

eKINDS Project Paper

Strategies for More Clearly Delineating, Characterizing, and Inferring the Natural History of Baramins III:

Evaluating Relationships and Proposing Post-Flood Dispersal, with Application to the Order Galliformes (Class: Aves)

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Abstract

In part I of this series, we laid out and applied a simple heuristic to the study of landfowl (traditional order Galliformes). We established that all families in this order share continuity consistent with them being identified as a created kind (baramin). In part II we took a closer look at the diversity and specializations that appear in various species of landfowl. Here, we continue our examination of the data, traditional characters as well as genome sequences, to understand relationships within the group, and propose likely routes of dispersal after the original ancestors of this baramin left the Ark.

All of the currently accepted genera and more than 85% of the world's landfowl have had their genomes examined in part or in whole, making this taxa ripe for baraminological study. Our analysis has upheld much of the traditional classification but has given insight especially into the large family Phasianidae, including both the pheasants and the Old World quail and partridges. Of the 12 identified landfowl groups, eight are within the family Phasianidae. All of the genera of this family can be assigned to a group either unequivocally, or with a high degree of probability. We explore the novel suggestion of the African Rock Partridge (*Ptilopachus*) as a possible link to the New World quail, and uphold this conclusion. Further findings are discussed under each of the constituent groups.

Finally, we show that dispersal of landfowl from the mountains of Ararat fits well with available data, with several lineages invading the New World, probably by more than one route.

Key Words: Landfowl, Galliformes, post-Flood dispersal, baramin, baraminology, natural history, Megapodiidae, megapodes, Cracidae, cracids, quail, Numididae, guineafowl, Phasianidae, pheasants, grouse, turkey, partridges, junglefowl

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Introduction

Landfowl are familiar to everyone. The domestic chicken (*Gallus gallus*) is the most abundant bird on Earth and is the most intensively studied. The landfowl which have commercial value—such as quail, grouse, and guineafowl—and those of avicultural interest—such as the brightly colored pheasants—are also well-known. The number of molecular studies devoted to landfowl is extensive and has been challenging to synthesize. Unfortunately, there are some species that are almost unknown to scientists because they occupy limited ranges in parts of the world where study is difficult. Many of the partridges are not spectacular in their plumage and have received limited attention. Nevertheless, there is abundant information, making this order attractive for detailed baraminological investigation.

The landmark baraminological study on landfowl is that of McConnachie (2007) and McConnachie and Brophy (2007, 2008). It is the most thorough prior study of any bird group, and synthesized data from morphology, the Biblical record, and hybridization. Their morphological analysis utilized data from Dyke et al. (2003). These data had been “pre-selected” for use in parsimony analyses and hence emphasized characters that were apomorphic within the landfowl. As a result, many characters used by Holman (1961, 1964) were omitted because they were considered to be plesiomorphic. In the end, the Dyke et al. cladistic analysis yielded a single character (the tomial notch) uniting the New World quail and only two (the breeding habits and large feet) attesting to the monophyly of the megapodes.

Given the bias of the Dyke dataset, it is not surprising that the study by McConnachie (2007) yielded four groups based on morphological characters. Hybrid data unites three of these four groups, leaving the megapodes as the only one of the five landfowl families where continuity could not be demonstrated with the core group. Thus, McConnachie and Brophy (2008) conservatively suggested the order Galliformes is comprised of two baramins, with the megapodes being separate from the rest.

However, that the landfowl represent a single monophyletic assemblage has never been seriously contested. The history of the classification of landfowl has been given in detail by Sibley and Ahlquist (1972, 1990). In part I of this series (Ahlquist and Lightner, 2019) we built on the pioneering work of McConnachie and Brophy (2007, 2008), though we assert that all Galliformes comprise a single baramin. We add a more thoroughly documented hybrid between cracids and a chicken, as well as append a list of numerous morphological characters that unite all landfowl. In part II (Ahlquist and Lightner, 2020) we examined diversity within landfowl; numerous families contain members with some impressive adaptations, while clearly retaining their identity as landfowl.

Establishing baraminic status and evaluating diversity within a group provide a basis for understanding relation-

ships within a baramin. Through the synthesis of available data, including morphological, physiological, behavioral, and genetic data, it is evident the landfowl have diversified into 12 identifiable groups (Figure 1). Four of these groups correspond to families: Megapodiidae (megapodes), Cracidae, Numididae (guineafowl), and Odontophoridae (New World quail). The remaining 8 groups are within the large, diverse family Phasianidae (pheasants and allies).

Megapodiidae (Megapodes)

Despite the unique breeding system, no one has denied the affinities of megapodes to landfowl. Although hybridization occurs among some megapode genera (McCarthy 2006, pp. 39–40), no hybrids are known between them and other landfowl. This is not surprising given the genetic distance between them and other families of landfowl, as well as the limited opportunities for potential hybridization to occur. All studies, whether morphological or molecular attest to a sister-group relationship of megapodes to other landfowl.

A study of relationships within Megapodiidae has produced conflicting opinions.

For the megapodes we consider five principal studies: Clark (1964), traditional characters; Dekker and Brom (1992), traditional characters; Mey (1999), parasites hosted by the birds; Birks and Edwards (2002), mitochondrial and nuclear DNA sequences; Harris et al. (2014), emphasis on biogeography and nesting habits.

In a broad sense these studies show similar relationships. A brush-turkey group consisting of the genera *Alectura*, *Leipoa*, *Aepyodius*, and *Talegalla* is sister to a second containing *Megapodius* and *Eulipoa*. The Maleo (*Macrocephalon*) clusters with each group twice.

The principal of using bird parasites as indices to relationships (Mey, 1999) is not new but requires explanation to the non-specialist. The underlying idea is simple: birds harboring similar parasites are likely to be closely related. In a secular sense one thinks of the parasites co-evolving with their hosts. The problems are twofold. One needs to determine accurately the relationships of the parasites; not always an easy task. The problem of secondary infestation (or accidental transfer) cannot always be accounted for. Nonetheless, some interesting systematic proposals have come out from this work.

One of the pioneering studies on feather lice is that of Rothschild and Clay (1952), which is a delightful read in spite of its age. Dame Miriam Rothschild was part of the Rothschild banking family and possessed the intelligence, motivation, and financial resources to devote her long and productive life to a study of bird parasites. She was the niece of the famous (and infamous) Lord Walter Rothschild who used his family fortune to amass a huge collection of birds at Tring, England.

This private collection, eventually dispersed to both the British Museum (Natural History Museum in London) and American Museum of Natural History, was one of the most important in the world.

Perhaps the best solution is to recognize *two* clades of megapodes, thus agreeing with Dekker and Brom (1992) and Harris et al. (2014), and differing from the parasite evidence of Mey (1999) and the molecular data of Birks and Edwards (2002), only in the placement of *Macrocephalon*. This produces a clear split between the two groups on the basis of incubation strategy and facilitates the interpretation of other features on an ancestral-descendant framework.

The first group (A) consists of *Alectura*, *Aepyodius*, *Leipoa*, and *Talegalla*. The second group (B) contains *Macrocephalon*, *Eulipoa*, and *Megapodius*. *Eulipoa* and *Megapodius* are clearly related to each other. Some authorities lump them into *Megapodius*. Those who do not (e.g., Jones et al., 1995) emphasize

three or four distinctive features of *Eulipoa*. (1) The strongly barred pattern of the upper parts, consisting of maroon and pale blue-grey bands, and seen also in the chicks. (2) The tarsus, toes, and claws are relatively, and absolutely, longer than in *Megapodius*. (3) The tail is relatively longer than in *Megapodius* with the central shafts of the feathers elongated, a feature unique among megapodes. (4) The birds fly at night to the islands at which they construct their burrows nocturnally.

