been built for a wide range of animals and plants, including all extant mammal species (Bininda-Emonds *et al.* 2007), seabirds (Kennedy & Page 2002), shorebirds (Thomas *et al.* 2004), oscine passerine birds (Jønsson & Fjeldså 2006), dinosaurs (Pisani *et al.* 2002), grasses (Salamin *et al.* 2002) and angiosperms (Davies *et al.* 2004). It is beyond the scope of this article to outline the arguments for and against supertree construction and the reader is directed instead to the relevant literature (e.g. Gatesy *et al.* 2002; Bininda-Emonds *et al.* 2003).

Here, we use the supertree method of matrix representation with parsimony (MRP; Baum 1992; Ragan 1992) to generate a robust estimate of species-level phylogenetic relationships within Galloanserae. The major objectives of this study are: (i) to provide a comprehensive, global view of the group's phylogenetic relationships; (ii) to compare this topology to other comprehensive fowl phylogenies based on the conventional analysis of molecular or morphological characters (e.g. Livezey 1997; Crowe *et al.* 2006); and (iii) to provide a phylogenetic framework for future comparative studies of fowl ecology, evolution, conservation and management.

Materials and methods

Source tree collection
Phylogenetic information for Galloanserae was collated from the published literature by searching online databases, the Web of Science and Zoological Record for the years 1971–2006. We used the following search terms: phylogen*, phenogram*, cladogram*, cladistic*, taxonom*, or fossil* (where the asterisks represent wildcards) in combination with any scientific name of each fowl order, family, subfamily, or genus (as given in Dickinson

2003) or any major fowl common name (e.g. fowl, game-bird, grouse, quail, pheasant, waterfowl, duck, goose, and swan). Additionally, we examined the references in the source articles we collected to obtain additional studies containing relevant phylogenetic information.

The protocol for inclusion or rejection of source trees was guided by the issues of data quality (e.g. data independence and duplication, see Gatesy *et al.* 2002) following the principles described in Bininda-Emonds *et al.* (2004b) and as implemented in Beck *et al.* (2006). Generally, only trees that were based on an actual analysis of a novel, independent data set were collected for our analysis. Reasons for the exclusion of potential source trees included the lack of any explicit underlying data set (e.g. as for taxonomies), the simple replication of the results of previous studies without any novel analysis, or an insufficient number of Galloanserae species for the tree to be phylogenetically informative in the context of this study. All nonindependent trees were retained at this stage, with corrections for any nonindependence being applied subsequently via down weighting (see below). Nonindependence could arise both between studies (e.g. through use of the same data set on an overlapping species sample) and/or within the same study (e.g. multiple analyses of the same data set using different optimization criteria). For example, gene trees derived from *MT-CYB* (cytochromeb) and *MT-RNR1* (12S rDNA) were held to be independent and independent from a tree based on morphological data, even if they all appeared in the same article. By contrast, all phylogenies based on *MT-CYB* would be classified as nonindependent, regardless of whether or not they occur in different articles or which optimization criteria was used for analysis.

A total of 400 phylogenetic trees derived from molecular and/or non-molecular (e.g. morphological or behavioral) data, and obtained using distance (e.g. neighbor-joining) or character-based methods (e.g. parsimony, maximum likelihood, and Bayesian analysis) were included initially as source trees. A topology equivalent to the classification of Dickinson (2003) was also included as a 'seed tree' to increase taxonomic overlap among source trees while providing only limited and usually uncontroversial phylogenetic information. The use of seed trees has been shown to improve the resolution of the supertree and to decrease computation time in simulation (Bininda-Emonds & Sanderson 2001) and when, suitably down weighted, does not distort the final topology compared to that dictated by the 'real' source trees (see Beck *et al.* 2006). All information in the source trees was coded and stored exactly as it appeared in the (i.e. without any correction for apparent typos and/or synonyms in taxon names) into the tree window of MacClare (Maddison & Maddison 2000).

Standardization of taxon names
The set of 400 source trees, despite not including all extant species of Galloanserae, contained a total of 1368

taxon names because of the inclusion of numerous typos and synonyms (including the use of common names) for a given species (e.g. 'Chicken' or '*Gallus Gallus* domestics' or '*Gallus Gallus* 1' for *Gallus Gallus*), of higher-level taxon names (e.g. *Gallus* or Galliformes), or of extinct species (e.g. the Turtlejawed Moa-nalo, Chelychely-nechen *quassus*) or of non-fowl species (e.g. the Rock Pigeon, *Columba livia*).

Therefore, where possible, the names of all terminal taxa were standardized to those in Dickinson (2003). Appropriate synonyms for unrecognized names were obtained primarily from the Integrated Taxonomic Information Service (ITIS: www.itis.gov) and secondarily from additional searches. All non-fowl species were synonymized to 'outgroup' and higher-level terminal taxa were synonymized to the type species of the taxon (e.g. both *Gallus* and Galliformes were synonymized to *Gallus Gallus*) following Bininda-Emonds *et al.* (2004b). Ambiguous names (e.g. 'Basal Anseriformes and Galliformes', 'Other Galliformes' or 'Partridge') and extinct taxa were pruned from the source trees. Synonymization was achieved using the Perl script synonoTree v2.1 (Bininda- Emonds *et al.* 2004b). SynonoTree also accounts for cases where the process of synonymization yields non-monophyletic species by outputting all possible permutations of a given source tree where each such species is represented only once in each of its possible placements. Finally, all trees containing the taxon 'outgroup' were rooted on this taxon, which was subsequently deleted. All other source trees were held to be unrooted. Trees that were synonymized so as to become phylogenetically uninformative (i.e. containing less than three or four species for rooted and unrooted trees, respectively) were deleted, as were any completely unresolved trees. Altogether the synonymization process reduced the number of source trees to 385 (from 108 published studies; including the seed tree) and 43 trees that represented additional permutations of 31 source trees. The identity of all trees, together with their final weights in the supertree analysis (see below) is provided in the online-only supplementary material I.

MRP supertree construction
Supertree construction used MRP, which represents by far the best investigated and most frequently used supertree method (Bininda-Emonds 2004). MRP operates by coding the topology of a tree as a series of binary pseudo characters, each pseudo character representing one informative node in the tree. Taxa derived from the node are scored as 1, those that are not, but are still present on the tree are scored as 0, and taxa present only on other trees in the entire set are scored as ?. The matrix representations of each tree are then combined into a single matrix for parsimony analysis. Normally an all-zero outgroup is added to the matrix. However, we used semi-rooted MRP coding (Bininda-Emonds *et al.* 2005) as implemented in the Perl script SuperMRP v1.2.1 in which

the outgroup was scored with zeros only for rooted trees; for unrooted trees, it was scored as ?

The final MRP matrix consisted of 4713 pseudo characters that were differentially weighted across trees to account for source-tree nonindependence, whether at the level of the underlying data or because of permutations of a given tree arising from non-monophyletic taxa, again following the guidelines of Bininda-Emonds *et al.* (2004b). The source trees were initially subdivided according to data type, with sets of nonindependent studies within each category being determined on a case-by-case basis: mixed-data analyses (six sets for seven trees), molecular data (83 sets for 236 trees), morphological data (1 set for 59 trees), other data types (13 sets for 22 trees), and unspecified data (13 sets for 13 trees). Weighting was applied in a hierarchical fashion, first according to data set nonindependence and then to permutation nonindependence. For example, pseudo characters for each of the 59 trees in the single morphological data set received a weight of 0.017 (= 1/59). However, the pseudo characters for the morphological study of Livezey (1991) were down weighted by an additional factor of two beyond this (to 0.008) to account for the two permutations of this tree generated by synonoTree. Similarly, weighting was applied separately for each set within a category. For example, of the 83 molecular data sets, those consisting of a single source tree received a relative weight of 1 (= 1/1), whereas those with five nonindependent trees (e.g. all *MT-CYB* trees) received a weight of 0.2 (= 1/5). Finally, the seed tree of Dickinson (2003) was given a weight of 0.001 (= at least six times smaller than any other source tree) to minimize its impact on the supertree topology beyond helping to stabilize the analysis. A nexus-formatted file listing the independent data sets and the weights applied to each is available from TreeBASE (Sanderson *et al.* 1994) under the study accession number xxx and matrix accession number xxx.

Parsimony analysis used PAUP* v4.0b10 (Swofford 2002) and employed a parsimony ratchet (Nixon 1999) consisting of 50 batches of 200 replicates initially, followed by a brute force search using all optimal trees found to that point as starting trees. During the reweighting steps, 25% of the MRP pseudo characters were selected at random and given a weight of two before being returned to their initial differential weights. Starting trees for each batch were obtained using a single random-addition sequence. All searches used TBR branch-swapping. Ratchet searches allowed only a single tree to be retained at any given step, whereas the terminal brute force search allowed multiple trees. All instructions for the ratchet were produced by the Perl script perlRat v1.0.9 and implemented in PAUP* as a PAUP block. The initial ratchet analysis saved a maximum of 10,050 equally most parsimonious trees. These trees then served as the starting trees for the extended brute-force search saving up to 100,000 trees. The strict consensus trees from the initial and ratchet and subsequent brute force searches were identical, hinting that the ratchet had reached a form of 'convergence' in that the additional equally most parsimonious solutions showed conflict with existing areas of incongruence rather than generating new conflict (and thereby decreasing resolution). The final supertree was held to be the strict consensus of the set of 100,000 equally most parsimonious solutions (each of length 1418.607). Both it and a majority-rule consensus of the same set of trees have been deposited with TreeBASE (study accession number S2245).

Differential support within the supertree was determined using the rQS index as implemented in QualiTree v1.2.1 (Bininda-Emonds 2003; Price *et al.* 2005), which measures the amount of support and disagreement for a given node in the supertree among the set of source trees. As such, it avoids the inherent nonindependence between MRP pseudo characters, which violates the assumptions underlying such conventional support measures as the bootstrap (Felsenstein 1985a) or Bremer support (Bremer 1988) and causing them to be invalid in this context. An rQS value varies between +1 and –1, indicating that all sources trees support or contradict the nodes in question, respectively. Empirically, rQS values usually tend to be slightly negative (e.g. Price *et al.* 2005; Beck *et al.* 2006), reflecting the fact that many phylogenies are uninformative for a given node (thereby scoring zero for it) and those that are informative tend to conflict with one another, even if slightly. Therefore, even slightly positive rQS values should be taken to indicate good support. All rQS values for each node on the supertree, together with how many source trees support, conflict, or are equivocal with a given node, are presented in the online-only supplementary material II. All Perl scripts used in this study are freely available from http://www.uni-oldenburg.de/molekularesystematik/33997.html or from the second author on request.

Results and discussion

Taxonomic coverage and resolution
Our fowl supertree includes 376 species, comprising over 83% of all 452 fowl species recognized by Dickinson (2003) (Table 1). All 162 Anseriformes species and 74% of all 290 Galliformes species are present in the supertree. The distribution of the 108 studies yielding source trees shows that the number of phylogenetic studies for fowls has increased rapidly since the late 1980s, with a sharp increase in particular for studies using molecular data, either alone or in combination with morphological or other data sources (Fig. 1). Overall, Galloanserae are relatively well-characterized phylogenetically. The number of source trees per fowl species present in the tree (1.0) was more than that in supertrees of well-studied mammalian groups of comparable size [e.g. 0.6 in primates or bats (Purvis 1995; Jones *et al.* 2002), and 0.7 in carnivores

Table 1 Information for major clades of Gallanserae, including number of taxa recognized and covered in this study and summary statistics for the supertrees. n/a, not available.

	Number of species recognized*	Number of species covered in this study	Percent coverage (%)	Percent resolution (%)		
				Strict consensus	Majority rule	rQS
Overall	452	376	83.2	81.1	96.3	0.265
Anseriformes	162	162	100	73.9	97.5	0.135
Anhimidae	3	3	100	100	100	0.091
Anseranatidae	1	1	100	0	0	0
Anatidae	158	158	100	72.6	97.5	0.044
Galliformes	290	214	73.8	86.9	95.8	0.252
Megapodiidae	22	17	77.3	93.8	93.8	0.099
Cracidae†	50	34	68	n/a	n/a	n/a
Numididae	6	6	100	100	100	0.026
Odontophoridae	32	13	40.6	91.7	100	0.021
Phasianidae†	180	144	80	n/a	n/a	n/a

* According to Dickinson (2003).
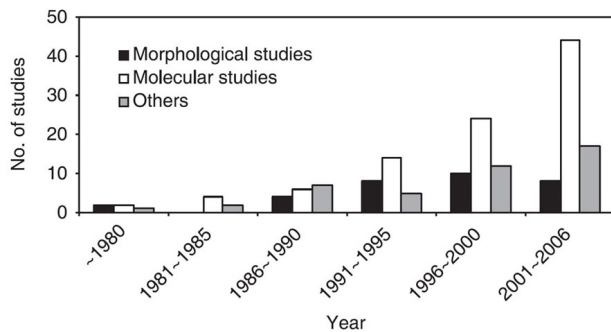† Cracidae and Phasianidae were not monophyletic in the supertrees.

Fig. 1. Temporal distribution of source trees included in the Galloanserae supertree.

(Bininda-Emonds *et al.* 1999)], despite our more conservative source tree inclusion protocol. The value continues to exceed those of the mammalian supertrees even when we calculate it for all extant species, including those not present on the tree (0.83) to make it comparable to the mammal values.

The supertree highlights that poorly characterized species (i.e. those missing from the tree entirely or those found in only a few source trees) tend to belong to groups that themselves are not well-studied. For instance, the majority of species missing in the supertree are assigned to either Odontophoridae (59% missing), Cracidae (32% missing), or Phasianidae (20% missing). The uneven distribution of missing species often appears associated with issues of geography and/or accessibility of the species. For example, species of the genus Odontophorus, which represents almost half of all species in Odontophoridae (15 of 32), are found in Neotropical forests, but the genus is represented by only a single species (*Odontophorus gujanensis*) in the supertree. Similarly, only a single species out of the 20 in Arborophila (*Arborophila torqueola*), which

generally inhabit Southeast Asian tropical forests or high alpine meadows in the Himalayas and often in widely scattered populations, was present in the supertree. Obviously, deriving a complete phylogenetic estimate of Galloanserae will require an increase in future research effort towards these and other missing species.

