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

Establishing Baraminic Status, with Application to the Order Galliformes (Class: Aves)

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Abstract

Baraminology is the study of created kinds, or baramins. A major goal of this branch of creationary science is identifying which species known today descended from a common kind of organism created at the beginning, as described in the opening chapter of Genesis. While numerous baramins have been tentatively identified, more work needs to be done to better establish and characterize these baramins. Here, using the galliform birds, or landfowl, as our example, we discuss and illustrate strategies that include examination of biblical data, tracking down hybridization data, opportunities for further studies using statistical baraminology, and incorporating rapidly accumulating molecular data. In the process we not only present further evidence substantiating that different families in the avian order Galliformes belong to a single baramin, but highlight future research opportunities that could further our understanding of this baramin. In future papers we will explore the diversity and relationships within this group and attempt to understand key aspects of their natural history from a biblical perspective.

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Introduction

One of the goals of baraminology is to identify species that are truly related because they descended from the same created kind, or baramin (Genesis 1:11–12, 21–22, 24–25). This information is valuable for a variety of reasons. It may allow detailed inferences about the design of organisms as it relates to their ability to reproduce and fill the earth. For example, it can help us discern what characteristics (coat color, beak size, etc.) were designed to vary, and to what extent. This can help guide investigations to identify the underlying causes of changes in these characteristics (Lightner, 2016). It may also help us as we attempt to delineate other baramins. Still further, it also allows specific inferences about the natural history of the kind.

Currently, while numerous baramins have been tentatively identified (Wood, 2016), there are no baramins that can be considered well-established, much less well-characterized from a biblical perspective. Lightner (2013) produced an estimate of 196 avian "ark kinds" based on available evidence, including hybridization and taxonomic placement. Independently, Ahlquist (unpublished) arrived at "around 216" avian baramins from a preliminary survey of the DNA X DNA hybridization data of Sibley and Ahlquist (1990).

In her paper, Lightner (2013) stressed the need for more research to clearly delimit baramins, and also emphasized that "considerable research needs to be done to evaluate the types of diversity typical within kinds and suggest the type of differences that may help delimit the boundaries of a kind." (p. 465). Toward that end, we will re-evaluate one putative baramin, augmenting Lightner's study with newer molecular data in combination with a re-evaluation of traditional avian taxonomic characters from a baraminological perspective. These data will be presented in greater detail in Part III of this series. In the process, we hope to lay out a strategy that will encourage and guide future baraminologic studies.

The "landfowl kind" tentatively identified by Lightner (2013) is equivalent to the order Galliformes of traditional classifications. This well-studied order comprises the chickens, pheasants, turkeys and allies, a total of nearly 300 species placed in five families (Gill and Donsker, 2019). As their name suggests, these birds have been most successful in colonizing open areas, grasslands, steppes, and even deserts, but they are found in nearly all terrestrial habitats including rain forests. The cracids are highly arboreal. Grouse live in boreal and Arctic regions. Landfowl are worldwide in distribution, exclusive of New Zealand (one extinct species), much of Polynesia, and Antarctica. A few have reached oceanic islands. They have not been successful in marshlands and the littoral (shore) zone. A more technical summary of the characteristics of landfowl appears in Appendix 1.

Here, we review the different lines of evidence important to establishing the baraminic status of the group; this includes lines of evidence not yet documented in the creationist literature. In part two of this series we will review the members of the group, highlighting some important diversity displayed within the baramin. Later in the series we evaluate relationships between the various members, and finally suggest possible routes for colonization by landfowl following the Genesis Flood.

Lines of Evidence

While some creationists may desire a "silver bullet" or single tool to assign organisms to a specific baramin, such a tool does not, and likely never will, exist. Instead, a more detailed and holistic approach is necessary to confidently assign organisms to a baramin, while delimiting the baramin as well. This may seem cumbersome to some, but we view it as an exciting, God-given challenge. By studying multiple aspects of organisms, we come to understand them better, and are able to more fully appreciate the beauty, marvelous design, unity and diversity God has placed in His creatures. Additionally, from a scientific perspective, multiple lines of evidence pointing to the same conclusion will demonstrate the robustness of a biblical model in biology.