In its simplest expression, wing loading is defined as the mass of the bird divided by the area of the wings. The lighter wing loading of members of Group B *Megapodius-Eulipoa* is obvious. The unknown is *Macrocephalon*.

A scan of the weights and wing lengths among *Macrocephalon* and the similar sized *Talegalla* and *Aepyodius* as given by Jones et al. (1995) shows no obvious differences, but this may not be a valid comparison. We may conjecture that since the Maleo had colonized Sulawesi, presumably from New Guinea, it may be a better flyer or at least possess the propensity to displace over water compared to the obligate mound builders.

Dekker and Brom (1992, p. 30) argue,

The maleo of Sulawesi, on the other hand, does use Sulawesi's beaches to incubate the eggs. In contrast to the megapodes of New Guinea, the forest-dwelling maleo is not a mound-builder but a burrow-nester which lays its eggs in volcanically heated soils. This may suggest that burrow-nesting at beaches can only be applied by species which are (or formerly were) burrow-nesters at volcanic soils. Burrow-nesting at beaches therefore seems to be derived from burrow-nesting at volcanic soils and not directly from mound-building.

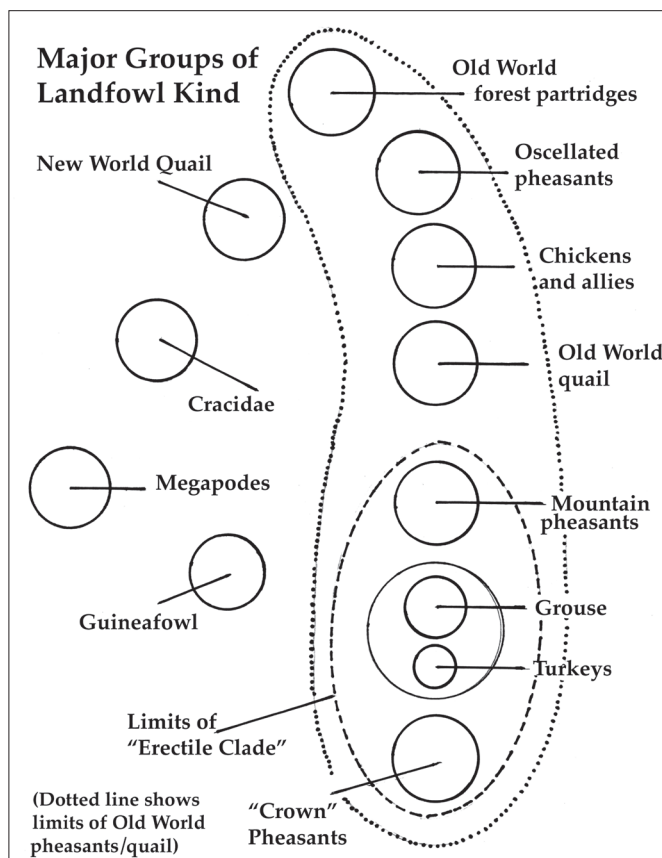


Figure 1. A simplified diagram depicting relationships within landfowl (Galliformes). Four families form smaller groups: New World quail (Odontophoridae); Cracidae; Megapodes, (Megapodiidae); and guineafowl (Numididae). The Old World pheasants and quail (Phasianidae) comprise a very large group, with numerous groups within it. Drawn by JA.

Cracidae (Chachalacas, Curassows, Guans)

Readers familiar with the Sibley-Ahlquist-Monroe (1988) classification of birds based largely on DNA evidence will note that the writers placed the Cracidae and Megapodiidae together in a separate suborder, the Craciformes. Here, we reach conclusions different from that of Sibley-Ahlquist-Monroe (1988) and in accord with those of Lightner (2013). Since Ahlquist was co-author of the 1988 classification, some comment is in order.

In Sibley and Ahlquist (1990) we entertained a relationship between cracids and megapodes despite the lack of unambiguous evidence. It was our conviction and intention, if not explicitly stated, to maintain some nodes in the hopes of stimulating further research. If we collapsed the node, it was an admission that we knew nothing or that we had no opinion regarding our own data or the data from other aspects of avian biology. Such was disingenuous.

The temporal framework of the Sibley and Ahlquist (1990) work was the secular geological time scale, including the ideas of continental drift and vicariance biogeography. As such, a putative relationship between cracids and megapodes was ten-

able via an ancient Gondwanaland (i.e., Australian-Antarctic-South American) connection. In a Genesis Flood scenario this is precluded.

More recent molecular evidence in favor of a cracid-megapode relationship has not been forthcoming (Crowe et al., 2006a, b; Cox et al., 2007; Kriegs et al., 2007; Wang et al., 2013; Kimball and Braun, 2014; Meiklejohn et al., 2014; Shen et al., 2014; Hosner et al., 2016; *inter alia*).

Given 25 years' hindsight, the number of comparisons ($n = 11$) reported for a cracid-megapode by Sibley and Ahlquist (1990) is too small to withstand statistical scrutiny. Inexplicably, they did not include melting curve data from a labeled megapode, although those values were used in their calculations. Thus, the elimination of Supraorder Craciformes is justified. A more plausible dispersal and invasion hypothesis is presented below under the heading Biogeography.

The fascinating and complex story of natural hybrids between cracids and other landfowl is told in Part I of this series. To summarize briefly, there existed a few reports in the literature which were not trustworthy. Anecdotal evidence of such hybrids abounded, though the genetic distance between cracids and the main landfowl families is relatively large. Many ornithologists were informed by villagers that chicken X cracid hybrids were frequent, yet specimens were not forthcoming. It was not until we discovered the work of Jose Ricardo Gunski (2001) who had produced and published work on such hybrids and backcrosses that the vexing question of cracid X phasianid hybrids had a definitive answer.

The question of relationships among the genera and species has received much discussion. Following are the genera of Cracidae recognized by Gill and Donsker (2016) with the number of species in parentheses; presumably their list implies a phylogenetic sequence: *Ortalis* (16), *Penelope* (15), *Pipile* (4), *Aburria* (1), *Chamaepetes* (2), *Penelopina* (1), *Oreophasis* (1), *Nothocrax* (1), *Mitu* (4), *Pauxi* (3), *Crax* (7). We use these names to unify our discussion.

The traditional groups are (a) the chachalacas (*Ortalis*), (b) the guans (*Penelope*, *Pipile*, *Aburria*, *Chamaepetes*, and *Penelopina*), and (c) the curassows (*Mitu*, *Pauxi*, and *Crax*). The basis for them are relative size, coloration, crest development, and bill shape. The relationships of the Horned Guan (*Oreophasis derbianus*) and the Nocturnal Curassow (*Nothocrax urumutum*) are debated. Principal papers are summarized below.

Vuilleumier (1965), Vaurie (1964, 1965a,b,c, 1966a,b, 1967a,b,c,d, 1968), and Delacour and Amadon (1973) have provided detailed accounts of relationships among the Cracidae based mainly on traditional characters. Their conclusions, however, are not easily entered into cladograms without doing the authors injustice. The papers are "must read" for the student of cracid relationships, so we cite them for their historical value.