Although the limit of 100 000 equally most parsimonious solutions was reached, the strict consensus of them was well resolved, containing 304 of a maximum possible 375 nodes (= 81.1%; Table 1). This degree of resolution was higher than that for many other supertrees of comparable scale, including those for primates (79%; Purvis 1995), carnivores (78%; Bininda-Emonds *et al.* 1999), marsupials (74%; Cardillo *et al.* 2004), bats (46%; Jones *et al.* 2002), whale and even-toed hoofed mammals (60%; Price *et al.* 2005), shorebirds (50%; Thomas *et al.* 2004), and seabirds (63%; Kennedy & Page 2002). Again, the degree of resolution varied across the tree and among the (monophyletic) families in particular, ranging from 73% for Anatidae to 100% for Anhimidae and Numididae. Smaller families tended to show greater resolution, possibly because of their being fewer nodes that are likely to vary, but even some relatively large families showed high resolution (e.g. 73% for the 15 species of Anatidae) indicating general consensus over their internal relationships. Some cases of decreased resolution among and within families appear to derive more from a lack of agreement among the source trees than from a lack of available information. For example, nearly full resolution (94%) for Megapodiidae was achieved on the basis of 373 pseudo characters. By contrast, relationships within *Coturnix* were completely unresolved despite having twice as much data available (726 pseudo characters). The occurrence of the poorly resolved groups in the supertree also highlights areas in need of more rigorous systematic analyses in the future.

Table 2. Genera that were either 'not monophyletic' or of 'questionable monophyly' (due to being unresolved with respect to another taxon) in the strict consensus supertree.

Family	Genus	Status	
Anseriformes			
Anatidae	Dendrocygna	Not monophyletic	Fig. 3(B)
Anatidae	Tachyeres	Questionable monophyly	Fig. 3(B)
Anatidae	Tadorna	Not monophyletic	Fig. 3(B,F)
Anatidae	Nettapus	Not monophyletic	Fig. 3(C)
Anatidae	Netta	Questionable monophyly	Fig. 3(B)
Anatidae	Aythya	Questionable monophyly	Fig. 3(B)
Anatidae	Melanitta	Not monophyletic	Fig. 3(B,D)
Anatidae	Bucephala	Not monophyletic	Fig. 3(B,E)
Galliformes			
Megapodiidae	Aepypodius	Not monophyletic	Fig. 3(I)
Cracidae	Pipile	Not monophyletic	Fig. 3(A)
Cracidae	Mitu	Not monophyletic	Fig. 3(A)
Cracidae	Pauxi	Not monophyletic	Fig. 3(A)
Cracidae	Ortalis	Questionable monophyly	Fig. 3(A)
Cracidae	Penelope	Questionable monophyly	Fig. 3(A)
Phasianidae	Francolinus	Not monophyletic	Fig. 3(L,O)
Phasianidae	Syrmaticus	Not monophyletic	Fig. 3(N)
Phasianidae	Coturnix	Questionable monophyly	Fig. 3(O)

To date, the most comprehensive phylogenies for Anseriformes and Galliformes (Livezey 1997 and Crowe *et al.* 2006, respectively) have been at the genus- and not species levels. These trees necessarily assume the monophyly of each genus, often forcing the wide range of ecological and evolutionary hypotheses that have been examined using these trees to be based on the average of the respective biological characters of the constituent species (e.g. Keane *et al.* 2005; Kolm*ar al.* 2007). Crucially, however, our species-level supertree showed that more than 30% of the polytypic genera were not monophyletic or of questionable monophyly (Table 2). This suggests that the results from the genus-level comparative studies using the average of the species' traits should be interpreted with caution until analogous species-level comparative studies are available.

Anseriformes–Galliformes relationships
The supertree supported the monophyly of each of the orders Anseriformes and Galliformes (Figs 2, 3), reflecting historical agreement on this point (but see Prager & Wilson 1976). In addition, both clades enjoyed high support as measured by the rQS index (0.252 for Anseriformes and 0.135 for Galliformes; node numbers 187 and 2, respectively), meaning that monophyly was directly specified by the majority of relevant source trees in each case.
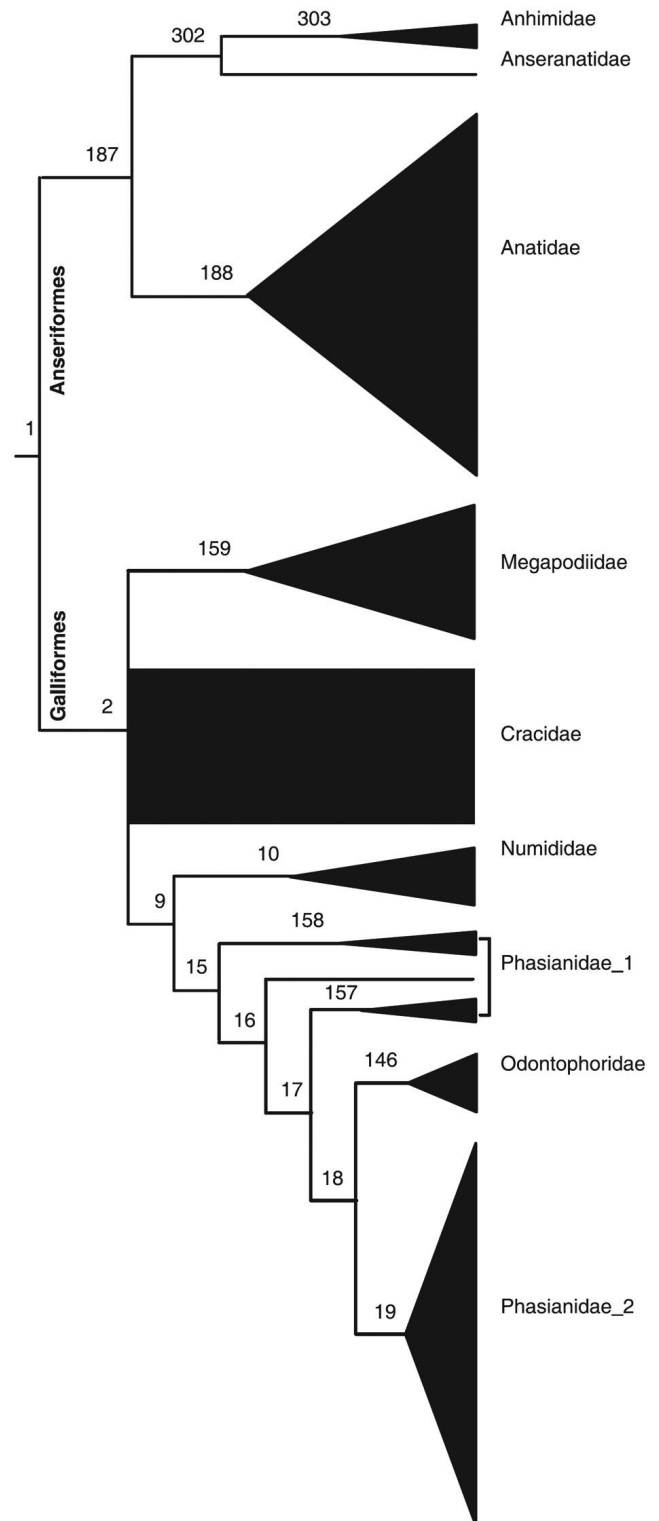

Fig. 2. Simplified representation of the Galloanserae supertree, showing interrelationships of and relative species richness of the major higher-level groups. Numbers on nodes represent node IDs.
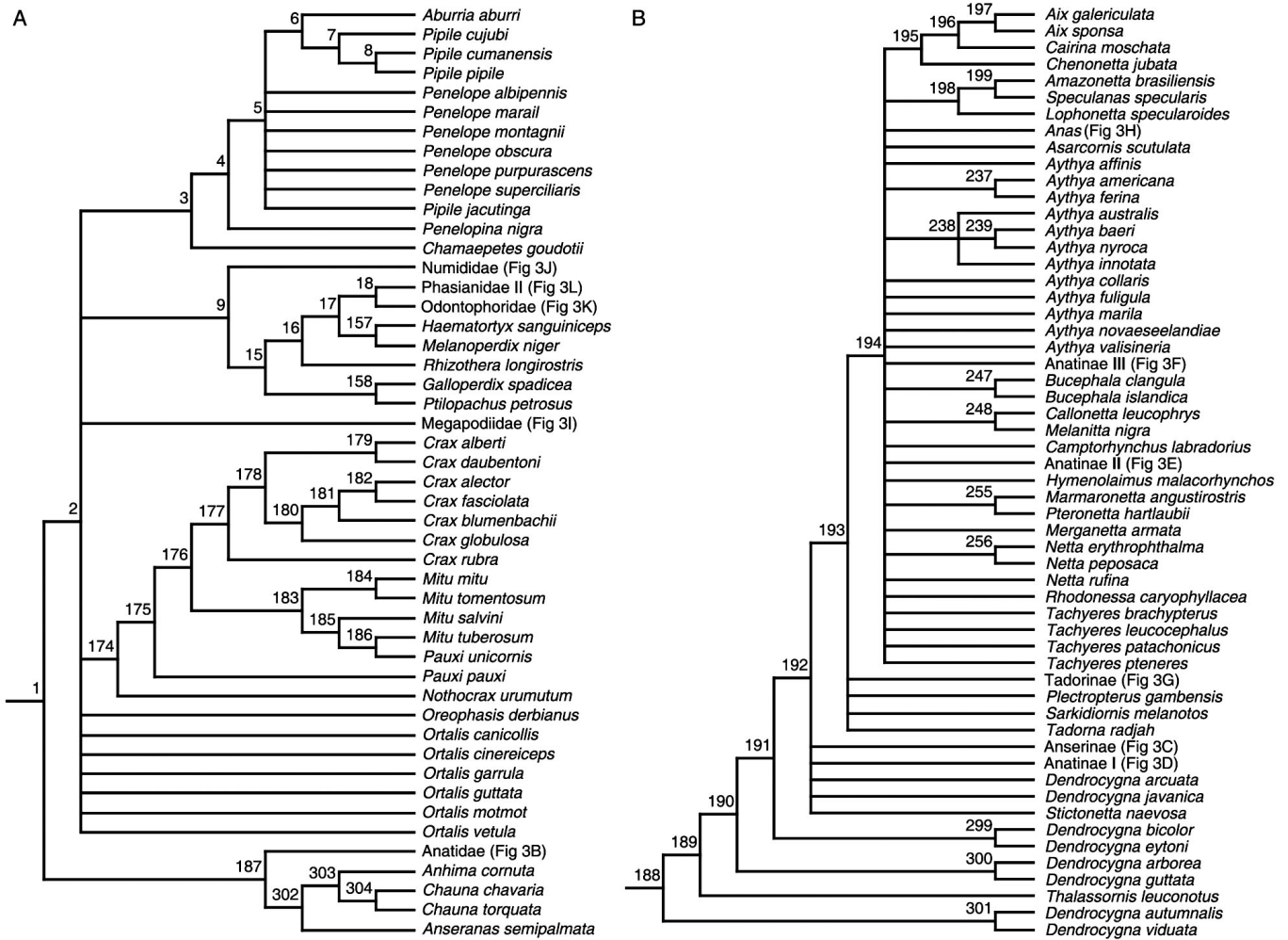
Fig. 3. A–P. Component supertrees of the fowl supertree showing species-level relationships.
—A. Galloanserae. —B. Anatidae. —C. Anserinae. —D. Anatinae I. —E. Anatinae II. —F. Anatinae III. —G. Tadorinae.
—H. Anas. —I. Megapodiidae. —J. Numididae. —K. Odontophoridae. —L. Phasianidae II. —M. Perdicinae. —N. Tetraoninae.
—O. Phasianinae I. —P. Phasianinae II. Numbers on nodes represent node IDs. rQS support values for each node on the
supertree are presented in supplementary material II.

Anseriformes

The supertree supported the partitioning of Anseri-
formes into the three traditional families (Fig. 2) Anhimi-
dae (screamers), the monotypic Anseranatidae (Magpie
Goose), and Anatidae (ducks, geese, and swans). Anati-
dae was the sister group to the two other families, which
was consistent with DNA-DNA hybridization (Sibley
& Ahlquist 1990), and nuclear and mitochondrial DNA
studies (e.g. Sorenson *et al.* 2003). This resolution, how-
ever, conflicted with some morphology-based topolo-
gies (e.g. Livezey 1997) and nuclear DNA studies (e.g.
RAG-2 exon; see Cracraft *et al.* 2004), where Anhimi-
dae formed the sister group. This uncertainty was also re-
flected in the slightly low rQS value (0.049; node num-
ber 302; Fig. 3A) for the clade containing both Anhimi-
dae and Anseranatidae.

Based on behavioral patterns, Delacour & Mayr (1945)
split Anatidae into the two subfamilies Anserinae and An-
atinae, a pattern followed by del Hoyo *et al.* (1992). This
classification was amended recently by Livezey (1997)
and Dickinson (2003), who each recognized five subfam-
ilies, splitting Dendrocygninae and the monotypic Stic-
tonettinae (Freckled Duck) from a redefined Anserinae,
and Tadorninae from Anatinae. However, the supertree
did not provide strong support for either scheme, with
only Anserinae sensu Livezey (1997) and Dickinson (2003)
being found to be monophyletic within a paraphyletic
Anatinae (Fig. 3B).