Biblical Evidence

Scripture provides some information that applies to avian kinds in general. For example, flying creatures were not only created according to their kinds, but also blessed and instructed to fill the earth (Genesis 1:20–22). This suggests that birds were designed to adapt to a wide variety of habitats, and a cosmopolitan distribution is expected to be common within created kinds. There may be some deviation from this, given that the world is cursed (Genesis 3:14–19). Yet God continues to uphold the world (Colossians 1:16–17), and a frequent cosmopolitan distribution of baramins would reflect His intent that the world be inhabited (Isaiah 45:18).

A second important detail involves the historic Global Flood. For most creatures on the Ark, only a single pair was preserved. Yet clean animals were preserved by sevens (Genesis 6:18–7:10). Where clean and unclean animals are discussed in more detail, it appears there were more clean birds than land animals. In fact, unclean birds are specified in a relatively short list. No landfowl are included in that list (Leviticus 11; Deuteronomy 14). Thus, clean birds, including landfowl, potentially carried more genetic diversity through the population bottleneck created by the Flood than most kinds. This doesn't mean all of it contributed to what we see today, however, because some of these birds would have been used for sacrifice or food, potentially before they had offspring (Genesis 8:20; 9:3).

The Bible does specifically mention some members of the Galliformes, both domestic and wild. A detailed examination has been presented by McConnachie (2007), and McConnachie and Brophy (2007, 2008). The results indicate the importance of these species at the time they are mentioned, but do not provide sufficient information to infer relationships within the landfowl or their relationship to other groups.

Hybridization

The existence of hybrids is generally regarded as the unambiguous indication that two species belong to the same kind (Marsh, 1947; Wood and Murray, 2003; Lightner et al., 2011, *inter alia*). Unfortunately, for many groups, hybrid data are lacking—whether from wild or captive birds. A few groups—notably the landfowl, waterfowl, hummingbirds, birds of paradise—contain numerous records of hybrids occurring in the wild, interspecific as well as intergeneric, that aid in assessing relationships. In wild birds, hybridization occurs most frequently in groups that have a polygynous mating system or others in which the pair bond is very short. In some cases, the pair-bond lasts no longer than copulation, although a female may spend some time in assessing the "best" male with whom to mate. The classic paper on these phenomena is Sibley (1957).

In some avian groups—including landfowl, waterfowl, pigeons, finches and tanagers—interest in aviculture has provided the source of many birds kept in captivity. Aviculturists have a monetary incentive in producing crosses among diverse taxa in hopes of obtaining colorful or otherwise interesting birds for the trade. This in turn has benefited the study of baraminology. The "scorecard" of the enterprising aviculturist is the unusual species he has managed to breed in captivity; it is even more rewarding if he can make viable crosses between exotic species. Unfortunately, aviculturists are not often scientists, and their successes are not published, at least in periodicals that are regularly searched by ornithologists. The principal sources of bird hybrids are the compendia by Gray (1958) and McCarthy (2006). They list hybrids connecting four (Phasianidae, Numididae, Odontophoridae, and Cracidae) of the five landfowl families.

The possibility of hybridization between cracids and other landfowl invites further comment. Gray (1958) as well as McCarthy (2006) listed several interfamilial hybrids involving cracids. They were accepted by McConnachie (2007), McConnachie and Brophy (2008), and Lightner (2013) as evidence for inclusion of the cracids within the landfowl kind.

Although some of the hybrid reports were from old literature and possibly of questionable veracity, Ruschi and Amdon (1959) published evidence of a putative hybrid involving a male guinea fowl (*Numida meleagris*) and a female guan (*Penelope superciliaris*), and provided a photograph of the bird. The photograph, as printed, is small and simply looks like a cracid. In the same paper they noted that Ruschi had observed in his aviaries probable hybrids of a male *Pipile jacutinga* X female domestic chicken (*Gallus gallus*) and a male *Crax blumenbachii* X female *Gallus gallus*.