There is general acceptance that the Cracidae consist of two groups: the smaller chachalacas and guans (*Ortalis*, *Penelope*, *Pipile*, *Aburria*, *Chamaepetes*, and *Penelopina*) and the larger curassows (*Nothocrax*, *Mitu*, *Pauxi*, and *Crax*). The problem species has been, and continues to be the Horned Guan (*Oreophasis derbianus*).

Of the two molecular data sets, one study (Pereira et al., 2002) places *Oreophasis* with a combined chachalaca-curassow group and the other (Frank-Hoeflich et al., 2007) places *Oreophasis* with the curassows and recognizes a second clade with the chachalacas and guans. Another paper (Pereira and Baker, 2004) has examined the relationships among the curassows using mitochondrial DNA (mtDNA). A discussion of this last paper is outside the scope of this review; however, the scenario of speciation within the 14 large curassows would be a fertile study for the baraminologist armed with different analytical techniques and the perspective of a single 'ice age' following the worldwide Flood.

The study by Frank-Hoeflich et al. (2007) is notable in that it utilized three sets of data, osteological, integumentary, plus behavioral, and molecular. These data are presented separately as well as in combined form. A suite of 74 morphological and behavioral characters placed *Oreophasis* at the base of a clade of chachalacas and guans. The mtDNA tree (661 base pairs from cytochrome *b* gene) recovers a clade consisting of *Ortalis* (chachalacas) plus the large curassows with *Oreophasis* as its sister. A combined tree of 661 molecular characters, 151 osteological characters, and 74 behavioral and morphological characters moves *Ortalis* to the clade with the guans and has *Oreophasis* as the basal lineage of the curassows.

Hosner et al. (2016) provided a more complete and better resolved picture of cracid relationships. They sampled 36 species of Cracidae plus nine from previous studies, giving a total of 47 of 55 currently recognized species or 85% coverage. Their data set included mtDNA, nuclear introns, and ultra-conserved sequences (UCEs) and strongly supported four groups: the curassows (*Crax*, *Mitu*, and *Pauxi*), the chachalacas (*Ortalis*), Horned Guan (*Oreophasis*), and the remaining guans (*Aburria*, *Chamaepetes*, *Penelope*, *Penelopina*, and *Pipile*).

Of these four groups two major clades are inferred. One (at left) includes the curassows, chachalacas, and Horned Guan; the second (at right) includes the remaining genera of guans, as follows:

<i>Oreophasis</i>	<i>Penelopina</i>
<i>Ortalis</i>	<i>Chamaepetes</i>
<i>Nothocrax</i>	<i>Penelope</i> , <i>Pipile</i> + <i>Aburria</i>
<i>Crax</i> , <i>Mitu</i> + <i>Pauxi</i>	

In our notation *Mitu*+*Pauxi* indicates that the species of each genus were interposed among one another. The difficulty of resolving the species of *Mitu* and *Pauxi*, in our opinion, is likely not a "failure" of the molecular data but most likely

represents the artificial constructs of each genus. Other studies, morphological as well as molecular, report conflicts in this area. Taxon sampling was not a problem as all four species of *Mitu* were represented and two of three species of *Pauxi*. The third species of *Pauxi*, the Sira Curassow (*P. koepckeae*), was described as a subspecies of *Pauxi unicornis* by Weske and Terborgh (1971) and is known from only a few specimens from a limited range in central Peru. A re-evaluation of the characters of the genera and their constituent species in light of the molecular data is needed.

The same is true of *Pipile*+*Aburria*. In this case the nuclear intron and UCE data separated *Aburria* from *Pipile*, whereas the mtDNA data did not. The authors commented that relationships among species of *Ortalis* and *Penelope* were only moderately resolved indicting the rapid and recent radiation of the two genera.

Overall, the authors favored a hypothesis of a North and Central American origin and radiation of Cracidae followed by a diversification in South America after the closure of the Panamanian water gap.

Numididae (Guineafowl)

The major study of the morphology of guineafowl is that of Crowe (1978) in which he clarified the multiple subspecies of the Helmeted Guineafowl (*Numida meleagris*) and provided a cladistic analysis of all the species. Crowe favored an Asian origin of this African endemic family.

Above the family level the relationships of the guineafowl are unambiguous. All molecular studies recover them as a sister-group to the Phasianidae plus Odontophoridae:

Megapodiidae
Cracidae
Numididae
Phasianidae, Odontophoridae

Asampling of the range of papers substantiating this include Crowe et al. (2006a); Crowe et al. (2006b); Kriegs et al. (2007); Kimball et al. (2011); Wang et al. (2013); Meiklejohn et al. (2014); and Hosner et al. (2016).

Of significance is the existence of reputable hybrids between *Numida* and *Gallus* (mainly), *Pavo*, and *Phasianus*; McCarthy (2006, pp. 51–53) devotes considerable space to the topic. Sibley and Ahlquist (1990) estimated at least a 10% difference across the genome between *Numida* and phasianids, making such a cross the most distant among birds. The guineafowl are more distant from phasianids than are the New World quail for which no reliable hybrids with phasianids exist.

It would be enlightening if a living *Numida* X phasianid hybrid could be genomically sampled. Given existing technology, and the existence of the complete genome of *Gallus*, such a hybrid could yield potentially valuable information

on the genetic architecture that led to such an improbable occurrence.

It is highly probable that guineafowl colonized Africa from Asia and diverged there. It is likely that the guineafowl were adapted to an open-country ecology; if so, then the presence of the two species of *Agelastes* in the rain forests of central and west Africa are a secondary specialization. This would explain the smaller size (crypsis) and loss of the spotting characteristic of *Numida*, *Guttera*, and *Acryllium* as being of little value in the low light of dense forests.

Phasianidae (Pheasants and Allies)

Grouse and turkeys

One can paraphrase a century of discourse on the relationships of these groups in a sentence. They are both unquestionably members of a large “phasianoid complex” but most discussion centers on whether they should be treated as families or subfamilies within this group. Taxonomic rank tells little about relationships. Hard data have not been forthcoming until recently.

Grouse are considered to be pheasants specialized for a boreal existence (Potapov and Sale, 2013). A number of pheasant genera live in mountainous regions of China, so it is easy to suggest an Old World origin for grouse. We may mention the eared-pheasants (*Crossoptilon*), monals (*Lophophorus*), and Koklass Pheasant (*Pucrasia*) that regularly breed at elevations of 3000–4000 meters or higher in eastern China. The snowcocks (*Tetraogallus*) are also high-altitude landfowl, living above the timber-line, but they are rightly viewed as offshoots of partridges (compare plumages to *Alectoris* and *Ammoperdix*), and their ecology is that of a partridge (open-country, seed-eaters).

Grouse, however, have a greater radiation in the New World. Only three genera (*Tetrastes*, *Tetrao*, and *Lyrurus*, each with two species) are exclusively Palearctic. Depending on one’s classification, *Falci pennis* has an Old and New World representative, and the ptarmigan (*Lagopus*) are Holarctic in distribution with one species, the White-tailed Ptarmigan (*Lagopus leucura*) being endemic to the New World. This leaves *Bonasa*, *Centrocerus*, *Dendragapus*, and *Tympanuchus* in the New World with eight species.

Grouse breed farther north than any birds, up to 83°30′N latitude in Greenland. Grouse in both hemispheres hardly penetrate below latitude 28° N, with the prairie chickens (*Tympanuchus*) ranging south to Texas, and the Ruffed Grouse (*Bonasa umbellus*) extending to the south Appalachians. In the Old World, the Chinese Grouse (*Tetrastes sewerzowi*) occurs where it can find favorable conditions in mixed boreal forests above 4,000 meters near the Sino-Tibetan border. Potapov and Sale (2013) rightly conclude that the ecological adaptations of

grouse restrict them to habitats that include significant periods of winter temperatures below freezing.