The supertree revealed a paraphyletic Dendrocygni-
nae with respect to the remaining Anatidae, placing it
as the first group to evolve in Anatidae (Fig. 3B). This
basal position of the subfamily reflected the majority of

C

D
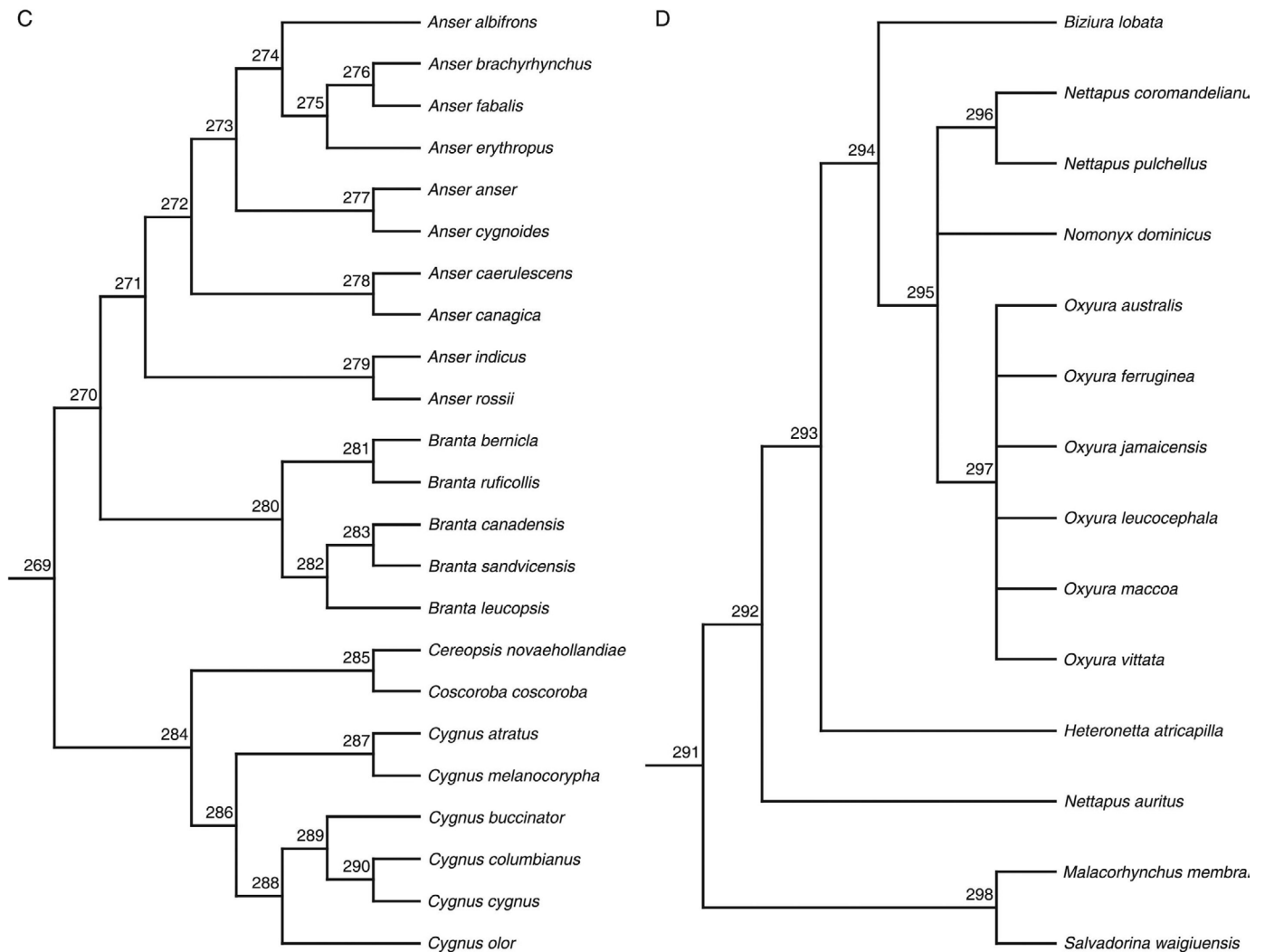
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the source topologies (e.g. Sibley & Ahlquist 1990; Livezey 1997). However, the internal relationships of Dendrocygninae in the supertree contradicted most traditional taxonomic groupings, including the monophyly of *Dendrocygna* (whistling ducks) and its sister group relationship with and *Thalassornis*.

The relative position of Stictonettinae also differed among the source references. Various authors have linked it with any of Dendrocygninae (Woolfenden 1961), Anserinae (Johnsgard 1965), or Tadorninae / Anatinae (Livezey 1997) based on morphological or behavioral characters. Our study also reflected this uncertainty, placing it in a polytomy with all other subfamilies (Fig. 3B).

Anserinae monophyly has been supported by both morphological (e.g. Livezey 1997) and molecular studies (e.g. Donne-Gousse *et al.* 2002), a fact reflected in our supertree (rQS = 0.042; node number 269; Fig. 3C), with 22 source trees supporting its monophyly and only six contradicting it. Resolution within Anserinae was complete and each of the three polytypic genera recognized by

Dickinson (2003) (*Anser*, *Branta*, and *Cygnus*) were recovered as monophyletic (Fig. 3C). *Anser* and *Branta* formed a clade (rQS = 0.042; node number 270; 20 source trees in agreement and only four in conflict), consistent with the majority of studies recognizing them as the tribe Anserini (true geese, e.g. Livezey 1997). However, disagreement among the source trees about the interrelationships of *Cygnus*, Coscoroba and Cereopsis lead the relative position of these genera being somewhat equivocal in the supertree (rQS = –0.003 for the clade as a whole and rQS = 0.003 for the grouping of Coscoroba and Cereopsis; Fig. 3C). For example, a morphological study (Livezey 1997) recognized the clade of *Cygnus* + Coscoroba as the tribe Cygnini (swans), and Cereopsis as the independent tribe Cereopsini, which was regarded as a distant relative to *Cygnus* + *Anser* + *Branta*. However, a recent molecular study placed Cereopsis and Coscoroba as sister genera, with *Cygnus* as sister to this clade (Donne- Gousse *et al.* 2002), as was found in this study (Fig. 3C). This latter branching pattern is also congruent with the disjunctive geographical origins
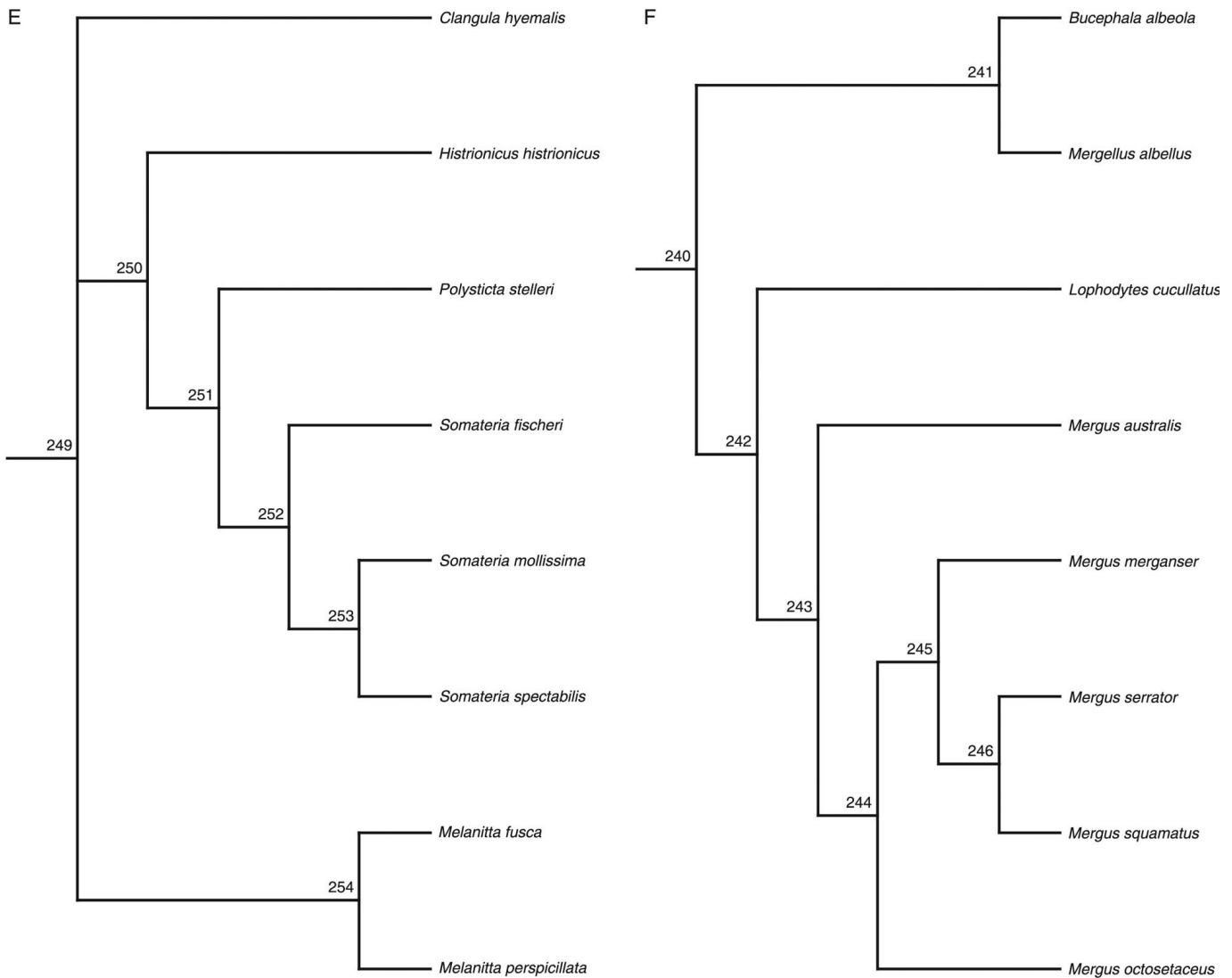
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of the genera, with *Cygnus* originating in the Northern Hemisphere and the other two genera coming from the Southern Hemisphere (Donne-Gousse *et al.* 2002).

Strong disagreement exists with respect to the compositions of and interrelationships between Tadorninae and Anatinae, which is reflected in the supertree by neither subfamily being recovered as monophyletic (Fig. 3B). Nor do the two subfamilies form a clade (although the majority of their members do cluster together), with Anserinae embedded within them. For instance, whereas Dickinson (2003) did not delineate any tribes for the subfamilies in his classification, del Hoyo *et al.* (1992) divided Tadorninae + Anatinae into eight tribes. Independently of this, Livezey (1997) also divided Tadorninae into three tribes and Anatinae into five tribes. However, despite the similar numbers of tribes erected by these two authors, few are identical in terms of their composition (e.g. Tadornini, comprising Tadorna, Chloephaga, Neochen, Alopochen,

and Cyanochen). Instead, different compositions are the rule. For example, whereas Livezey (1997) included Hymenolaimus in Merganettini (Tadorninae), del Hoyo *et al.* 1992 considered it to be part of Anatini (Anatinae).

This supertree reflected these disagreements, with only the tribe Malacorhynchini (comprising *Malacorhynchus* and *Salvadorina*) being recovered unequivocally as monophyletic (Tadornini was monophyletic in the majority-rule supertree), and then strongly so, with 12 source trees supporting the clade and none opposing it (rQS = 0.031; node number 298; Fig. 3D). Moreover, whereas Malacorhynchini formed a clade with Oxyurini (*Heteronetta*, *Biziura*, *Nomonyx*, and *Oxyura*, but also unconventionally including *Nettapus*), this clade was positioned as part of a polytomy with Anserinae (or basal to it in the majority-rule supertree), hinting at the possible non monophyly of Tadornine + Anatinae (Fig. 3B). Again, however, this uncertainty simply reflects historical disagreement. For
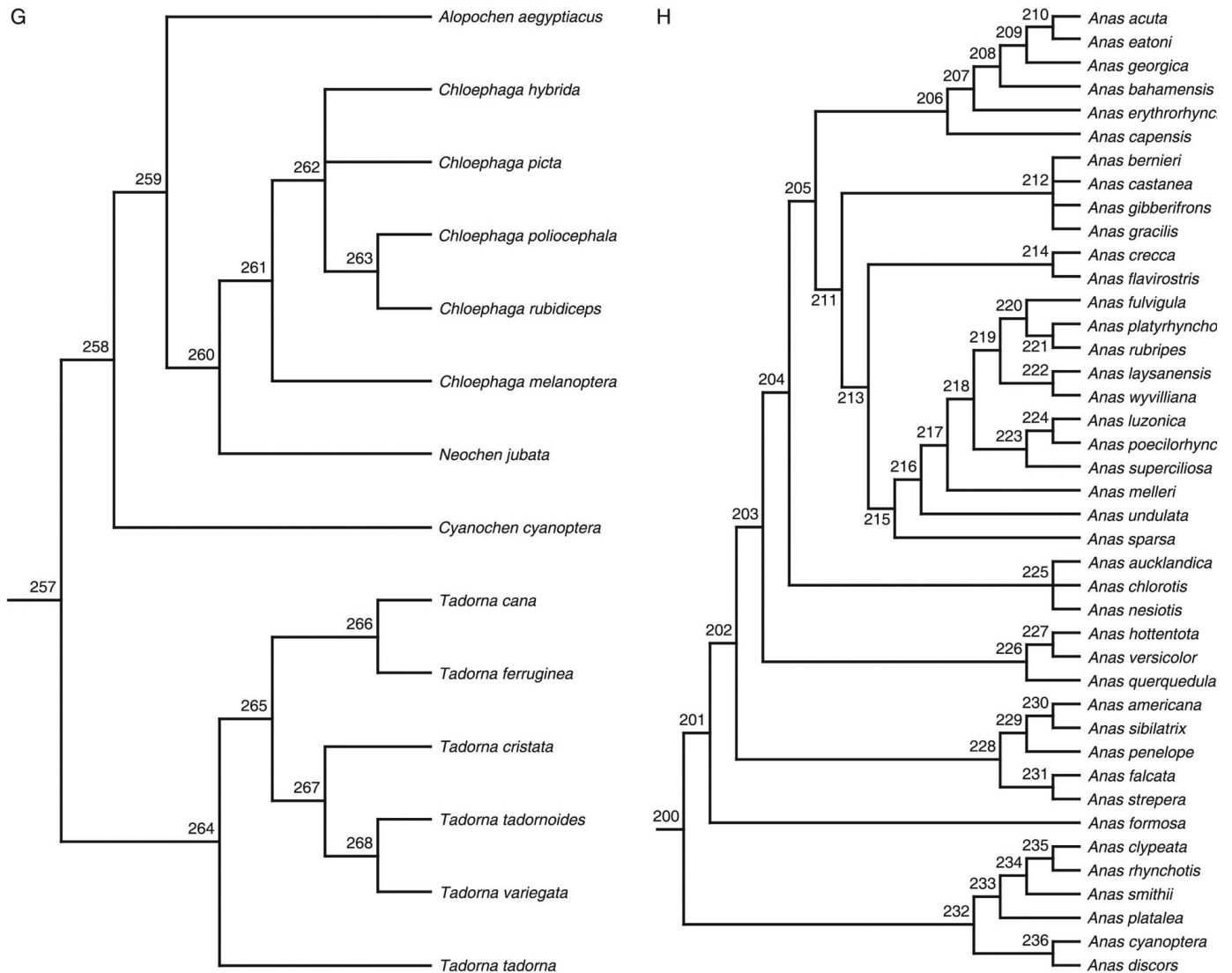
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example, the DNA-DNA hybridization study of Sibley & Ahlquist (1990) placed the Oxyura as sister to the remaining Anatidae, which is broadly consistent with our results, but Malacorhynchini in Anatinae, and therefore not directly related to Oxyura. By contrast, morphological evidence (e.g. Livezey 1997) tends to place Malacorhynchini at the base of the whole Anatinae. Thus, the relative positions of Malacorhynchini and Oxyurini appear to differ between molecular and morphological data. This conflict was also reflected in the rQS value of –0.018 for the relationship between Malacorhynchini and its sister clade, with six source trees in agreement and 17 source trees in disagreement with this arrangement (node number 291; Fig. 3D).