This evidence was later disavowed by Amadon in a monograph of the Cracidae (Delacour and Amadon 1973, p. 5).

> The Cracidae stand well apart from these other families of gallinaceous birds. Hybrids are known between such diverse types as pheasants, guineafowl, and turkeys, but not between cracids and other galliforms. All reports to the contrary are erroneous, including one (Ruschi and Amadon) to which the junior author was unfortunately a party.

The reasons for this change of attitude by Amadon are not given, perhaps out of deference to his Brazilian colleague. One might surmise that the "open" nature of Ruschi's aviaries combined with inattention to detail may have been factors, but this is conjecture. None of the principals is alive to provide details. Accordingly, Ahlquist wrote to Mary LeCroy and Helen Hays, both long-time employees in the ornithology department of the American Museum Natural History, to see if they recalled any discussions of the hybrids.

Ms. LeCroy responded (*in litt.*, July 3, 2016), "I knew nothing about this supposed hybrid guinea fowl x cracid! I mentioned your letter to George Barrowclough [curator of birds]. It surprised him, too, but he did remember that there is a guinea fowl x chicken in our collection." She also said that, to the best of her knowledge, Ruschi's specimens are still in Brazil.

If any of the hybrids have been saved, it would be possible to extract DNA from a piece of dried skin. Given the substantial genetic gap between cracids and other galliforms, even degraded DNA would provide an answer to the bird's parentage.

Ahlquist also wrote to Paul Johnsgard of the University of Nebraska-Lincoln, an authority on waterfowl and landfowl, especially their hybrids. Dr. Johnsgard graciously replied (*in litt.*, May 29, 2016) that he could not add to the discussion.

Fortunately, the story does not end in deadlock. The numerous putative hybrids cited by Gray (1958) and McCarthy (2006) seem to fall into the categories of "anecdotes," "hearsay accounts," "unsubstantiated claims," and "ambiguous documentation." The numerous and persistent reports of cracid X phasianid hybrids, however, suggest that such probably exist.

Gunski et al. (2001) report on viable F1 hybrids between *G. gallus* and *Crax fasciolata*. They showed that the 2n chromosome number of *Crax fasciolata* is 88 whereas that of *Gallus* is 78 and that hybrids had 2n = 83. The F1 birds showed differences between the fourth and eighth chromosome pairs as well as the sex chromosomes. Unexpectedly, they were able to obtain viable F2 hybrids with individuals bearing differences in both number and morphology of chromosomes. Thus, the vexing question of cracid X phasianid hybrids has a definitive answer!

Despite the unique breeding system (highlighted in part II of this series), 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, nor should they be expected, given the genetic distance between them. The absence of hybrid data and these differences are major considerations that have led to some creationists proposing that the megapodes constitute a separate baramin (McConnachie and Brophy, 2008). However, all studies, whether morphological or molecular, attest to a sister-group relationship of megapodes to other landfowl. Part III of this series will summarize and analyze the results of more than two dozen papers from morphology, behavior, ecology, and genomic DNA sequences to hypothesize relationships among all landfowl and to provide a reasonable post-Flood dispersal of the groups around the world.

As valuable as hybrid data are, their lack says nothing about the relationship of different species. In addition to lack of reproductivity opportunity, various other barriers can arise that prevent organisms within the same baramin from being able to hybridize. Biologists recognize five such categories: (1) mechanical isolation in which the reproductive organs are incompatible; (2) temporal isolation in which the breeding seasons are different; (3) behavioral isolation in which the displays, including vocalizations, of species are different; (4) habitat isolation in which breeding localities are not the same; (5) gametic isolation in which sperm and egg are not compatible or where the chromosomal components are so different that a zygote cannot be formed.

For these reasons, other methods have been developed to help assess if two organisms under consideration belong to the same baramin.