The large size and accompanying morphological peculiarities of turkeys have not yielded many clues to their relationships. Sibley and Ahlquist (1990; see Fig. 357, p. 842) provided an answer in placing both grouse and turkeys in the same clade but, inexplicably, never discussed their finding nor attempted any follow-up to it. That did not preclude other investigators from observing this finding and adding data in support of it.

Virtually every study has concurred in a sister-group relationship of grouse and turkeys. Supporting studies include the following papers, but are not limited solely to them: Kaiser et al. (2007) noted a sister-group relationship between grouse and turkeys on the basis of insertion pattern of CR1 retrotransposons, a conclusion which was supported by a similar study by Kriegs et al. (2007). Complete mitochondrial genomes (Shen et al., 2010) support the relationship, as do over 15,000 sites, primarily from nuclear introns but also including three mitochondrial regions (Pereira and Baker, 2004; Kimball and Braun, 2008; 2014; Kimball et al., 2011).

Moreover, these investigators have found that the turkey-grouse group is nested among other groups in the larger pheasant-partridge assemblage, and this has had implications in rending asunder the traditional Phasianinae and Perdiciinae, as we shall see below.

The first molecular study to examine relationships among grouse was that of Ellsworth et al. (1995) who compared restriction fragment polymorphisms of mtDNA. They concluded that the prairie chickens (*Tympanuchus*) were the first to differentiate with *Bonasa* and *Dendragapus* being most derived. This agreed with a study by Short (1967) in placing the prairie chickens first and suggesting that the earliest grouse were grassland dwellers. Short's analysis was based on characters of egg color, natal plumages, number of tail feathers, feather color patterns, and others. Allowing for his merged genera, Short's "tree" reduces to:

Tympanuchus
 Bonasa
 Centrocercus
 Dendragapus
 Lagopus, Tetrao

Subsequent studies based on DNA sequences are in contradiction. Although details differ among them, a consistent pattern emerges in placing *Bonasa* and *Tetrastes* sister to the remaining grouse and *Tympanuchus* as most derived. Gutierrez et al. (2000); Crowe et al. (2006ab); Wang et al. (2013); Hosner et al. (2016); *inter alia* have variations on this perspective. Parsons et al. (2016) provided well-resolved relationships among all 19 species of grouse using mtDNA, nuclear intron, and nuclear UCE sequences.

We agree with Parsons et al. (2016, p. 130) that the "ancestor of the turkeys and grouse dispersed to the New World prior to diversification." If they have assessed the relationships correctly, then there would be a recolonization to the Old World with the hazel grouse (*Tetrastes bonasia* and *T. swerzowi*), two species of ptarmigan (*Lagopus lagopus* and *L. muta*), and the capercaillies (*Tetrao*) and black grouse (*Lyrurus*), with one recolonization from Old to New World in *Falci pennis canadensis*. Since their data do not indicate strict monophyly of *F. canadensis*, it may be necessary to reconsider the generic allocation of *F. canadensis*, which formerly was placed in a monotypic genus *Canachites*.

Finally, it is worthwhile pointing out that the display postures of grouse and turkeys are quite similar. The lekking behavior, fanned tail, drawn-in neck, and drooped wings all are suggestive, but given the variety of postures in typical pheasants can hardly be considered conclusive.

"Typical" pheasants (Phasianinae)

When we turn to the remainder of the phasianoid complex, we are met with a group of diverse taxa and a number of taxonomic studies, most of them molecular in nature. It is indeed gratifying that so many of them have been produced in the three decades since the Sibley and Ahlquist (1990) work concluded. Especially satisfying are the efforts to examine a wide range of species and to include in the authorship one or more ornithologists who have lent their expertise in the areas of morphology, ecology, and biogeography in analyzing and interpreting the significance of the data. We have reached a point where an integration of the molecular data with that of "natural history" is to be lauded.

These studies differ among one another in the nature of the sequence data collected, the number of species examined, and the methods of data analysis. To simplify discussion we concentrate on the most important general studies of landfowl (Pereira and Baker, 2004; Crowe et al., 2006 a,b; Kaiser et al., 2007; Krieg et al., 2007; Kimball and Braun, 2008, 2014; Kan et al., 2010; Shen et al., 2010, 2014; Wang et al., 2013; Meiklejohn et al., 2014; Hosner et al., 2016). This eliminates repetition of the citations of individual studies and provides a broad picture, namely, the eight Phasianidae groups that emerge from a synthesis of all the data. We have cited smaller studies and portions of the longer papers where they have special bearing on the major groups.

To our knowledge all genera of landfowl have been studied; thus, the constituents of these groups are more or less consistent. As expected, there are outliers, genera or species that seem not to fit well given our state of knowledge. This is not to be disparaged and is understandable for several reasons, as noted below.

1. Some genera branched off early in rapid sequence. These deep branches are often difficult to disentangle. Every

molecular study has commented on a rapid diversification of landfowl. This phenomenon is readily understood in a Genesis Flood scenario where the lineages branched from one another in a matter of a few hundred years. There are correspondingly few gaps to separate groups.

2. As already pointed out, different studies use different sources of sequence data. Some, such as those derived from mtDNA, are most effective in resolving taxa that have recently differentiated and give little “signal” at deeper levels. Other sequences, particularly those from slowly changing nuclear DNA genes or UCEs, are effective at resolving deeper-branch lengths.
3. Different labs have employed different numbers of species. It is obvious that, within limits, a sparse coverage of taxa will yield different patterns of relationships than a study that employs a wider coverage. Even examining 100% of landfowl will not guarantee a fully resolved tree, due to the limitations posed in item (2).
4. Not all taxa can be represented by fresh material. It is astonishing, and laudable, that usable DNA samples can be obtained from dried material (especially toe pads) of old museum specimens. That these sources yield somewhat degraded DNA is, of course, known to the investigators, and they are careful not to overestimate the conclusions to those derived from such specimens. Given the factors of time, funding (or lack thereof), and political conditions, it is not possible to obtain fresh samples of all desired taxa. We are fortunate, therefore, to have some, albeit imperfect data rather than none.
5. For a variety of reasons different laboratories utilize different methods of data analysis, and each research group has its reasons for doing so. To attempt to take a position on the validity of these methods is beyond the scope of this paper and would engage the authors in endless debate. Suffice it to say that analytical methods can lead to different conclusions. Constructively, they can help an investigator evaluate the validity of his data.
6. Further, we have the taxonomic equivalent of the theologians’ *hapax legomena*, those species represented (so far) by a single sample in a single study. We have no context in which to evaluate what the data from that sample tells us. In some cases, its morphological characters are unambiguous; in others they are difficult to evaluate, especially when the molecular and traditional evidence are not congruent.
7. Finally, we have used our own knowledge and taxonomic judgment in accepting, rejecting, or modifying the conclusions of others. In each instance we have stated that this represents our opinion, and we attempt to give reasons for our conclusions.

Using these data from the studies mentioned above, we are able to postulate groups within the Phasianinae (typical pheasants) plus *Perdicinae* (Old World quail) (Figure 1). These groups are approximate and not all papers agree with the placement of some genera. The grouse and turkeys, which comprise two related groups, have already been discussed because their constituents are unambiguous; a grouse is a grouse and a turkey is a turkey; there are no “problem” genera. We defer a discussion of the Rock Partridge (*Ptilopachus*) and the New World quail (*Odontophoridae*) until the end because they represent a special case.