Resolution within the remaining members of Tadorninae and Anatinae (which formed a clade) was generally poor (Fig. 3B,D–H), with the clade displaying a large basal polytomy and the poor resolution also extending from the tribal-level down through the genus- and species-levels. Only 46% (6 of 13) of the polytypic genera within Tadorninae + Anatinae were monophyletic in the supertree, and the entire clade was less than 70% resolved. The majority-rule supertree reveals better overall resolution for this clade (97%), and at the species- and the genus-levels in these subfamilies in particular. Resolution, however, remained poor at the higher taxonomic levels.

Galliformes

Traditionally, the relative positions between Megapodiidae (megapodes) and Cracidae (chachalacas, curassows, and guans), and among Numididae (guineafowls), Odontophoridae (New World quails), and Phasianidae (partridges, turkeys, grouse, and pheasants) have been contentious. Some authors suggested a sister-group relationship between Megapodiidae and Cracidae, designating them as the superfamily Cracoidea (Wetmore 1960),
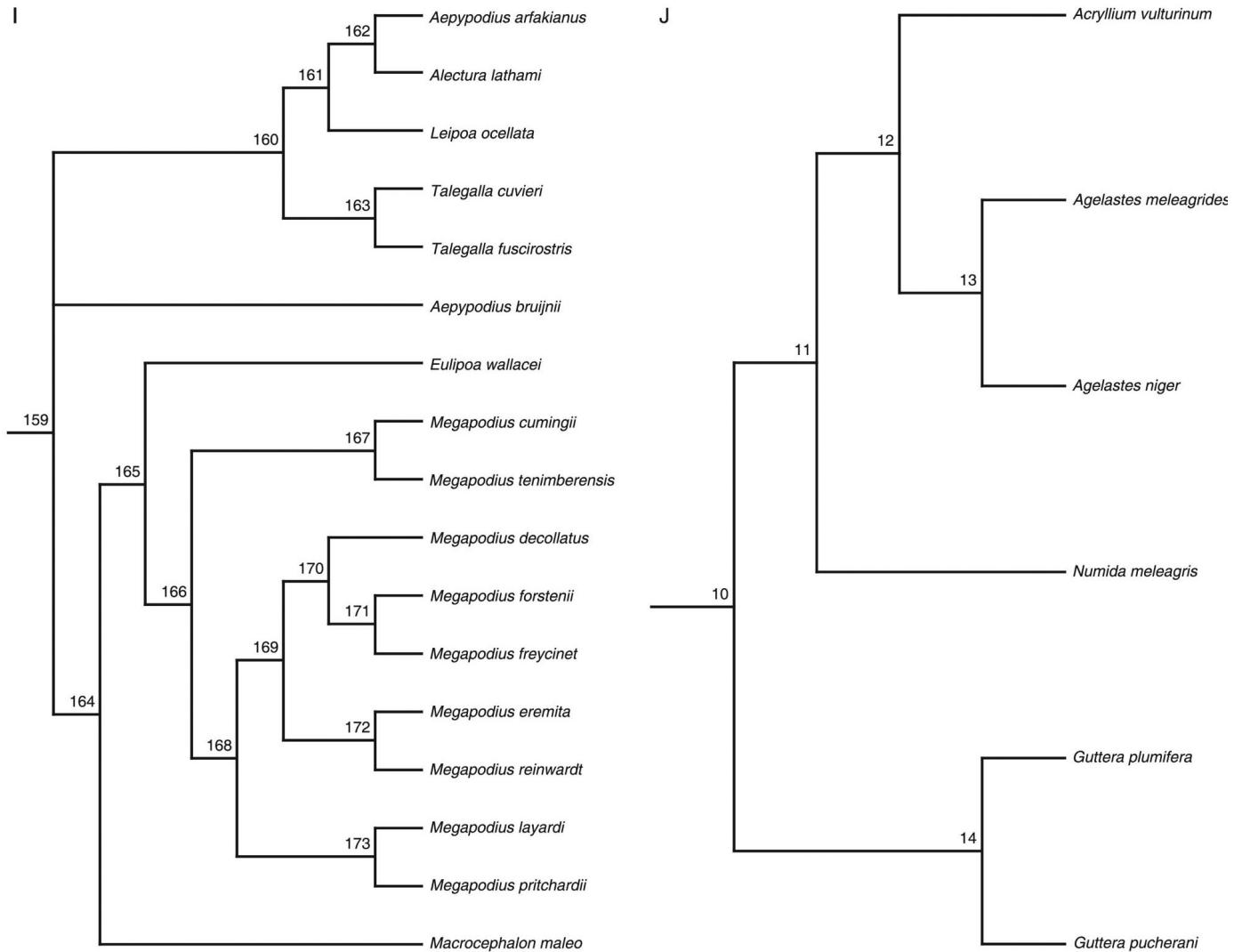
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the suborder Craci (del Hoyo *et al.* 1994), or even as the independent order Craciformes (Sibley & Ahlquist 1990). However, more recent phylogenies based on morphology (e.g. Dyke *et al.* 2003), molecular data (e.g. Dimcheff *et al.* 2002) or their combination (e.g. Crowe *et al.* 2006) all tend to support Megapodiidae as being sister to the remaining Galliformes (including Cracidae), with Cracidae then being sister to the remaining forms. Although relationships among these groups were unresolved in the strict consensus supertree (Fig. 3A), the majority-rule supertree broadly reflected this latter pattern, supporting the sequential sister-group relationships of Megapodiidae and Cracidae (with the exception of *Ortalis vetula*, thereby making Cracidae non-monophyletic), and the remaining Galliformes; these groups formed part of a large polytomy in the strict-consensus supertree (Figs 2, 3). Support for these sequential sister-group relationships also comes from recent studies based on transposon data (Kriegs *et*

al. 2007) that were published after completion of the supertree analyses.

Our supertree supported Numididae as being sister to the remaining families Odontophoridae and Phasianidae, with the clade comprising all three families having a high rQS value of 0.252 (node number 9; Fig. 3A). This arrangement agrees with those derived from nuclear (e.g. Armstrong *et al.* 2001), mitochondrial (e.g. Dimcheff *et al.* 2002), and combined morphological and molecular data (e.g. Crowe *et al.* 2006). That being said, the position of Odontophoridae remains largely unresolved. For example, recent phylogenetic trees derived from DNA–DNA hybridization (e.g. Sibley & Ahlquist 1990), morphological (e.g. Dyke *et al.* 2003), and combined morphological and molecular data (e.g. Crowe *et al.* 2006) place the family in a variety of positions within Phasianidae. Our supertree follows suit and recovers Odontophoridae as a relatively basal group within Phasianidae. However, it is

K

- 151 — *Callipepla californica*, *Callipepla gambelii*
- 150 — *Callipepla douglasii*
- 149 — *Callipepla squamata*
- 148
- 152 — *Colinus cristatus*, *Colinus virginianus*
- *Oreortyx pictus*
- 147
- 156 — *Cyrtonyx montezumae*, *Dactylortyx thoracicus*
- 155
- 154 — *Rhynchortyx cinctus*
- 153 — *Odontophorus gujanensis*
- *Dendrortyx macroura*
- 146
- *Philortyx fasciatus*

L

- 23 — Phasianinae I (Fig 3O)
- 37 — Tetraoninae (Fig 3N)
- 55 — *Meleagris gallopavo*, *Meleagris ocellata*
- 36
- 35
- 56 — *Perdix dauurica*, *Perdix perdix*
- Phasianinae II (Fig 3P)
- 22
- 91 — *Bambusicola thoracicus*
- 94 — *Gallus gallus*, *Gallus sonneratii*
- 93
- 92 — *Gallus lafayettii*, *Gallus varius*
- 90
- 99 — *Francolinus africanus*
- 101 — *Francolinus levaillantoides*, *Francolinus psilolaemus*
- 98 — *Francolinus shelleyi*
- 97
- 102 — *Francolinus finschi*, *Francolinus laevaillantii*
- *Francolinus streptophorus*
- 21
- 96
- 106 — *Francolinus albogularis*, *Francolinus schlegelii*
- 105
- 104 — *Francolinus coqui*
- 103 — *Francolinus lathami*
- 95 — *Francolinus sephaena*
- *Francolinus pondicerianus*
- 20
- 108 — *Francolinus francolinus*, *Francolinus pictus*
- 107 — *Francolinus pintadeanus*
- *Francolinus gularis*
- Perdicinae (Fig 3M)
- 19
- 145 — *Arborophila torqueola*, *Caloperdix oculeus*
- 144
- 143 — *Rollulus rouloul*
- *Xenoperdix udzungwensis*

Fig. 3. Continued.

noteworthy that most phylogenetic studies have included only a few species of Odontophoridae, such that we lack robust phylogenetic information for more than half of all species of this family. Thus, the relative position of Odontophoridae indicated here should likewise be regarded as tentative and should be revisited in the future with increased taxon sampling.

The monophyly of Megapodiidae was supported in the supertree (rQS = 0.099; node number 159; Fig. 3I) and relationships within the family were largely congruent with several traditional species-level phylogenies (e.g. Jones *et al.* 1995; Birks & Edwards 2002; Crowe *et al.* 2006). Support for the monophyly of the genus *Megapodius* in particular was strong, with 10 source trees supporting it and none directly opposing it (rQS = 0.026; node number 166). Macrocephalon was recovered as the sister to the clade of Eulipoa + *Megapodius* (rQS = 0.023; node number 164). Monophyly of *Aepypodius* was not supported.

The source trees did not support Cracidae monophyly absolutely (Fig. 3A), although the family is monophyletic in the majority-rule supertree (and found in 94% of all 100 000 equally most parsimonious solutions). Much of the conflict can be traced to the historical uncertainty regarding the two genera *Oreophasis* and *Ortalis*, which have been placed within either Cracinae (e.g. Crowe *et al.* 2006) or Penelopinae (e.g. del Hoyo *et al.* 1994; Dickinson 2003). The strict-consensus supertree makes no definitive statement to resolve this conflict (Fig. 3A); however, the majority-rule supertree suggests that the affinities of the two genera lie with Cracinae. However, *Ortalis* was not recovered as monophyletic in either supertree. Recent analyses combining molecular data with osteological, integumentary and behavioral characters placed *Oreophasis* and *Ortalis* within Penelopinae and not Cracinae, and with fairly robust bootstrap support (Frank- Hoeflich *et al.* 2007). As such, placement of these genera should still be regarded as tentative
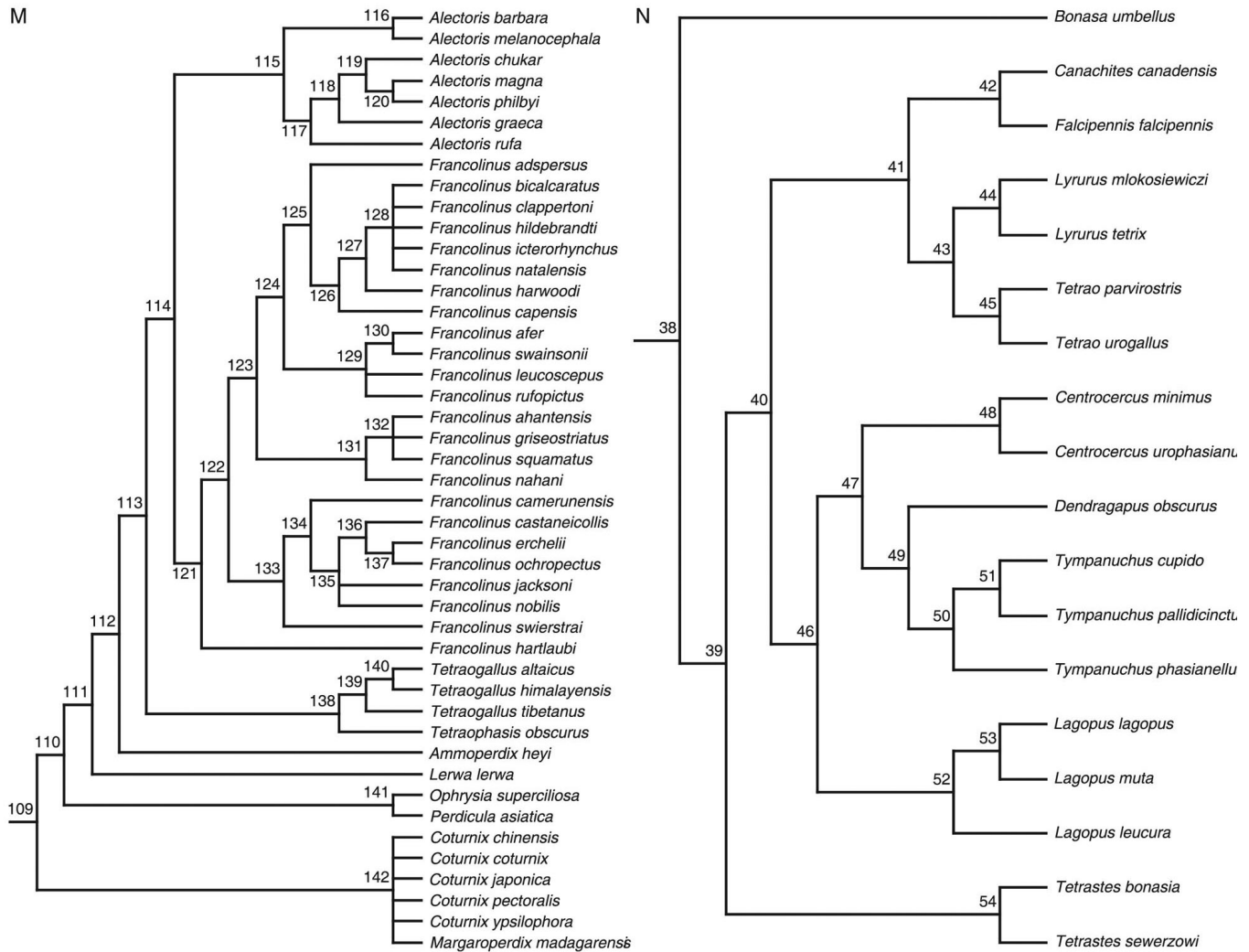
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and should be revisited with increased taxon sampling and possibly the use of other, novel data types. Beyond this, the subfamilies Cracinae (curassows) and Penelopinae (chachalacas and guans) were found to be monophyletic, although the degree of resolution within each varied considerably. Support for Cracinae was strong, with 26 source trees directly supporting and none directly contradicting it (rQS=0.068; node number 174; Fig. 3A). By contrast, relationships within Penelopinae were unclear, largely because of the non-monophyly of *Penelope*.