Statistical Baraminology

To address the need to identify baraminic status even in the absence of useful hybrid data, a number of statistical baraminology tools have been developed (reviewed in Wood, 2006). Generally, datasets assembled by scientists doing cladistic studies are used. Both baraminic distance correlation (BDC) and multidimensional scaling (MDS) have been used on datasets for various bird taxa (Wood, 2005, 2008). The interpretation of the results is not always clear, especially when the datasets do not appear to be holistic. For example, some of the avian datasets were limited to characters based on the syrinx. A study specifically dealing with landfowl suggested there was discontinuity between taxa that are known to have hybridized (McConnachie and Brophy, 2008). We agree with these authors that this emphasizes the need for multiple lines of evidence to establish baramins. We also suggest that the emphasis should be on congruence—not consensus—among the data. This is given in the flow chart below, but the principles are meant for data other than molecular sources. As we will explore in Part III of this series, the ideal is congruence among data sets. Congruence, as opposed to conflict, is achievable more often than frequently anticipated.

A major source of anatomical data on birds has been produced by Livezey and Zusi (2006), but has yet to be used in statistical baraminology. The authors have identified and described 2954 characters, evaluated the character states for each, and analyzed them for 185 exemplar taxa using cladistic techniques. Their monograph features 36 pages of drawings showing the essential skeletal features and includes a CD with the complete 185 X 2954 data matrix. Separately, they have published the taxonomic results from their analyses (Livezey and Zusi, 2007).

Since the authors did not sample species extensively in any group, baraminologists will need to seek out skeletons and do some original research. This is true especially for the songbirds (Passeriformes) which tend to be relatively uniform overall and offer the investigator fewer characters. The baraminologist seeking to work with any passerine group may well break new ground in discovering suitable characters. Potentially, such an undertaking could be quite valuable.

The characters utilized by Livezey and Zusi are mainly osteological; therefore, they can be employed without having extensive training in anatomy. One would need to become familiar with the avian skeleton, preferably through an instructor; obtain access to a museum collection; have a binocular dissecting microscope, ideally equipped for photography; and exercise appropriate care with fragile bird bones.

We suggest a flow chart for such a study.

1. Choose a group and visit a museum or assemble material via a loan.
2. Determine which characters may provide suitable signal for relationships within the group of interest.
3. Code the characters appropriately.
4. Analyze the data using standard baraminological methods, or
5. Better yet, devise an original analytical protocol and write the code for it.

This involves a good deal of work, but the enterprising investigator could produce a study of considerable significance.

Recently, another statistical tool has been developed that uses molecular data (O'Micks, 2017). This involves comparing proteome data using an all-versus-all comparison. This technique demonstrates clear discontinuity between humans and all simians (apes and monkeys; Lightner and Cserhati, 2019). Currently, the major limitation of this technique is the lack of full proteome data from enough species to make good comparisons on taxa of interest. For example, Lightner and Cserhati (2019) include four species from Galliformes and two from Anseriformes in their analysis. However, this only includes species from three of the five galliform families. Further, when only two species group together, as in Anseriformes, one cannot calculate a p value. Thus, there is insufficient data to make a strong case for Anseriformes being a separate kind, rather than just a distinct lineage within the same kind as the galliform birds. When both taxa are better represented, this technique may provide a much clearer picture.

DNA Evidence

A major goal of the papers in this series is to bring together the body of molecular evidence, especially that from DNA, and to synthesize it in a context that is suitable for determining avian baramins and inferring their natural history. We understand that God made DNA in correspondence to the way birds live. In other words, given a God of organization, we expect songbirds like a robin and a sparrow to have more of their DNA in common than either would with a duck. Take away the time scale and evolutionary (i.e., *universal* common ancestry) assumptions, and we expect to derive a network in two (or, really three) dimensions of how the realm of birds is organized.

After decades of work in molecular systematics, Dr. Ahlquist (co-author of this paper), provides the following personal perspective.