If our discussion seems to be biased toward the work of Crowe’s group, it is not because we believe their data to be superior in all cases;] of DNA bases, and utilized more thorough analyses. Their studies have been carried out over 30 years. Their taxonomy (although cladistic) is holistic, embracing an array of attributes including morphology, behavior, advertising vocalizations, ecology, and biogeography.

The groups are listed below, not in a taxonomic sequence, with discussion from individual studies as necessary along with our comments. Several of the scientific names may be confusing to the non-specialist. However, Madge and McGowan (2002) provide a succinct identification guide to all the pheasants with full-color illustrations of each.

Mountain Pheasants

The mountain pheasant group, includes *Tragopan*, *Lophophorus*, *Tetraophasis*, and possibly *Lerwa* and *Ithaginis*. This group was not recognized as distinct by Crowe et al. (2006a) who included it in their subfamily Phasianinae, which comprise the crown pheasants.

Grouse and Turkeys

These two groups were discussed in detail above. There is consistent relationship of turkeys (*Meleagris*, subfamily Meleagridinae) and grouse (subfamily Tetraoninae, grouse and capercaillie (*Falcapennis*, *Dendragapus*, *Tetrao*, *Lyrurus*, *Bonasa*, *Tetrastes*, *Centrocercus*), ptarmigans (*Lagopus*), prairie-chickens (*Tympanuchus*). All studies recover them as sister to each other, although nested within the Phasianidae.

The location of the Koklass Pheasant (*Pucrasia*) at the base of a grouse-turkey group is intriguing. MtDNA alone does not recover this branch, suggesting that the Koklass is an outlier to typical pheasants (Bush and Strobeck, 2003; Huang and Ke, 2015). With the addition of nuclear genes and wider taxon sampling, the relationship becomes clearer (Wang et al., 2013; Kimball and Braun, 2014; Hosner et al., 2016). We accept this classification as tentative, pending an investigation of morphological characters for congruence. *Pucrasia* is somewhat of an aberrant pheasant with no obvious close relatives. It is found over a discontinuous range in montane

forests from 2000–4000 meters from the Himalayas through western China to Manchuria.

Note that the Grey Partridge (*Perdix*) in some molecular studies branches at the base of this group (Crowe et al., 2016a, b). This intriguing suggestion deserves further study.

Crown pheasants

The “crown” pheasants, also called gallopheasants, include *Catreus*, *Lophura*, *Crossoptilon*, *Phasianus*, *Chrysolophus*, *Syrmatiscus*, and possibly the grey partridges *Perdix*. With the exception of *Perdix* this group includes the typical pheasants, characterized by elongated tail feathers with characteristic barring.

Turkeys, grouse, mountain pheasants and crown pheasants comprise a larger group called the “erectile clade” (Kimball and Braun, 2008). Various members of the landfowl possess bare regions on their heads; however, the ability to *erect rapidly* such combs or wattles is restricted to members of this assemblage, which has been definitively established by Hosner et al. (2016). In their study *Perdix* is recovered as a sister-group to the gallopheasants (crown pheasants); the Koklass Pheasant *Pucrasia* is basal to the turkeys and grouse; and the Snow Partridge *Lerwa* forms the first dichotomy to this erectile clade.

Forest partridges

This corresponds roughly to the subfamily Arborophilinae of Crowe et al. (2006a) and contains Old World partridges, also appropriately termed forest partridges, that are sister (meaning ancestral) to the rest of the Phasianidae: *Rollulus*, Black Partridge (*Melanoperdix*), Ferruginous Partridge (*Caloperdix*), hill partridges (*Arborophila*), and *Xenoperdix*. All members of this group are found in southeast Asia and western Indonesia with the exception of the recently discovered *Xenoperdix* which is African (Dinesen et al., 1994; Bowie and Fjeldsa, 2005).

The skeptical systematist would have predicted that the former *Perdicinae* (Old World quail and partridges) was potentially ripe for surprises. Of 108 species the genera *Francolinus* comprising 41 species and *Arborophila* with 21 form the largest groups (57% of total species). The characters used in determining relationships have included the number and presence of tarsal spurs, the number of tail feathers, and relative lengths of the tail and wings. Otherwise, with the exception of a few genera, the plumage is designed for crypsis of ground dwelling birds and not for taxonomic insight. The advent of molecular data has provided such surprises, and the task is to determine how the molecular and morphological data dovetail with each other.

Old World quail and partridges

This assemblage consists of Old World quail/partridges including snowcocks (*Tetraogallus*), sand partridge (*Ammoperdix*), *Alectoris* partridges, quails (*Coturnix* and *Excalfactoria*),

Madagascan Partridge (*Margaroperdix*), bush quails (*Perdicula*), spur-fowls (*Pternistis*, formerly *Francolinus*), and the Snow Mountain Partridge (*Anurophasis*). Three or four smaller “sub-groups” are seen among these genera.

Junglefowl and allies

The “chicken” group or subfamily Gallinae of Crowe et al. (2006a) includes the bamboo-partridges (*Bambusicola*), junglefowls (*Gallus*), francolins of the genera *Scelopoptila* (formerly *Francolinus*), *Peliperdix* (formerly *Francolinus*), *Dendroperdix* (formerly *Francolinus*), and *Francolinus*.

Considering that the chicken (*Gallus gallus*) is arguably the best known bird on Earth—whether from its economic importance as food for man, its use as the “standard bird” in anatomical, embryological, physiological, and immunological studies, or a host of other criteria—it is surprising that conclusive evidence of its near relatives was not established until relatively recently. Fumihito et al. (1995) discovered a clear link between *Gallus* and bamboo partridges (*Bambusicola*) using a relatively small set of sequences of mtDNA. Subsequent studies have confirmed this. For a discussion of francolins please see subheading ‘Rock Partridge’ below.

Thus, the chicken and the junglefowl (*Gallus*) consistently fall outside of the main pheasant assemblage. Of their characters Madge and McGowan (2002, p. 292) write:

Junglefowl form a very familiar and distinctive genus, indeed they are sufficiently distinct that it is difficult to consider them ‘pheasants’ at all. They have no close relatives and almost form their own subgroup. Cocks have a prominent flashy coronal comb, throat wattles and ear lappets, and extensive bare facial skin. Tails are laterally compressed of 14–16 feathers, those of cocks with elongated, rather soft-sifted, decurving central feathers which fall either side of the supporting shorter feathers of the ridged tail. Neck, back, and rump feathers are elongated and usually pointed, forming hackles in cocks (these are shed following breeding in some species). Legs are relatively long. those of cocks bearing a single spur, hens usually unspurred.

Ocellated pheasants

This is the subfamily Pavoninae of Crowe et al. (2006a) and is referred to as the ocellated clade by Hosner et al. (2016). Members include *Pavo*, *Afropavo*, *Argusianus*, *Rheinardia*, and *Polyplectron*. (*Galloperdix* and *Haematortyx* apparently cluster here as well; see below.)

Kimball et al. (1997) provided the first clear evidence from mtDNA for the affinities of the Congo Peafowl (*Afropavo*) to the typical peafowl (*Pavo*), thus confirming the earlier immunological data of Mainardi (1963). Further, Kimball et al. (2001) examined complete mitochondrial cytochrome b (CYB) and control region sequences, as well as sequences from intron G

of the nuclear ovomucoid gene (OVOG) to derive relationships among the peacock-pheasants (*Polyplectron*). Their data established the reality of this group, the members of which are characterized by the presence of ornamental eye-spots (ocelli) variously on the tail, tail coverts, flight feathers, wing coverts and the mantle. The included genera are *Polyplectron*, two peafowl (*Pavo*), the Congo Peafowl (*Afropavo*), and the two argus pheasants (*Argusianus* and *Rheinardia*).