Monophyly of Numididae was directly supported by 12 source trees and contradicted by only two (rQS=0.026; node number 10; Fig. 3J). The species-level relationships in the family were completely resolved and each of the two polytypic genera (*Agelastes* and *Guttera*) was monophyletic. The branching pattern within the family disagreed with that presented by Crowe (1978), but was identical to that based later on combined morphological and molecular data (Crowe *et al.* 2006).

Similarly, monophyly of Odontophoridae was also supported, being present in eight source trees and none directly contradicting it (rQS = 0.021; node number 146; Fig. 3K). Relationships within the family were largely consistent with those based on a wide range of data types, including osteological (e.g. Holman 1961), ecological (e.g. Johnsgard 1983), allozyme (e.g. Gutierrez *et al.* 1983), and combined morphological and molecular data (e.g. Crowe *et al.* 2006). *Philortyx* fasciatus has been grouped traditionally with some genera adapted to the forest edge, such as *Colinus*, *Callipepla*, and *Oreortyx* (e.g. Holman 1961; Johnsgard 1983), but our supertree placed it as sister to the remaining Odontophoridae. Again, however, this relationship, and all other relationships within the family, should be interpreted with some degree of caution given the poor phylogenetic sampling effort in the family to date.

Within a polyphyletic Phasianidae, sequential sister-group relationships of the four subfamilies Perdicinae (partridges), Meleagridinae (turkeys), Tetraoninae
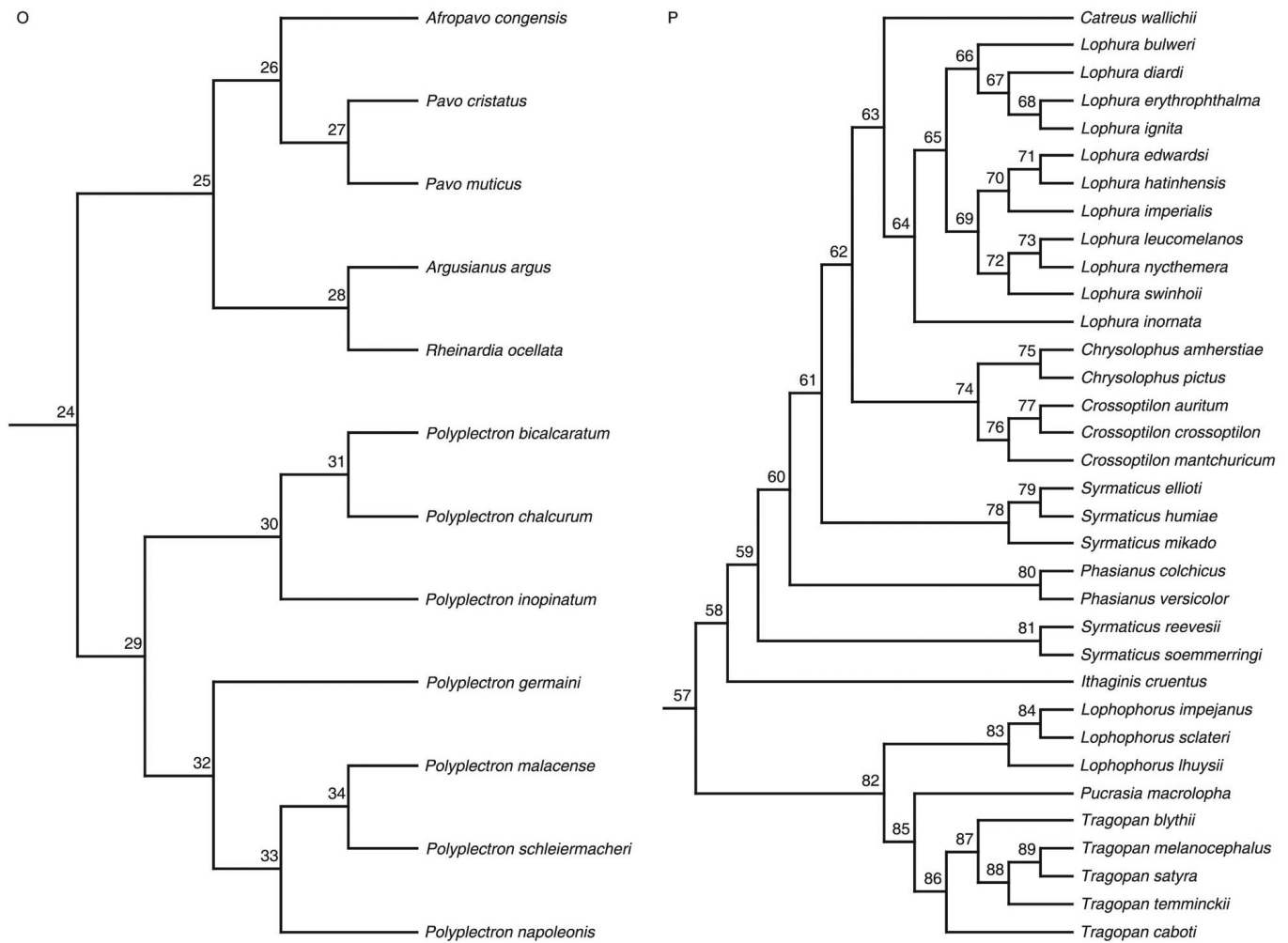
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(grouses), and Phasianinae (pheasants) were broadly recovered in the supertree, albeit with some exceptions (Fig. 3A,L–P). The supertree revealed seven subdivisions of Perdicinae, six of which were monophyletic. The first was a paraphyletic assemblage of Rhizothera and the monotypic genera *Galloperdix*, *Ptilopachus*, *Haematortyx*, and *Melanoperdix* situated basal to Odontophoridae and the remaining Phasianidae (Fig. 3A). Among these genera, a sister-group relationship between *Galloperdix* and Ptilopachus was recovered, concurring with the results of Crowe *et al.* (2006). The second group (rQS = 0.042; node number 143; Fig. 3L) included *Xenoperdix*, *Rollulus*, *Arborophila*, and *Caloperdix*. The species composition and branching pattern within the group was in agreement with Crowe *et al.* (2006), who designated this group as Arborophilinae. Similarly, the third group (rQS = 0.044; node number 109; Fig. 3M) corresponds to Coturnicinae of Crowe *et al.* (2006) and comprises Old World quails, the partridges *Coturnix* and *Alectoris*, and some *Francolinus* species. Relationships within *Coturnix* were unresolved, however,

and its monophyly could also not be assured. The fourth group (rQS = –0.013; node number 107; Fig. 3L) consisted of Francolinus gularis, F. pictus, F. pintadeanus, and F. francolinus. In the fifth group, the monotypic Bambusicola formed a clade with the four species of *Gallus* (Fig. 3L). Although *Gallus* is typically allocated to Phasianinae, the grouping found in our supertree does find support in Crowe *et al.* (2006), who named it Gallininae. In addition, the sister-group relationship between Bambusicola and *Gallus* was highly supported with an rQS value of 0.075 (node number 91; Fig. 3L). The sixth group (rQS = –0.018; node number 95; Fig. 3L) consisted of the remaining Francolinus species, meaning that the supertree did not support the monophyly of the 41 species of Francolinus. Some authors, however, have suggested on the basis of morphological and molecular data that this genus be subdivided into at least five different genera (Pternistis, Francolinus, Dendroperdix, Peliperdix, and Scleroptila, e.g.Crowe *et al.* 1992; Crowe *et al.* 2006). Although our results did not reflect these generic designations exactly,

branching patterns within Francolinus and its relation-ships with other genera were largely congruent with those in Crowe *et al.* (1992). The final group, the genus *Perdix* (rQS = 0.031; node number 56; Fig. 3L), was placed as the sister taxon to the clade of Meleagridinae + Tetra-oninae, albeit with some uncertainty (rQS = –0.005; node number 36; Fig. 3L), with 30 source trees contradicting this placement and 28 supporting it.

The sister-group relationship of Meleagridinae (two species in the genus *Meleagris*) and Tetraoninae was also not strongly supported (rQS = 0.003; node number 37; Fig. 3L), although the monophyly of each showed better support (rQS = 0.018 and 0.106; node number 55 and 38; Fig. 3L, N). Relationships within Tetraoninae were con-gruent with molecular (e.g. Gutierrez *et al.* 2000; Dim-cheff *et al.* 2002; Drovetski 2002) and combined morpho-logical and molecular data (e.g. Crowe *et al.* 2006). The only exception was the position of Lagopus, with the low rQS value of the clade containing Lagopus and its sister group (–0.062; node number 46; Fig. 3N) suggesting dis-agreement among the source trees.

The remaining Phasianinae (with the exception of *Gallus*) was split into the peafowl (e.g. *Pavo* and *Polyplec-tron*; rQS = –0.003; node number 24; Fig. 3O) and pheas-ant groups (e.g. *Lophura* and *Tragopan*; rQS = 0.005; node number 57; Fig. 3P) separated by the clade comprising *Perdix*, Meleagridinae, and Tetraoninae. Apart from this, the species composition and branching pattern within each group was highly congruent with phylogenetic trees based on molecular and morphological data (e.g. Crowe *et al.* 2006).

Conclusion

Our supertree represents a first attempt to derive a com-prehensive species-level phylogeny of Galloanserae, again highlighting the power of a traditional supertree approach (*sensu* Bininda- Emonds 2004) in this regard. Those areas where the supertree was either poorly re-solved or incomplete tend to reflect gaps in the existing phylogenetic database (either ongoing disagreement and/ or a lack of sufficient, robust phylogenetic information), and highlight areas in need of more study. Some of this missing information could perhaps be gleaned from tax-onomies and other studies that are not based on the direct analysis of primary character data. However, given that strong disagreement often exists within the studies we have included here, we felt it prudent not to include these additional sources. Like any phylogenetic hypothesis, our supertree is naturally open to further revision and resolu-tion. In the meantime, however, it will provide a valuable foundation to understand the diverse biology of Galloan-serae in a robust phylogenetic framework.

Supporting Information

Additional Supporting Information may be found following the References.

Supplementary Material I (25 pages)
Source trees used to construct the galloanserae supertree sub-divided according to the independent data set they contributed to. The relative weights for the pseudo characters associated with each source tree are also provided. Number of permuta-tions refers to the number of trees that resulted from the syn-onymization process because of having to accommodate non-monophyletic taxa.

Supplementary Material II (12 pages)
rQS values for the strict consensus supertree, indicating nodal support (± SE) among the set of source trees together with the number of source trees supporting, conflicting or equivocal with a given node. Node numbers refer to Figs 2 and 3.

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Supplementary Material I

Source trees used to construct the galloanserae supertree subdivided according to the independent data set
they contributed to. The relative weights for the pseudocharacters associated with each source tree
are also provided. Number of permutations refers to the number of trees that resulted from the
synonymization process because of having to accommodate non-monophyletic taxa.

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mix 01	A 09 09	McCracken *et al*. (1999)	Fig 5a		0.500
Mix 01	A 09 10	McCracken *et al*. (1999)	Fig 5b		0.500
Mix 02	G 63 08	Bloomer & Crowe (1998)	Fig 7		1.000
Mix 03	G 89 09	Crowe *et al*. (2006)	Fig 4		0.500
Mix 04	G 64 06	Crowe *et al*. (1992)	Fig 3c		1.000
Mix 06	G 75 02	Randi *et al*. (1991)	Fig 1b		1.000
Mol 01	G 04 03	Kimball *et al*. (1999)	Fig 4		0.250
Mol 01	G 14 05	Kornegay *et al*. (1993)	Fig 5b		0.250
Mol 01	G 14 07	Kornegay *et al*. (1993)	Fig 6b		0.250
Mol 01	G 37 02	Avise *et al*. (1994)	Fig 1 (right)		0.250
Mol 02	G 05 03	Nishibori *et al*. (2004)	Fig 1c		0.500
Mol 02	G 051 03	Nishibori *et al*. (2002)	Fig 1c		0.500
Mol 03	G 48 02	Nishibori *et al*. (2005)	Fig 1b	2	0.500
Mol 04	A 16 01	Zimmer *et al*. (1994)	Fig 3a		0.143
Mol 04	A 16 02	Zimmer *et al*. (1994)	Fig 3b		0.143
Mol 04	A 16 03	Zimmer *et al*. (1994)	Fig 3c		0.143
Mol 04	G 31 09	Garcia-Moreno *et al*. (2003)	Fig a1 (12S ML analysis)		0.143
Mol 04	G 31 10	Garcia-Moreno *et al*. (2003)	Fig a1 12S		0.143

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 04	G 31 11	Garcia-Moreno *et al*. (2003)	POY (equal weights) Fig a1 12S (tv and gaps 2x over ts)		0.143
Mol 04	G 89 13	Crowe *et al*. (2006)	Fig 8	2	0.071
Mol 05	G 17 01	Sorenson *et al*. (2003)	Fig 1		0.500
Mol 05	G 17 02	Sorenson *et al*. (2003)	Fig 2		0.500
Mol 06	G 31 01	Garcia-Moreno *et al*. (2003)	Fig 2b		0.333
Mol 06	G 31 13	Garcia-Moreno *et al*. (2003)	Fig a2 (coding mtDNA)		0.333
Mol 06	G 31 18	Garcia-Moreno *et al*. (2003)	Fig a2 (all mtDNA)		0.333
Mol 07	G 02 01	Dimcheff *et al*. (2002)	Fig 2		0.333
Mol 07	G 02 02	Dimcheff *et al*. (2002)	Fig 3		0.333
Mol 07	G 39 01	Dimcheff *et al*. (2000)	Fig 6		0.333
Mol 08	G 02 03	Dimcheff *et al*. (2002)	Fig 4		0.500
Mol 08	G 45 01	Pereira & Baker (2006)	Fig 1		0.500
Mol 09	A 09 04	McCracken *et al*. (1999)	Fig 2a		0.018
Mol 09	A 09 05	McCracken *et al*. (1999)	Fig 2b		0.018
Mol 09	A 09 06	McCracken *et al*. (1999)	Fig 2c		0.018
Mol 09	A 09 07	McCracken *et al*. (1999)	Fig 3		0.018
Mol 09	A 14 01	Sraml *et al*. (1996)	Fig 1		0.018
Mol 09	A 14 02	Sraml *et al*. (1996)	Fig 2		0.018
Mol 09	A 14 03	Sraml *et al*. (1996)	Fig 3		0.018
Mol 09	G 01 02	Armstrong *et al*. (2001)	Fig right		0.018