> From the early days of electrophoretic comparisons of protein systems, such as egg-white, we were aware that the ultimate source of genetic information for determining relationships among birds lay in the DNA itself. In the meantime, we had to be content with indirect methods. The elucidation of the genetic code (amino acid codons) was proceeding, the determination of amino acid sequences of individual proteins was in its infancy, and Robert Holley had not yet published the nucleotide sequence of the first yeast alanine transfer RNA.
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> In our naiveté, we assumed that reading off the genetic message for a bird would be not much more difficult that reading this sentence. Repeated DNA had not yet been discovered, nor had introns, transposable elements, and a variety of sequences that were initially (and erroneously) termed "junk" DNA. Once the group at the Carnegie Institution in Washington applied DNA hybridization in microorganisms, we jumped on the bandwagon (1964) only to be defeated by the extensive existence of repeated sequences, the pitfalls of radio-labeling avian DNA in tissue culture, and a host of other technical problems. When we returned to DNA hybridization in 1974—after a decade of mixed success using multiple electrophoretic procedures, immunological methods, two-dimensional peptide mapping, and amino acid composition of peptides—most of the technical difficulties had been worked out to the point where birdwatchers could apply the method.
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> At the time it was feasible to sequence DNAs, although the available methods precluded the investigation of large numbers of taxa. We were interested in the "big picture" of avian relationships and chose DNA hybridization as the means toward worldwide coverage. As a result, we were excoriated for using phenetic data (by the cladists) and pilloried for not assembling complete data matrices (not enough time). We were making a minimum of 125 comparisons per week, sometimes as many as 250. That would have been impossible with sequencing methods. Given over 30 years of 20/20 hindsight and retrospection, we would have missed many facets of bird relationships had we done otherwise. Of course, we made mistakes, but others were stimulated to take up the cudgel.
>
> Some sought to augment our work with better techniques (sequences) and additional taxa; others strove to prove us wrong at any cost. In the end it makes little difference, for more and better data were produced, and they continue to be gathered at an exponential rate. The work undertaken by ourselves, by Herbert Dessauer on reptiles at Louisiana State University Medical School and Morris Goodman on primates at Wayne State University opened the floodgates for a generation of investigation.

The use of DNA turns out to be not so simple as reading off a sequence of nucleotides. Over the past several decades, scientists have discovered a variety of epigenetic factors that, in effect, change the meaning of the original sequence. In this case the Greek prefix επί- means "over" or "beyond" and can refer to factors that modify, turn off, or change the expression of a gene, apart from the sequence itself. These epigenetic factors are by no means well understood, but they may have played a role in the rapid diversification of species in the years following the Flood.

DNA sequence data are being generated rapidly. Our burden is to synthesize the mass of these data relative to the definition of baramins. This brings us to the task of how to accomplish that goal. Essentially, successive approximation plays a pivotal role in the process.

What follows is a flow chart employing the same strategies that Sibley and Ahlquist used implicitly or explicitly in their previous work. Part III of this series will further address the relevance of this flow chart wherein we apply the principles to numerous studies that have been published on landfowl.

It is interesting to note that little is said about the analytical procedures used by experimenters. Each lab has its own preferred method of analysis. To argue over which methods are better will produce a Gordian knot tangential to what we need to accomplish. For the most part, we leave the statistical debates to those who have the time and expertise to engage in them.