In a broader sense one might argue that lack of ocelli is ancestral in landfowl, that it is gained as a derived character in the peafowl group, and subsequently lost in one or more taxa. In the initial paper (Kimball et al., 2001) a loss is clear in the Bronze-winged Peacock-Pheasant (*Polyplectron chalcuroides*) and the Congo Peafowl (*Afropavo*). The writers claim that ocelli are lost also in the Crested Argus (*Rheinardia*), but this depends on how one defines ocelli. In their narrow definition, requiring an iridescent patch as a component of the ocellus, they are correct. On the other hand a look at the plumage of the Crested Argus reveals a multitude of spots lacking only the iridescence. It might be preferable to code the character in three states: 0 = ocelli absent; 1 = ocelli present; 2 = ocelli modified. In this case there are only two losses of ocelli, and the character in *Rheinardia* becomes apomorphic.

In subsequent papers, Sun et al. (2014) and Hosner et al. (2016) added two species of spurfowl (*Galloperdix*) and the Crimson-headed partridge (*Haematortyx*) to the dataset, and they clustered with *Polyplectron*, between that genus and the peafowl. This surprising finding suggests five losses of ocelli. However, it might be premature to accept the placement of the two quail-like genera within these pheasants without further corroboration. The natural inclination is to “expect” *Haematortyx* and *Galloperdix* to cluster among the other quail (forest partridges) sister to the remaining Phasianidae. The genetic differences are too great to permit this. We would, therefore, prefer to amend the members of this group to include possibly the Crimson-headed Partridge (*Haematortyx*) and spurfowl (*Galloperdix*) with a precise placement awaiting further evidence.

The Rock Partridge (and New World quail)

We reserve a separate section for this interesting bird. No taxonomic inquiry would be complete without one enigmatic member to challenge the *status quo*. Most writers have commented on the distinctiveness of *Ptilopachus petrosus*. Mackworth-Praed and Grant (1970, p. 195) wrote, “A very distinct and aberrant monotypic genus with peculiar characteristics.” Johnsgard (1988, p. 242–243) noted that its most likely relatives are the Asian genera *Bambusicola* and *Galloperdix*.

It is one matter to note the distinctiveness of a taxon but quite different to provide actual evidence of relationships. Over three decades Timothy Crowe and colleagues have attempted

to accomplish that. Their work on African landfowl extends back 40 years (Crowe, 1978). He and his colleagues have built up an array of evidence from various sources in assessing relationships among the landfowl, especially the African francolins. Crowe’s data range from traditional morphology (external and skeletal characters), behavioral features, ecology, and vocalizations, as well as molecular data from mitochondrial and nuclear genes. Their synthesis, involving all data, exemplify the methods that we outlined previously, namely a holistic approach of successive approximations.

The name *Francolinus* derives directly from the French *francolin* and that from the Italian *francolino*, meaning a grouse. Lewis and Short (1879) do not give any Latin word resembling “francolinus.” In its traditional application the genus *Francolinus* comprises 41 species, the most speciose of the landfowl. The hill partridges (*Arborophila*) make up another 21 species. Together they comprise nearly 15% of landfowl species. Hall (1963) made a thorough study of the francolins based mainly on plumage and other characteristics. She supported monophyly of *Francolinus* and separated them into eight groups, with the exception of four species (*F. lathami*, *F. pondicerianus*, *F. nahani*, and *F. gularis*) that did not fit well. In Hall’s view the francolins were distinguished from the other *Perdicinae* (quail) on the basis of a long, hooked bill, a short tail of 14 feathers, an upright stance, and, in a majority of species, tarsal spurs in the males.

Milstein and Wolff (1987) reached different conclusions, separating two major groups, an Asian (containing the genera *Francolinus* and *Ortygornis*) and an African (*Pternistis*, *Scleroptila*, *Dendroperdix* and *Peliperdix*). They were using the “oversplit” genera of Wolters (1975). They did not, however, challenge the monophyly of the group.

Crowe et al. (1992), following up on the previous study of Crowe and Crowe (1985), established the paraphyly, if not polyphyly, of the francolins using a combination of mtDNA sequences and 25 morphobehavioral characters. Bloomer and Crowe (1998, p. 236) provided additional evidence for 20 francolin species:

quail-francolins (including *Scleroptila*, *Dendroperdix*, *Peliperdix*, and *Ortygornis* species) are small, ground-roosting birds with chestnut and white striped or barred dorsal plumage and high-pitched tonal calls. Partridge-francolins (*Francolinus* and *Pternistis* species) are larger, tree-roosting birds with dark dorsal plumage vermiculated with white or buff and emit lower pitched raucous calls.

The sister group to the partridge francolins is an assemblage of Old World partridges including *Alectoris*, *Coturnix*, and *Margaroperdix* (monotypic of Madagascar).

Dyke et al. (2003) carried out a study of the Galliformes using cladistic analyses of 102 characters, 89 of which were osteological and the remaining 13 involved plumage. The

study is valuable in that the characters and character states are described, and illustrations of the less obvious ones are provided. The results overall confirmed the traditional groups of the landfowl, but grouped both New and Old World quail together and were unable to resolve relationships among the pheasants. The placement of the quails together is not unexpected due to “convergent” similarities in morphology and the fact that many of the characters listed by Holman (1961) as being distinctive of the Odontophoridae were considered to be symplesiomorphic (“shared primitive”) and hence not amenable to cladistic analysis.

In the “final” analysis (Crowe et al., 2006a) the large genus *Pternistis* of francolins is in our Old World quail and partridge group (above), equivalent to Crowe’s subfamily Coturnicinae. The remaining francolins (*Francolinus*, *Dendroperdix*, *Peliperdix*, *Scleroptila*) are in Crowe’s subfamily Gallininae (our junglefowl and allies) which includes the bamboo-partridges (*Bambusicola*), and junglefowls (*Gallus*), and is in turn sister to the peafowl and peacock-pheasants. This study concluded that the francolins originated in Africa and subsequently spread into Asia.

As these studies were unfolding, the question of the Rock Partridge (*Ptilopachus petrosus*) was coming into focus. The prevailing opinion shared by Hall (1963), Johnsgard (1988), *inter alia*, was that *Ptilopachus* has its nearest relatives in southeast Asia with species such as the forest partridges (*Gallopardix*, and *Bambusicola*).

Such an alliance is possible. The Congo Peafowl has its closest relatives with the peafowl (*Pavo*) and peacock pheasants of southeast Asia (Kimball et al., 1997), and the recently discovered African forest partridges *Xenoperdix udzungwensis* and *X. obscuratus* are most closely allied to the Asian forest partridges (*Rollulus*, *Caloperdix*, and *Arborophila*) (Dinesen et al., 1994; Bowie and Fjeldsa, 2005). In these latter cases, the authors presented evidence that Asia and Africa were formerly linked via continuous rain forest, and that present desert conditions through the Middle East and Arabian Peninsula are recent phenomena.

With *Ptilopachus* a different scene was created when the molecular data showed that it, as well as Nahan’s Francolin (*Francolinus nahani*), are actually sister to the New World quail (Odontophoridae). As is the case with other molecular “epiphanies,” this remarkable finding led to the investigation of other evidence.