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 09	G 04 01	Kimball *et al.* (1999)	Fig 2		0.018
Mol 09	G 04 02	Kimball *et al.* (1999)	Fig 3		0.018
Mol 09	G 09 01	Kimball *et al.* (1997)	Fig 1a		0.018
Mol 09	G 09 03	Kimball *et al.* (1997)	Fig 2a		0.018
Mol 09	G 10 01	Randi (1996)	Fig 5a		0.018
Mol 09	G 10 02	Randi (1996)	Fig 5b		0.018
Mol 09	G 10 03	Randi (1996)	Fig 6a		0.018
Mol 09	G 10 04	Randi (1996)	Fig 6b		0.018
Mol 09	G 14 04	Kornegay *et al.* (1993)	Fig 5a		0.018
Mol 09	G 14 06	Kornegay *et al.* (1993)	Fig 6a		0.018
Mol 09	G 31 07	Garcia-Moreno *et al.* (2003)	Fig a1 (cytochrome b)		0.018
Mol 09	G 31 16	Garcia-Moreno *et al.* (2003)	Fig a2 (cytochrome b)		0.018
Mol 09	G 33 03	Zhan & Zhang (2005)	Fig 2c		0.018
Mol 09	G 33 04	Zhan & Zhang (2005)	Fig 4a		0.018
Mol 09	G 35 01	Shibusawa *et al.* (2004a)	Fig 4		0.018
Mol 09	G 37 01	Avise *et al.* (1994)	Fig 1 (left)		0.018
Mol 09	G 37 03	Avise *et al.* (1994)	Fig 2 (left)		0.018
Mol 09	G 37 04	Avise *et al.* (1994)	Fig 2 (right)		0.018
Mol 09	G 63 02	Bloomer & Crowe (1998)	Fig 3		0.018
Mol 09	G 63 03	Bloomer & Crowe (1998)	Fig 4a		0.018
Mol 09	G 63 04	Bloomer & Crowe (1998)	Fig 4b		0.018
Mol 09	G 63 05	Bloomer & Crowe (1998)	Fig 4c		0.018
Mol 09	G 63 06	Bloomer & Crowe (1998)	Fig 5		0.018
Mol 09	G 65 01	Bush & Strobeck (2003)	Fig 1		0.018

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 09	G 65 02	Bush & Strobeck (2003)	Fig 2		0.018
Mol 09	G 65 03	Bush & Strobeck (2003)	Fig 3		0.018
Mol 09	G 69 04	Kimball *et al.* (2001)	Fig 2b3		0.018
Mol 09	G 69 07	Kimball *et al.* (2001)	Fig 3		0.018
Mol 09	G 71 01	Luzhang *et al.* (2005)	Fig 3		0.018
Mol 09	G 78 01	Ellsworth *et al.* (1996)	Fig 1		0.018
Mol 09	G 78 02	Ellsworth *et al.* (1996)	Fig 2a		0.018
Mol 09	G 78 03	Ellsworth *et al.* (1996)	Fig 2b		0.018
Mol 09	G 78 04	Ellsworth *et al.* (1996)	Fig 2c		0.018
Mol 09	G 78 05	Ellsworth *et al.* (1996)	Fig 3		0.018
Mol 09	G 81 01	Gutierrez *et al.* (2000)	Fig 1a		0.018
Mol 09	G 81 02	Gutierrez *et al.* (2000)	Fig 1b		0.018
Mol 09	G 81 03	Gutierrez *et al.* (2000)	Fig 1c		0.018
Mol 09	G 81 04	Gutierrez *et al.* (2000)	Fig 1d		0.018
Mol 09	G 84 03	Zhan *et al.* (2003)	Fig 2a		0.018
Mol 09	G 84 04	Zhan *et al.* (2003)	Fig 2b		0.018
Mol 09	G 85 01	Tsam *et al.* (2003)	Fig 3a		0.018
Mol 09	G 85 02	Tsam *et al.* (2003)	Fig 3b		0.018
Mol 09	G 85 03	Tsam *et al.* (2003)	Fig 3c		0.018
Mol 09	G 88 01	Wen *et al.* (2005)	Fig 2a		0.018
Mol 09	G 88 02	Wen *et al.* (2005)	Fig 2b		0.018
Mol 09	G 88 03	Wen *et al.* (2005)	Fig 2c		0.018
Mol 09	G 89 10	Crowe *et al.* (2006)	Fig 5	3	0.006
Mol 09	G 90 01	Butorina *et al.* (2000)	Fig 4		0.018
Mol 10	G 70 02	Lucchini *et al.* (2001)	Fig 3		1.000
Mol 11	A 06 02	Kennedy & Spencer (2000)	Fig 3		1.000

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 12	A 06 03	Kennedy & Spencer (2000)	Fig 5		1.000
Mol 13	A 10 02	McCracken & Sorenson (2005)	Fig 4a		0.500
Mol 13	A 10 03	McCracken & Sorenson (2005)	Fig 4b		0.500
Mol 14	G 81 05	Gutierrez *et al.* (2000)	Fig 1e		0.500
Mol 14	G 81 06	Gutierrez *et al.* (2000)	Fig 1f		0.500
Mol 15	A 11 01	Paxinos *et al.* (2002)	Fig 4	2	0.042
Mol 15	G 33 06	Zhan & Zhang (2005)	Fig 4c		0.083
Mol 15	G 62 01	Randi *et al.* (2001)	Fig 4a		0.083
Mol 15	G 62 02	Randi *et al.* (2001)	Fig 4b		0.083
Mol 15	G 62 03	Randi *et al.* (2001)	Fig 4c		0.083
Mol 15	G 69 03	Kimball *et al.* (2001)	Fig 2b2		0.083
Mol 15	G 72 01	Moulin *et al.* (2003)	Fig 2		0.083
Mol 15	G 74 05	Randi *et al.* (2000)	Fig 6d		0.083
Mol 15	G 74 08	Randi *et al.* (2000)	Fig 6g		0.083
Mol 15	G 74 09	Randi *et al.* (2000)	Fig 6h		0.083
Mol 15	G 86 01	Wu *et al.* (2005)	Fig 1		0.083
Mol 15	G 86 02	Wu *et al.* (2005)	Fig 2		0.083
Mol 16	A 01 13	Donne-Gousse *et al.* (2002)	Fig 7c		0.500
Mol 16	G 53 02	Grau *et al.* (2005)	Fig 2		0.500
Mol 17	G 31 03	Garcia-Moreno *et al.* (2003)	Fig 2d		1.000
Mol 18	A 01 12	Donne-Gousse *et al.* (2002)	Fig 7b		0.091
Mol 18	A 03 01	Johnson & Sorenson (1998)	Fig 1	4	0.023
Mol 18	A 03 02	Johnson & Sorenson (1998)	Fig 2	4	0.023
Mol 18	A 05 01	Johnson & Sorenson (1999)	Fig 1	2	0.045
Mol 18	G 05 01	Nishibori *et al.* (2004)	Fig 1a		0.091
Mol 18	G 05 02	Nishibori *et al.* (2004)	Fig 1b		0.091

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 18	G 051 01	Nishibori *et al.* (2002)	Fig 1a		0.091
Mol 18	G 051 02	Nishibori *et al.* (2002)	Fig 1b		0.091
Mol 18	G 57 01	Zink & Balckwell (1998)	Fig 3a		0.091
Mol 18	G 57 02	Zink & Balckwell (1998)	Fig 3b		0.091
Mol 18	G 80 01	Wada *et al.* (2004)	Fig 1		0.091
Mol 19	G 54 01	Pereira & Baker (2004)	Fig 2		0.500
Mol 19	G 54 02	Pereira & Baker (2004)	Fig 3		0.500
Mol 20	G 54 03	Pereira & Baker (2004)	Fig 5a		0.500
Mol 20	G 54 04	Pereira & Baker (2004)	Fig 5b		0.500
Mol 21	A 01 04	Donne-Gousse *et al.* (2002)	Fig 4a		0.032
Mol 21	A 01 05	Donne-Gousse *et al.* (2002)	Fig 4b		0.032
Mol 21	A 01 06	Donne-Gousse *et al.* (2002)	Fig 4c		0.032
Mol 21	A 01 07	Donne-Gousse *et al.* (2002)	Fig 4d		0.032
Mol 21	A 01 08	Donne-Gousse *et al.* (2002)	Fig 5a		0.032
Mol 21	A 01 09	Donne-Gousse *et al.* (2002)	Fig 5b		0.032
Mol 21	A 01 11	Donne-Gousse *et al.* (2002)	Fig 7a		0.032
Mol 21	A 10 01	McCracken & Sorenson (2005)	Fig 2		0.032
Mol 21	A 12 05	Peters *et al.* (2005)	Fig 5		0.032
Mol 21	A 12 06	Peters *et al.* (2005)	Fig 6		0.032
Mol 21	A 13 01	Ruokonen *et al.* (2000)	Fig 2a		0.032
Mol 21	A 13 02	Ruokonen *et al.* (2000)	Fig 2b	2	0.016
Mol 21	A 15 01	Young & Rhymer (1998)	Fig 2		0.032
Mol 21	G 04 04	Kimball *et al.* (1999)	Fig 5		0.032
Mol 21	G 09 02	Kimball *et al.* (1997)	Fig 1b		0.032
Mol 21	G 09 04	Kimball *et al.* (1997)	Fig 2b		0.032
Mol 21	G 33 05	Zhan & Zhang (2005)	Fig 4b		0.032

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 21	G 46 01	Akishinonomiya *et al.* (1995)	Fig 1		0.032
Mol 21	G 46 02	Akishinonomiya *et al.* (1995)	Fig 2		0.032
Mol 21	G 59 04	Drovetski (2002)	Fig 4	4	0.008
Mol 21	G 66 01	Akishinonomiya *et al.* (1996)	Fig 2		0.032
Mol 21	G 67 01	Hennache *et al.* (2003)	Fig 2	3	0.011
Mol 21	G 69 05	Kimball *et al.* (2001)	Fig 2b4		0.032
Mol 21	G 70 01	Lucchini *et al.* (2001)	Fig 2		0.032
Mol 21	G 73 01	Randi & Lucchini (1998)	Fig 7		0.032
Mol 21	G 74 01	Randi *et al.* (2000)	Fig 5		0.032
Mol 21	G 74 02	Randi *et al.* (2000)	Fig 6a		0.032
Mol 21	G 74 03	Randi *et al.* (2000)	Fig 6b		0.032
Mol 21	G 74 04	Randi *et al.* (2000)	Fig 6c		0.032
Mol 21	G 89 08	Crowe *et al.* (2006)	Fig 3f	2	0.016
Mol 21	G 89 12	Crowe *et al.* (2006)	Fig 7	3	0.011
Mol 22	G 31 05	Garcia-Moreno *et al.* (2003)	Fig a1 (ND1)		0.500
Mol 22	G 31 14	Garcia-Moreno *et al.* (2003)	Fig a2 (ND1)		0.500
Mol 23	G 48 01	Nishibori *et al.* (2005)	Fig 1a	2	0.250
Mol 23	G 48 03	Nishibori *et al.* (2005)	Fig 1c	2	0.250
Mol 24	G 31 06	Garcia-Moreno *et al.* (2003)	Fig a1 (ND2)		0.200
Mol 24	G 31 15	Garcia-Moreno *et al.* (2003)	Fig a2 (ND2)		0.200
Mol 24	G 55 02	Birks & Edwards (2002)	Fig 5 (right)	2	0.100
Mol 24	G 55 04	Birks & Edwards (2002)	Fig 6 (right)	2	0.100
Mol 24	G 89 11	Crowe *et al.* (2006)	Fig 6	2	0.100
Mol 25	A 07 01	Kessler & Avise (1984)	Fig 2 (upper)		0.333
Mol 25	A 07 02	Kessler & Avise (1984)	Fig 2 (lower)		0.333
Mol 25	A 07 03	Kessler & Avise (1984)	Fig 3	3	0.333

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 26	A 18 01	Tuohy *et al.* (1992)	Fig 7		1.000
Mol 27	G 49 01	Munechika *et al.* (1997)	Fig 1		1.000
Mol 28	G 61 01	Ellsworth *et al.* (1995)	Fig 1		0.500
Mol 28	G 61 02	Ellsworth *et al.* (1995)	Fig 2		0.500
Mol 29	G 64 05	Crowe *et al.* (1992)	Fig 3b		0.500
Mol 29	G 64 07	Crowe *et al.* (1992)	Fig 4		0.500
Mol 31	G 37 05	Avise *et al.* (1994)	Fig 4		1.000
Mol 32	G 52 03	Pereira *et al.* (2002)	Fig 4		0.500
Mol 32	G 52 04	Pereira *et al.* (2002)	Fig 5		0.500
Mol 33	G 31 04	Garcia-Moreno *et al.* (2003)	Fig a1 (all characters)		0.500
Mol 33	G 31 19	Garcia-Moreno *et al.* (2003)	Fig a2 (all protein genes)		0.500
Mol 34	G 69 02	Kimball *et al.* (2001)	Fig 2b1		1.000
Mol 35	A 10 04	McCracken & Sorenson (2005)	Fig 5 (upper)		0.500
Mol 35	A 10 05	McCracken & Sorenson (2005)	Fig 5 (lower)		0.500
Mol 36	G 28 04	Cracraft *et al.* (2004)	Fig 275		1.000
Mol 37	G 55 05	Birks & Edwards (2002)	Fig 7	2	0.500
Mol 38	G 59 05	Drovetski (2002)	Fig 5		1.000
Mol 39	G 26 01	van Tuinen & Hedges (2001)	Fig 3		1.000
Mol 42	A 17 01	Madsen *et al.* (1988)	Fig 2		0.250
Mol 42	G 19 03	Sibley & Ahlquist (1990)	Fig 328		0.250
Mol 42	G 19 05	Sibley & Ahlquist (1990)	Fig 354		0.250
Mol 42	G 19 06	Sibley & Ahlquist (1990)	Fig 357		0.250
Mol 43	G 18 02	Eguchi *et al.* (2000)	Fig 6b		0.500
Mol 43	G 50 01	Eguchi *et al.* (1995)	Fig 4a		0.500

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 44	G 18 01	Eguchi *et al.* (2000)	Fig 6a		0.500
Mol 44	G 50 02	Eguchi *et al.* (1995)	Fig 4b		0.500
Mol 45	G 18 03	Eguchi *et al.* (2000)	Fig 6c		0.500
Mol 45	G 50 03	Eguchi *et al.* (1995)	Fig 4c		0.500
Mol 47	G 13 01	Jolles *et al.* (1979)	Fig 3		0.500
Mol 47	G 14 08	Kornegay *et al.* (1993)	Fig 8		0.500
Mol 48	G 12 01	Henderson *et al.* (1981)	Fig 7		1.000
Mol 49	G 08 01	Gutierrez *et al.* (1983)	Fig 1		0.250
Mol 49	G 08 02	Gutierrez *et al.* (1983)	Fig 2		0.250
Mol 49	G 08 03	Gutierrez *et al.* (1983)	Fig 3 left		0.250
Mol 49	G 08 04	Gutierrez *et al.* (1983)	Fig 3 right		0.250
Mol 50	G 59 03	Drovetski (2002)	Fig 3	2	0.500
Mol 51	G 07 01	Smith *et al.* (2005)	Fig 1	4	0.125
Mol 51	G 07 02	Smith *et al.* (2005)	Fig 2	2	0.250
Mol 52	G 38 01	Hedges *et al.* (1995)	Fig 2a		1.000
Mol 53	G 59 02	Drovetski (2002)	Fig 2		1.000
Mol 54	A 12 03	Peters *et al.* (2005)	Fig 4a	2	0.125
Mol 54	A 12 04	Peters *et al.* (2005)	Fig 4b	2	0.125
Mol 55	A 04 01	John *et al.* (2005)	Fig 4		1.000
Mol 56	G 48 05	Nishibori *et al.* (2005)	Fig 3		1.000
Mol 57	G 31 02	Garcia-Moreno *et al.* (2003)	Fig 2c		0.200
Mol 57	G 31 08	Garcia-Moreno *et al.* (2003)	Fig a1 (Cmos)		0.200
Mol 57	G 31 12	Garcia-Moreno *et al.* (2003)	Fig a2 (Cmos)		0.200
Mol 57	G 31 17	Garcia-Moreno *et al.* (2003)	Fig a2 (all characters)		0.200
Mol 57	G 58 01	Butorina & Solovenchuk (2004)	Fig 2		0.200

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 59	G 28 07	Cracraft *et al.* (2004)	Fig 278		1.000
Mol 60	G 24 01	Fain & Houde (2004)	Fig 2		1.000
Mol 61	G 79 01	Backstrom *et al.* (2005)	Fig 1		1.000
Mol 62	G 17 03	Sorenson *et al.* (2003)	Fig 3		1.000
Mol 63	G 48 04	Nishibori *et al.* (2005)	Fig 2	2	0.500
Mol 64	G 01 01	Armstrong *et al.* (2001)	Fig left		0.333
Mol 64	G 69 06	Kimball *et al.* (2001)	Fig 2b5		0.333
Mol 64	G 89 14	Crowe *et al.* (2006)	Fig 9	2	0.167
Mol 65	G 41 01	Pimentel-Smith *et al.* (2001)	Fig 1		1.000
Mol 66	G 28 05	Cracraft *et al.* (2004)	Fig 277a		1.000
Mol 67	G 55 01	Birks & Edwards (2002)	Fig 5 (left)		0.500
Mol 67	G 55 03	Birks & Edwards (2002)	Fig 6 (left)		0.500
Mol 68	G 59 01	Drovetski (2002)	Fig 1		1.000
Mol 69	G 15 05	Prager & Wilson (1976)	Fig 3a		0.500
Mol 69	G 15 06	Prager & Wilson (1976)	Fig 3b		0.500
Mol 71	G 11 01	Kathleen *et al.* (1986)	Fig 3I		1.000
Mol 72	G 36 01	Helm-Bychowski & Wilson (1986)	Fig 3I		1.000
Mol 73	G 15 07	Prager & Wilson (1976)	Fig 4a		0.500
Mol 73	G 15 08	Prager & Wilson (1976)	Fig 4b		0.500
Mol 74	G 15 03	Prager & Wilson (1976)	Fig 2a		0.500
Mol 74	G 15 04	Prager & Wilson (1976)	Fig 2b		0.500
Mol 75	G 15 11	Prager & Wilson (1976)	Fig 7		1.000
Mol 76	G 75 05	Randi *et al.* (1991)	Fig 2a		0.250
Mol 76	G 75 06	Randi *et al.* (1991)	Fig 2b		0.250
Mol 76	G 75 07	Randi *et al.* (1991)	Fig 2c		0.250
Mol 76	G 75 08	Randi *et al.* (1991)	Fig 2d		0.250

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Mol 77	G 76 01	Randi *et al.* (1992)	Fig 2a		0.500
Mol 77	G 76 02	Randi *et al.* (1992)	Fig 2b		0.500
Mol 79	A 19 02	Patton & Avise (1986)	Fig 2		0.333
Mol 79	A 19 03	Patton & Avise (1986)	Fig 3		0.333
Mol 79	A 19 04	Patton & Avise (1986)	Fig 4		0.333
Mol 80	A 30 09	Livezey (1997)	Fig 7c		1.000
Mol 81	G 28 02	Cracraft *et al.* (2004)	Fig 273		1.000
Mol 82	A 01 10	Donne-Gousse *et al.* (2002)	Fig 6		1.000
Mol 83	G 70 03	Lucchini *et al.* (2001)	Fig 4		1.000
Morph	A 02 01	Ericson (1997)	Fig 33		0.017
Morph	A 02 02	Ericson (1997)	Fig 34		0.017
Morph	A 02 03	Ericson (1997)	Fig 35		0.017
Morph	A 02 04	Ericson (1997)	Fig 36		0.017
Morph	A 09 01	McCracken *et al.* (1999)	Fig 1a		0.017
Morph	A 09 02	McCracken *et al.* (1999)	Fig 1ba		0.017
Morph	A 09 03	McCracken *et al.* (1999)	Fig 1b2		0.017
Morph	A 09 08	McCracken *et al.* (1999)	Fig 4		0.017
Morph	A 09 11	McCracken *et al.* (1999)	Fig 6a		0.017
Morph	A 20 01	Livezey (1986a)	Fig 1		0.017
Morph	A 21 02	Livezey (1986b)	Fig 2		0.017
Morph	A 22 01	Livezey (1989)	Fig 1		0.017
Morph	A 23 01	Livezey (1991)	Fig 1	2	0.008
Morph	A 24 01	Livezey (1995a)	Fig 1a		0.017
Morph	A 24 02	Livezey (1995a)	Fig 1b		0.017
Morph	A 24 03	Livezey (1995a)	Fig 1c		0.017
Morph	A 24 04	Livezey (1995a)	Fig 2		0.017

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Morph	A 24 05	Livezey (1995a)	Fig 3		0.017
Morph	A 25 01	Livezey (1995b)	Fig 1		0.017
Morph	A 25 02	Livezey (1995b)	Fig 2		0.017
Morph	A 26 01	Livezey (1995c)	Fig 1		0.017
Morph	A 26 02	Livezey (1995c)	Fig 2		0.017
Morph	A 27 01	Livezey (1996a)	Fig 1		0.017
Morph	A 27 02	Livezey (1996a)	Fig 2		0.017
Morph	A 27 04	Livezey (1996c)	Fig 4		0.017
Morph	A 28 01	Livezey (1996c)	Fig 1		0.017
Morph	A 28 02	Livezey (1996c)	Fig 2		0.017
Morph	A 28 03	Livezey (1996c)	Fig 3		0.017
Morph	A 28 04	Livezey (1996c)	Fig 4		0.017
Morph	A 28 05	Livezey (1996c)	Fig 5		0.017
Morph	A 28 06	Livezey (1996c)	Fig 6		0.017
Morph	A 28 07	Livezey (1996c)	Fig 7		0.017
Morph	A 28 08	Livezey (1996c)	Fig 8		0.017
Morph	A 28 09	Livezey (1996c)	Fig 9		0.017
Morph	A 28 10	Livezey (1996c)	Fig 10		0.017
Morph	A 28 11	Livezey (1996)	Fig 11		0.017
Morph	A 29 01	Livezey (1996b)	Fig 1		0.017
Morph	A 29 02	Livezey (1996b)	Fig 2		0.017
Morph	A 29 03	Livezey (1996b)	Fig 3		0.017
Morph	A 30 01	Livezey (1997a)	Fig 1		0.017
Morph	A 30 02	Livezey (1997a)	Fig 2		0.017
Morph	A 30 03	Livezey (1997a)	Fig 3		0.017
Morph	A 30 04	Livezey (1997a)	Fig 4		0.017

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Morph	A 30 05	Livezey (1997a)	Fig 5		0.017
Morph	A 30 06	Livezey (1997b)	Fig 6		0.017
Morph	A 32 01	Livezey (1997b)	Fig 1		0.017
Morph	A 32 02	Livezey (1997b)	Fig 2		0.017
Morph	A 33 01	Livezey & Martin (1988)	Fig 10a		0.017
Morph	A 33 02	Livezey & Martin (1988)	Fig 10b		0.017
Morph	A 33 03	Livezey & Martin (1988)	Fig 10c		0.017
Morph	A 33 04	Livezey & Martin (1988)	Fig 10d		0.017
Morph	A 33 05	Livezey & Martin (1988)	Fig 10e		0.017
Morph	A 33 06	Livezey & Martin (1988)	Fig 10f		0.017
Morph	A 34 01	Bourdon (2005)	Fig 2		0.017
Morph	G 32 01	Livezey & Zusi (2001)	Fig 2b		0.017
Morph	G 32 04	Livezey & Zusi (2001)	Fig 3		0.017
Morph	G 34 01	Dyke (2003)	Fig 2		0.017
Morph	G 44 02	Gulas-Wroblewski & Wroblewski (2003)	Fig 4		0.017
Morph	G 56 02	Jones *et al.* (1995)	Fig 22		0.017
Morph	G 63 07	Bloomer & Crowe (1998)	Fig 6		0.017
Other 01	A 09 12	McCracken *et al.* (1999)	Fig 9a		0.250
Other 01	A 09 13	McCracken *et al.* (1999)	Fig 9b		0.250
Other 01	A 09 14	McCracken *et al.* (1999)	Fig 9c		0.250
Other 01	A 09 15	McCracken *et al.* (1999)	Fig 9d		0.250
Other 02	G 64 02	Crowe *et al.* (1992)	Fig 1b		0.333
Other 02	G 64 03	Crowe *et al.* (1992)	Fig 1c		0.333
Other 02	G 64 04	Crowe *et al.* (1992)	Fig 3a		0.333
Other 03	G 91 02	Crowe (1978)	Fig 47		0.500

Data set	Tree ID	Reference	Tree source	Number of permuations	Relative weight
Other 03	G 91 03	Crowe (1978)	Fig 53		0.500
Other 04	G 23 01	Johnsgard (1999)	Fig 1		0.500
Other 04	G 23 02	Johnsgard (1999)	Fig 2		0.500
Other 05	G 03 01	Dike *et al*. (2003)	Fig 2	2	0.250
Other 05	G 03 02	Dike *et al*. (2003)	Fig 3	2	0.250
Other 06	G 74 06	Randi *et al*. (2000)	Fig 6e		1.000
Other 07	G 72 02	Moulin *et al*. (2003)	Fig 3		1.000
Other 08	G 06 01	Shibusawa *et al*. (2004b)	Fig 6		1.000
Other 09	G 16 01	Stock & Bunch (1982)	Fig 10		1.000
Other 11	G 20 01	Johnsgard (1983)	Fig 1		1.000
Other 12	G 21 02	Johnsgard (1973)	Fig 1 (down)		1.000
Other 13	G 22 02	Johnsgard (1988)	Fig 3		1.000
Unsp 01	A 01 01	Donne-Gousse *et al*. (2002)	Fig 1a		1.000
Unsp 02	A 30 08	Livezey (1997)	Fig 7b		1.000
Unsp 03	G 09 05	Kimball *et al*. (1997)	Fig 3a		1.000
Unsp 07	G 28 08	Cracraft *et al*. (2004)	Fig 2710		1.000
Unsp 08	G 33 02	Zhan & Zhang (2005)	Fig 2b		1.000
Unsp 09	G 52 01	Pereira *et al*. (2002)	Fig 2a		1.000
Unsp 10	G 52 02	Pereira *et al*. (2002)	Fig 2b		1.000
Unsp 11	G 53 01	Grau *et al*. (2005)	Fig 1		1.000
Unsp 12	G 56 01	Jones *et al*. (1995)	Fig 21		1.000
Unsp 13	G 63 01	Bloomer & Crowe (1998)	Fig 1		1.000
Tax	Tax	Dickinson (2003)			0.001

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Supplementary Material II

rQS values for the strict consensus supertree, indicating nodal support (± SE) among the set of source trees together with the number of source trees supporting, conflicting or equivocal with a given node. Node numbers refer to Figs 2 and 3.