In her 1963 study, Hall was unable to place the small, dark, forest-dwelling *Francolinus nahani* into any of her eight groups. Bowie et al. (2013) observed that both *Ptilopachus* and *F. nahani* share small size, bare red skin around the eye, lack tarsal spurs, and are not sexually dimorphic. Both taxa regularly cock their tails in the manner of a bantam hen. This was confirmed for *F. nahani* by Cohen et al. (2012) with photographs of wild birds. The calls of both taxa consist of a series of whistles which

suggest the calls of New World quail rather than typical francolins or spurfowl. Sande et al. (2009) provide additional field observations on the elusive and endangered Nahan’s Francolin.

Cohen et al. (2012) also provided sonograms of the calls of *Ptilopachus* and *F. nahani*. The syringeal structure and vocalizations of francolins were studied by Mandiwana-Neudani et al. (2011, 2014). The results of the first study showed differences between the two groups of francolins. The second was more ingenious in that the authors demonstrated that the sonograms of francolin advertising calls could be broken down into individual units (called strophes) and then analyzed cladistically. Although the number of resulting characters was small (n=9), the results separated the two francolin groups but were ambiguous in determining statistically significant groups of species.

The results are contrary to the generally perceived notion that bird vocalizations are dependent upon ecology (Morton, 1975), or are species-specific, and hence are unlikely indicators of relationship. There is, on the other hand, a great deal of information in a sonogram, and these data suggest that some of this information may be relevant for taxonomy.

Bowie et al. (2013) concluded that the Rock Partridge and Nahan’s Francolin are similar enough to warrant their placement into a single genus, *Ptilopachus*, and as a subfamily Ptilopachinae within the Odontophoridae. Furthermore, the dispersion of the ancestor to the New World quail likely was via a North Atlantic land bridge, as has been shown for various plants (Tiffney, 1985; Milne, 2006). This biogeographic scenario was challenged by Hosner et al. (2016) who favored a Bering Land Bridge route. The differences in the conclusions rest on the allocation of the fossils and the secular dates utilized. Given the vagaries presented by both, we favor the North Atlantic connection simply because it is shorter.

We emphasize that the conclusions regarding *Ptilopachus* derive not solely on the DNA evidence, but on the congruence of several lines of data including external morphology, behavior, and vocalizations.

Crowe et al. (2006a, p. 521) made two important conclusions regarding the use of molecular data:

It is phylogenetically more sensible to analyze all character data partitions in combination rather than use a divisive “process”—partition approach as the different partitions in combination complement one another. Discarding [morphological behavioral] and non-coding molecular characters results in massive losses of phylogenetic resolution and nodal support, particularly at deeper nodes within Galliformes.

Unresolved Relationships

As of this writing, the DNAs of *all* landfowl genera listed by Gill and Donsker (2016) or recognized since 1990 have been sequenced to a greater or lesser extent. The results have been

gratifying, as reasonable, robust hypotheses of relationships have been proposed. Also satisfying is that these relationships are not in conflict with a reconsideration of traditional characters of anatomy, behavior, vocalizations, or ecology. In no small measure such congruence has been due to the efforts of the investigators who have been aware of the biology of the landfowl as well as the analyses of the molecular data themselves.

Despite the amount of data that have accumulated regarding landfowl, relationships of several “problem” genera remain. Of typical pheasants, the Koklass (*Pucrasia macrolopha*) and Blood Pheasant (*Ithaginis cruentus*) have been difficult to place consistently. Traditionally both have been thought to fall within the *Tragopan-Lophophorus* cluster of pheasants.

On the basis of molecular data *Pucrasia* most often appears basal to the grouse-turkey assemblage, or basal to the main pheasant group. *Ithaginis* appears to be an outlier to pheasants with no close relatives. While neither of these findings is unacceptable—the *Pucrasia*-grouse-turkey group is, in fact, appealing—we feel that more data are needed to have a high degree of confidence in existing results.

Biogeography

In a Genesis Flood scenario biogeographical dispersal is aided by having a *locus a quo*, a place of origin, namely disembarking from the Ark on or near Mount Ararat.

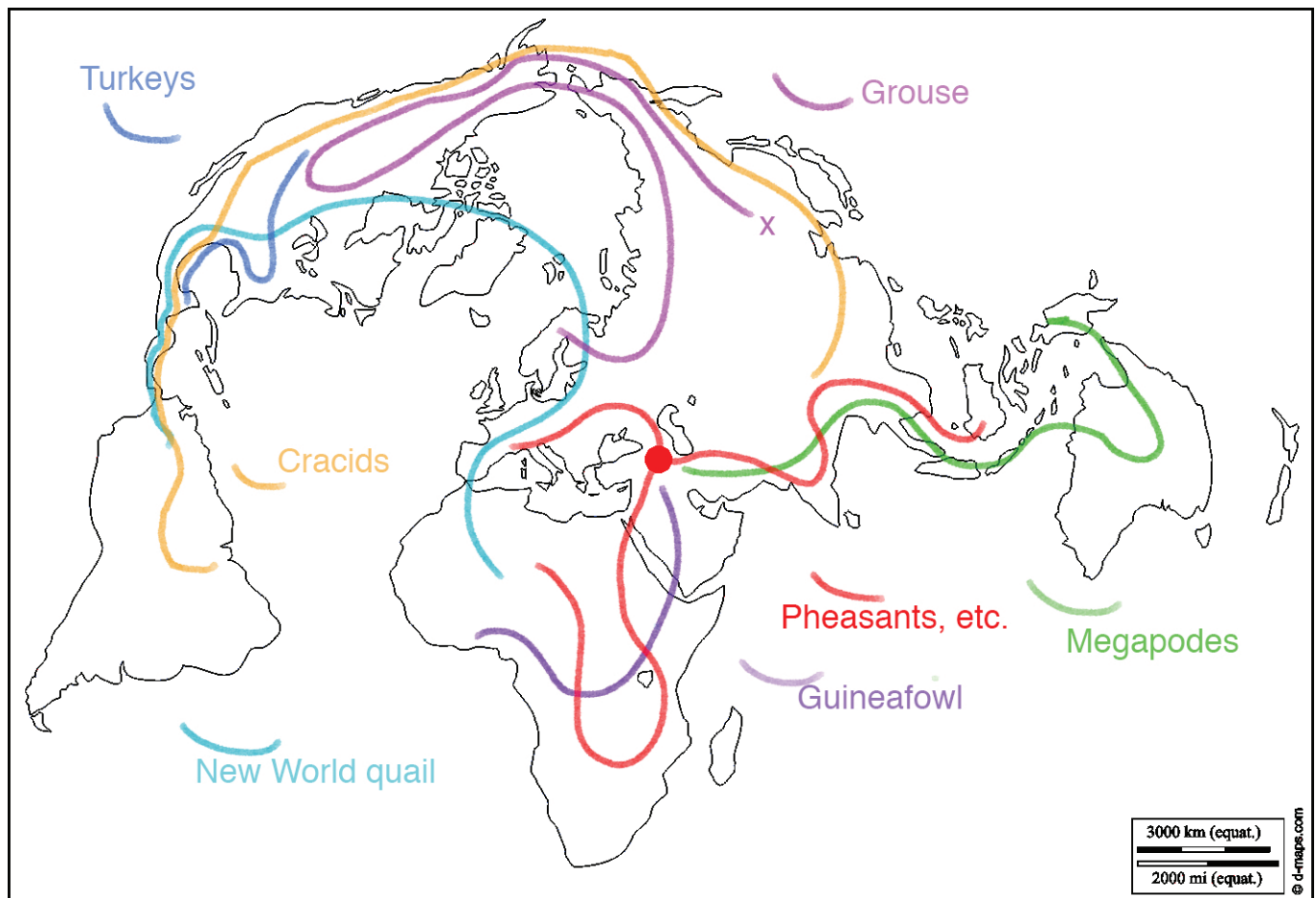


Figure 2. A diagram depicting major landfowl dispersal after leaving the Ark. The megapodes (green) dispersed toward Australasia; the cracids (brown) colonized the New World, probably from Asia. A radiation of guineafowl (deep blue) took place in Africa. It appears New World quail (light blue) colonized the New World from an ancestor in Africa, likely entering via a different route than used by the cracids. The pheasants (red) radiated throughout the old world (Europe, Africa, and Asia); not shown is the grouse invasion of the New World, from which the turkeys may have developed. Map used courtesy d-maps with data added by JA.