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
1	376	0.265 ± 0.023	102	0	283
2	214	0.252 ± 0.023	99	2	284
3	13	0.055 ± 0.012	22	1	362
4	12	0.000 ± 0.011	9	9	367
5	11	0.034 ± 0.014	21	8	356
6	4	0.039 ± 0.011	16	1	368
7	3	0.008 ± 0.005	3	0	382
8	2	0.008 ± 0.005	3	0	382
9	163	0.252 ± 0.024	104	7	274
10	6	0.026 ± 0.010	12	2	371
11	4	0.047 ± 0.012	20	2	363
12	3	0.018 ± 0.009	10	3	372
13	2	0.005 ± 0.004	2	0	383
14	2	0.005 ± 0.004	2	0	383
15	157	0.018 ± 0.011	12	5	368
16	155	-0.018 ± 0.007	0	7	378
17	154	-0.016 ± 0.006	0	6	379
18	152	-0.023 ± 0.024	40	49	296
19	139	0.005 ± 0.013	13	11	361
20	135	0.213 ± 0.027	103	21	261

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
21	90	-0.034 ± 0.017	15	28	342
22	86	0.000 ± 0.028	56	56	273
23	68	-0.094 ± 0.023	22	58	305
24	12	-0.003 ± 0.015	16	17	352
25	5	0.034 ± 0.014	21	8	356
26	3	0.094 ± 0.015	37	1	347
27	2	0.036 ± 0.010	14	0	371
28	2	0.047 ± 0.011	18	0	367
29	7	0.021 ± 0.007	8	0	377
30	3	0.013 ± 0.007	6	1	378
31	2	0.016 ± 0.007	7	1	377
32	4	0.008 ± 0.007	5	2	378
33	3	0.013 ± 0.007	6	1	378
34	2	0.005 ± 0.004	2	0	383
35	56	0.148 ± 0.025	80	23	282
36	22	-0.005 ± 0.020	28	30	327
37	20	0.003 ± 0.022	37	36	312
38	18	0.106 ± 0.019	50	9	326
39	17	0.008 ± 0.017	24	21	340
40	15	0.148 ± 0.020	63	6	316
41	6	-0.026 ± 0.019	22	32	331
42	2	0.021 ± 0.015	21	13	351
43	4	0.055 ± 0.015	28	7	350
44	2	0.052 ± 0.013	24	4	357
45	2	0.055 ± 0.014	25	4	356
46	9	-0.062 ± 0.020	17	41	327

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
47	6	0.034 ± 0.019	32	19	334
48	2	0.021 ± 0.007	8	0	377
49	4	0.039 ± 0.019	34	19	332
50	3	0.049 ± 0.014	25	6	354
51	2	-0.013 ± 0.015	13	18	354
52	3	0.029 ± 0.017	26	15	344
53	2	0.096 ± 0.015	37	0	348
54	2	0.075 ± 0.013	29	0	356
55	2	0.018 ± 0.008	8	1	376
56	2	0.031 ± 0.009	12	0	373
57	34	0.005 ± 0.018	24	22	339
58	25	0.008 ± 0.013	14	11	360
59	24	0.088 ± 0.015	36	2	347
60	22	0.016 ± 0.018	26	20	339
61	20	-0.023 ± 0.009	2	11	372
62	17	0.023 ± 0.017	26	17	342
63	12	0.016 ± 0.013	16	10	359
64	11	0.013 ± 0.006	5	0	380
65	10	0.005 ± 0.007	5	3	377
66	4	-0.003 ± 0.006	2	3	380
67	3	-0.003 ± 0.006	2	3	380
68	2	-0.003 ± 0.006	2	3	380
69	6	0.034 ± 0.009	13	0	372
70	3	0.008 ± 0.006	4	1	380
71	2	0.013 ± 0.007	6	1	378
72	3	0.005 ± 0.008	6	4	375

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
73	2	0.018 ± 0.007	7	0	378
74	5	0.023 ± 0.014	19	10	356
75	2	0.013 ± 0.006	5	0	380
76	3	0.034 ± 0.009	13	0	372
77	2	-0.016 ± 0.008	2	8	375
78	3	0.026 ± 0.008	10	0	375
79	2	0.026 ± 0.008	10	0	375
80	2	0.005 ± 0.004	2	0	383
81	2	-0.003 ± 0.007	3	4	378
82	9	-0.003 ± 0.015	16	17	352
83	3	0.010 ± 0.005	4	0	381
84	2	0.005 ± 0.005	3	1	381
85	6	0.021 ± 0.015	20	12	353
86	5	0.044 ± 0.010	17	0	368
87	4	0.018 ± 0.009	9	2	374
88	3	-0.010 ± 0.010	5	9	371
89	2	-0.003 ± 0.007	3	4	378
90	18	0.010 ± 0.016	20	16	349
91	5	0.075 ± 0.017	37	8	340
92	4	0.073 ± 0.013	28	0	357
93	3	0.029 ± 0.011	14	3	368
94	2	0.005 ± 0.013	13	11	361
95	13	-0.018 ± 0.009	2	9	374
96	12	0.003 ± 0.010	8	7	370
97	7	0.005 ± 0.005	3	1	381
98	6	0.018 ± 0.010	11	4	370

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
99	4	0.029 ± 0.010	13	2	370
100	3	0.013 ± 0.010	10	5	370
101	2	0.005 ± 0.005	3	1	381
102	2	-0.013 ± 0.009	3	8	374
103	5	-0.013 ± 0.010	5	10	370
104	4	0.005 ± 0.005	3	1	381
105	3	0.010 ± 0.005	4	0	381
106	2	0.010 ± 0.005	4	0	381
107	4	-0.013 ± 0.009	3	8	374
108	3	0.013 ± 0.006	5	0	380
109	45	0.044 ± 0.022	43	26	316
110	39	-0.018 ± 0.011	5	12	368
111	37	-0.008 ± 0.005	0	3	382
112	36	-0.031 ± 0.009	0	12	373
113	35	-0.005 ± 0.012	9	11	365
114	31	-0.008 ± 0.010	6	9	370
115	7	0.052 ± 0.011	20	0	365
116	2	-0.003 ± 0.011	8	9	368
117	5	0.057 ± 0.013	24	2	359
118	4	0.026 ± 0.012	15	5	365
119	3	0.047 ± 0.011	19	1	365
120	2	0.044 ± 0.010	17	0	368
121	24	0.023 ± 0.010	12	3	370
122	23	0.013 ± 0.009	8	3	374
123	16	0.013 ± 0.009	8	3	374
124	12	0.003 ± 0.010	8	7	370

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
125	8	-0.003 ± 0.010	7	8	370
126	7	0.005 ± 0.010	9	7	369
127	6	0.005 ± 0.005	3	1	381
128	5	-0.008 ± 0.009	4	7	374
129	4	0.016 ± 0.007	7	1	377
130	2	0.018 ± 0.010	11	4	370
131	4	0.000 ± 0.005	2	2	381
132	3	0.010 ± 0.005	4	0	381
133	7	0.010 ± 0.005	4	0	381
134	6	0.000 ± 0.005	2	2	381
135	5	0.000 ± 0.005	2	2	381
136	3	0.005 ± 0.005	3	1	381
137	2	0.010 ± 0.005	4	0	381
138	4	0.005 ± 0.004	2	0	383
139	3	0.005 ± 0.004	2	0	383
140	2	0.005 ± 0.004	2	0	383
141	2	0.005 ± 0.004	2	0	383
142	6	0.099 ± 0.017	43	5	337
143	4	0.042 ± 0.010	16	0	369
144	3	0.005 ± 0.009	7	5	373
145	2	-0.003 ± 0.005	1	2	382
146	13	0.021 ± 0.007	8	0	377
147	12	0.065 ± 0.015	29	4	352
148	7	0.026 ± 0.015	21	11	353
149	6	0.068 ± 0.015	31	5	349
150	4	0.018 ± 0.007	7	0	378

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
151	2	0.031 ± 0.009	12	0	373
152	2	0.026 ± 0.008	10	0	375
153	5	0.005 ± 0.004	2	0	383
154	4	0.016 ± 0.006	6	0	379
155	3	0.005 ± 0.004	2	0	383
156	2	0.005 ± 0.004	2	0	383
157	2	0.005 ± 0.004	2	0	383
158	2	-0.003 ± 0.005	1	2	382
159	17	0.099 ± 0.015	38	0	347
160	5	0.021 ± 0.009	10	2	373
161	3	0.026 ± 0.012	16	6	363
162	2	0.021 ± 0.008	9	1	375
163	2	0.003 ± 0.003	1	0	384
164	11	0.023 ± 0.013	18	9	358
165	10	0.036 ± 0.010	14	0	371
166	9	0.026 ± 0.008	10	0	375
167	2	0.018 ± 0.007	7	0	378
168	7	0.026 ± 0.008	10	0	375
169	5	0.016 ± 0.008	8	2	375
170	3	0.018 ± 0.007	7	0	378
171	2	0.008 ± 0.007	5	2	378
172	2	0.021 ± 0.008	9	1	375
173	2	0.026 ± 0.008	10	0	375
174	14	0.068 ± 0.013	26	0	359
175	13	-0.003 ± 0.012	10	11	364
176	12	-0.003 ± 0.012	11	12	362

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
177	7	0.013 ± 0.006	5	0	380
178	6	0.003 ± 0.006	3	2	380
179	2	0.008 ± 0.006	4	1	380
180	4	0.013 ± 0.006	5	0	380
181	3	0.008 ± 0.006	4	1	380
182	2	0.013 ± 0.006	5	0	380
183	5	0.021 ± 0.010	12	4	369
184	2	0.000 ± 0.007	4	4	377
185	3	0.016 ± 0.007	7	1	377
186	2	0.000 ± 0.007	4	4	377
187	162	0.135 ± 0.017	52	0	333
188	158	0.044 ± 0.010	17	0	368
189	156	0.044 ± 0.011	18	1	366
190	155	0.010 ± 0.006	5	1	379
191	153	0.049 ± 0.012	20	1	364
192	151	0.177 ± 0.022	77	9	299
193	111	0.039 ± 0.017	30	15	340
194	94	0.062 ± 0.021	44	20	321
195	4	-0.029 ± 0.012	6	17	362
196	3	0.042 ± 0.011	18	2	365
197	2	0.008 ± 0.005	3	0	382
198	3	0.008 ± 0.011	10	7	368
199	2	0.023 ± 0.009	11	2	372
200	41	0.062 ± 0.015	30	6	349
201	35	-0.026 ± 0.010	2	12	371
202	34	0.010 ± 0.016	20	16	349

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
203	29	-0.026 ± 0.010	2	12	371
204	26	0.029 ± 0.010	13	2	370
205	23	0.042 ± 0.016	28	12	345
206	6	0.023 ± 0.009	11	2	372
207	5	0.023 ± 0.009	11	2	372
208	4	0.039 ± 0.011	17	2	366
209	3	0.034 ± 0.009	13	0	372
210	2	0.008 ± 0.005	3	0	382
211	17	0.016 ± 0.011	12	6	367
212	4	0.036 ± 0.011	16	2	367
213	13	0.008 ± 0.015	17	14	354
214	2	0.013 ± 0.009	9	4	372
215	11	0.036 ± 0.010	14	0	371
216	10	0.036 ± 0.010	14	0	371
217	9	0.026 ± 0.010	12	2	371
218	8	0.029 ± 0.010	13	2	370
219	5	0.008 ± 0.009	8	5	372
220	3	0.000 ± 0.011	9	9	367
221	2	0.005 ± 0.010	9	7	369
222	2	0.008 ± 0.005	3	0	382
223	3	0.008 ± 0.009	8	5	372
224	2	-0.003 ± 0.009	6	7	372
225	3	0.039 ± 0.010	15	0	370
226	3	0.003 ± 0.009	7	6	372
227	2	0.013 ± 0.009	9	4	372
228	5	0.078 ± 0.014	30	0	355

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
229	3	0.049 ± 0.011	19	0	366
230	2	0.034 ± 0.011	16	3	366
231	2	0.039 ± 0.011	17	2	366
232	6	0.057 ± 0.012	22	0	363
233	4	0.023 ± 0.009	11	2	372
234	3	0.023 ± 0.009	11	2	372
235	2	0.034 ± 0.009	13	0	372
236	2	0.036 ± 0.010	15	1	369
237	2	0.010 ± 0.005	4	0	381
238	4	0.010 ± 0.005	4	0	381
239	2	0.010 ± 0.005	4	0	381
240	8	0.016 ± 0.009	9	3	373
241	2	0.005 ± 0.007	5	3	377
242	6	0.018 ± 0.009	9	2	374
243	5	0.010 ± 0.005	4	0	381
244	4	0.010 ± 0.005	4	0	381
245	3	0.010 ± 0.005	4	0	381
246	2	0.010 ± 0.005	4	0	381
247	2	0.008 ± 0.005	3	0	382
248	2	0.008 ± 0.009	7	4	374
249	8	0.005 ± 0.011	10	8	367
250	5	-0.003 ± 0.007	3	4	378
251	4	-0.003 ± 0.007	3	4	378
252	3	0.008 ± 0.005	3	0	382
253	2	0.008 ± 0.005	3	0	382
254	2	0.008 ± 0.005	3	0	382

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
255	2	-0.013 ± 0.007	1	6	378
256	2	0.010 ± 0.005	4	0	381
257	14	0.057 ± 0.015	28	6	351
258	8	0.042 ± 0.011	17	1	367
259	7	0.042 ± 0.013	21	5	359
260	6	0.047 ± 0.011	18	0	367
261	5	0.008 ± 0.005	3	0	382
262	4	0.008 ± 0.005	3	0	382
263	2	0.008 ± 0.005	3	0	382
264	6	0.003 ± 0.006	3	2	380
265	5	0.016 ± 0.006	6	0	379
266	2	0.008 ± 0.005	3	0	382
267	3	0.008 ± 0.005	3	0	382
268	2	0.008 ± 0.005	3	0	382
269	23	0.042 ± 0.014	22	6	357
270	15	0.042 ± 0.013	20	4	361
271	10	0.023 ± 0.010	12	3	370
272	8	0.013 ± 0.010	10	5	370
273	6	0.005 ± 0.009	7	5	373
274	4	0.016 ± 0.009	9	3	373
275	3	0.003 ± 0.007	4	3	378
276	2	0.013 ± 0.007	6	1	378
277	2	-0.005 ± 0.005	1	3	381
278	2	-0.003 ± 0.007	3	4	378
279	2	-0.008 ± 0.007	2	5	378
280	5	0.023 ± 0.008	9	0	376

Node number	Clade size	rQS ± SE	Number of matches	Number of mismatches	Number of equivocal matches
281	2	-0.003 ± 0.008	4	5	376
282	3	0.008 ± 0.008	6	3	376
283	2	0.010 ± 0.006	5	1	379
284	8	-0.003 ± 0.012	11	12	362
285	2	0.003 ± 0.011	9	8	368
286	6	0.010 ± 0.005	4	0	381
287	2	0.010 ± 0.005	4	0	381
288	4	0.021 ± 0.007	8	0	377
289	3	0.010 ± 0.005	4	0	381
290	2	0.010 ± 0.005	4	0	381
291	14	-0.018 ± 0.011	6	13	366
292	12	-0.003 ± 0.007	3	4	378
293	11	0.013 ± 0.010	10	5	370
294	10	0.005 ± 0.011	10	8	367
295	9	0.003 ± 0.012	12	11	362
296	2	0.016 ± 0.006	6	0	379
297	6	0.055 ± 0.012	21	0	364
298	2	0.031 ± 0.009	12	0	373
299	2	0.013 ± 0.008	7	2	376
300	2	0.016 ± 0.006	6	0	379
301	2	0.031 ± 0.009	12	0	373
302	4	0.049 ± 0.018	33	14	338
303	3	0.091 ± 0.015	36	1	348
304	2	0.005 ± 0.004	2	0	383