On all grounds an Old World origin and primary radiation of the landfowl kind is justified. Following that approach, the principal dispersals are given below in probable chronological sequence (Figure 2).

1. The megapodes represent the first dispersal to the Australo-Papuan region, probably via land bridges from Asia and thence to outlying islands. Although megapodes are seemingly sedentary, they have proven to be good colonizers of islands, and even partly-grown young birds have been observed flying at sea many miles from land.
2. The Cracidae next colonized the New World from Asia, presumably via a Bering Land Bridge, and became centered in Central and tropical South America. Since living cracids are sensitive to cold temperatures an alternative, but less probable, hypothesis involves colonization directly across the Pacific by rafting.
3. A small but distinct radiation of the Numididae (guineafowl) took place in Africa. There are no geographical problems for these birds colonizing Africa from Asia.
4. The Odontophorinae form a second invasion of the New World. If a relationship to the African Rock Partridge (*Ptilopachus*) is maintained, then the most parsimonious route of colonization would be from the Old World via a North Atlantic land bridge. Such has not been invoked for birds, but is well known for plants (Tiffney, 1985; Milne, 2006) in the early Tertiary (post-Flood).
5. The grouse are clearly a boreal component of the pheasants and an offshoot therefrom. Based on present-day distributions, their dispersion to the North America is easily accounted for via the Bering Land Bridge. Given the probable close relationship of grouse and turkeys, a diversification of the latter in the New World is likely. Ancillary evidence for this scenario is that of the 20 species of grouse (recognized by Potapov and Sale, 2013), two are Holarctic in distribution, seven are Palearctic, and eleven are found in the New World.

Lucchini et al., (2001, p. 157) examined the probable geographical origin of grouse using mtDNA sequence data with a parsimony analysis of possible colonizing events:

Use of DIVA with the phylogeny showing *Lagopus* linked to the *Tympanuchus*–*Centrocerus*–*Dendragapus* clade ... the distribution of each species classified as present/absent in four different areas, and the assumption that ancestral stocks were limited to, at maximum, two areas, showed that the most optimal reconstruction required 18 dispersals ... The ancestral area of the grouse was inferred to be the western part of the Nearctic ... According to the most optimal scenario, the grouse have dispersed out of the Nearctic on at least three occasions: in the ancestors to the Palearctic *Bonasa*, in the ancestors to the circumpolar *Lagopus mutus*/*L. lagopus*, and in the clade leading to *Tetrao*/*Falci pennis*. However, it

is equally parsimonious to assume that ancestors of *Tetrao* have dispersed independently into the Palearctic and that speciation in *Falci pennis* is the result of a vicariance event when the rise of the Bering Sea split a previously continuous ancestral *Falci pennis* stock into two reproductively isolated populations.

This hypothesis is reasonable. Of typical phasianids the widespread Ring-necked Pheasant (*Phasianus colchicus*) extends farthest north, being found north of Korea. It is, however, more of an open-country bird and shuns high mountainous forests. Of the truly montane pheasants the Koklass (*Pucrasia macrolopha*) and Brown Eared-pheasant (*Crossoptilon mantchuricum*) have the most northerly distributions, breeding in northeastern China. This does not preclude a former distribution (pre-Ice Age) into regions such as Beringia, but we lack conclusive data.

6. Given that the relationships among the large assemblage of pheasants, partridges, and Old World quail are imperfectly known, it is premature to attempt a fine geographical analysis of their radiation. We have noted above some aspects, namely the division of the francolins and affinities of the Congo Peacock.

Conclusions and Perspectives

The landfowl are defended as an unambiguous example of a Biblical kind (baramin). The congruence of morphological, biological, and genetic evidence permits the recognition of the main lineages within landfowl—megapodes, cracids, guinea fowl, New World quail, grouse plus turkeys, and a large assemblage of pheasants, partridges, and Old World quail—and probable pathways of their post-Flood colonization and diversification. Studies along several lines suggest sub-groups within the pheasant–Old World quail assemblage. It is premature to make definitive conclusions, but we have suggested several interim cognatum groups that are loosely upheld by biochemical as well as traditional data.

It may be at first perplexing that so many species of landfowl differing vastly in size, breeding habits, general ecology, and especially plumage diversity can be derived from a single pair of birds on the Ark. However, astounding diversity has been observed to arise within domesticated species, as well. Creationists recognize the importance of created diversity (Jeanson and Lisle, 2016) as well as designed mechanisms affecting genetic change (homologous recombination, gene conversion, transposable elements, etc.; briefly summarized and referenced in Lightner, 2016). While more random processes and natural selection may have played some role in shaping diversity, too, there is no question God created his creatures with the ability to reproduce and adapt, filling the world with an astounding array of diversity even within a created kind.

It would be informative to have contributions from a baraminological perspective on four aspects of using molecular sequences:

1. A discussion of the relative value of various types of molecular data: mtDNA, various nuclear DNA sequences, UCEs, retroposons, etc.
2. A primer on the methods of data analysis giving the rationale, practice, and meaning of each for systematics. Such a study would explain to the nonspecialist how such manipulations are *not* a matter of tossing sequences into a mythical black box and having “truth” emerge.
3. Given that nearly all secular methods of DNA sequence analysis involve some evolutionary assumptions, the enterprising baraminologist could adapt existing protocols or write his own programs without evolutionary anlagen. This would require not much more than mathematical talent, the ability to write code, and a computer. Data in the form of DNA sequences abound and are accessible. The participant need not learn cloning, reading a sequencing gel, nor engage in forming his own biochemical laboratory.
4. Perhaps the most exciting prospect is that of proteomes. Here, all protein-coding genes are utilized and the data may be analyzed using statistical methods of baraminology, thus eliminating evolutionary assumptions and biases. Lightner and Cserhati (2019, p. 137) have compared the proteomes of humans plus Neanderthals and Denisovans and found them to be distinct from all other primate groups:

This supports the humanity of Neanderthals and Denisovans, as much as it contradicts evolutionary narratives about common descent between humans and apes. In conjunction with other lines of evidence of human morphological, cognitive, and genetic (including non-protein coding regions) distinctiveness, it clearly demonstrates that the evolutionary ideas on the origin of man have no plausible scientific foundation.

Cserhati and Ahlquist (2019) compared the proteomes of a number of the nightjars (avian order Caprimulgiformes) and found evidence for paraphyly if not polyphyly. Among several possible baramins suggested by the authors, the most intriguing supports a baramin consisting of swifts, hummingbirds, and the New Guinea family of owl-nightjars (Caprimulgiformes: Aegothelidae). Once one compares the skulls of Aegothelidae with a typical swift, the similarities become apparent.

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