1. A new study of DNA sequences can be expected to produce several results. (a). Most of the clusters of allegedly related species will be similar to those produced during the first 150 years of avian systematics. (b). Some of the results will initially be contrary to conventional wisdom but upon further reflection will be reasonable. (c). A few suggestions will be greeted by such terms and phrases as "outlandish," "impossible," "make no sense at all," and the like.
2. Ideally, other labs will have produced data on the same group(s). Likely, they will include the sequences of different genes, a different array of taxa, and different analyses. Such studies should yield several to many clusters containing approximately the same species. These examples of congruence give one confidence in reality of such clusters. If the "outliers" or "difficult" taxa appear in these studies, this suggests that we need to determine if there is other evidence in support.
3. DNA data do not exist in a vacuum. It is our contention that if the clusters of species, as suggested by the molecular evidence, are real, then there will be evidence from other sources in congruence, or agreement. At this point, the search for additional evidence will extend to all attributes, including but not limited to morphology, behavior, song, ecology, life history, etc. Some of these characters are not quantifiable, and a few border on being almost anecdotal, but years of experience as a taxonomist teach that "good data, like nuggets of gold, are where you find them."
4. Most clusters will emerge as being unambiguous. Most problem taxa will be found to be not so problematic after all. The important point is that we assemble as much evidence as reasonable and not rely on one or a few characters. Since our search is heuristic, it is unlikely to be biased in favor of DNA sequences wherein there are "thousands" of characters. In this respect our conclusions also will be holistic. Central to the above discussion is an example, and we provide such in our discussion of the relationships of the Rock Partridge (*Ptilopacus petrosus*) as outlined in a subsequent paper. Finally, a few species will remain recalcitrant until more and better data are found. We will list these as *incertae sedis*.
5. DNA sequence data are often available as appended or supplementary materials with a published paper. They are also accessible via GenBank. Therefore, baraminologists can reanalyze them using algorithms that are not dependent on evolutionary assumptions, or a molecular clock. Further, we challenge a statistically astute investigator to develop new computer methods to meet these needs.

Other Characters

Many characteristics of birds are not quantifiable, hence are not accommodated by statistical barminology. These include, but are certainly not limited to, behavior, song, ecology, and life history traits. An ornithologist will be aware of numerous subtle features—whether derived from field work or museum specimens—that could indicate or corroborate possible relationships.

Conclusions

Clearly delimiting the boundaries of a baramin is a first and necessary step in the science of baraminology. This cannot be done by applying a single "test," but requires intense study and consideration of additional lines of evidence, even in the better studied groups such as landfowl. More molecular evidence will be provided in Part III of this series, where relationships among landfowl and their natural history is inferred. Evidence from all sources should be considered, including pertinent biblical comments, hybridization data, morphologic and molecular data, and more subtle evidence based on extensive study of the group. In the process, baraminologists will gain a deeper appreciation for awesome patterns and design in God's creatures.

This insight naturally leads to other aspects of baraminologic study. By assessing diversity within a group, we can begin to describe what types of characters vary, and how. We can gain a deeper understanding of how God provided for His creatures to reproduce and fill the earth. This can be extended beyond a morphologic description, as we investigate ecological and molecular aspects that effect such changes. Future papers in this series will explore these areas in more detail as they apply to landfowl, and hopefully spark an interest in other creation researchers to study the awesome works of the LORD in his creation.

For you make me glad
by your deeds, O LORD;
I sing for joy
at the works of your hands.
How great are your works, O LORD,
how profound your thoughts!
Psalm 92:4–5 (NIV)

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Appendix 1. A Definition of Landfowl

Were a non-specialist presented a series of photographs of birds, likely he could correctly identify most, if not all, of the

Landfowl Kind. Asked, however, to define what characteristics led to his conclusions, he would be lost beyond a few generalizations. A skilled bird watcher can identify a flying bird accurately at great distance based on an "overall impression," "Gestalt," or "jizz," none of which can be easily put into words. This is similar to—but less formalized than—the cognitum concept (Sanders and Wise, 2003; Sanders, 2010; Lightner et al., 2011).

The heart of baraminology is discontinuity, especially in a matter as fundamental as the definition of a baramin. Wood and Murray (2003, p. 81) define discontinuity as "a significant difference between two sets of organisms detected in a holistic analysis." A few avian baramins, such as hummingbirds and parrots, can be defined in a sentence or two. Others require a combination of anatomical characters in order to achieve clarity. In some instances, where the principal diagnosis is based on genetic characters (DNA sequences), we seek consistent clusters from the evidence of several to many genes, ideally coupled with a congruent suite of features such as morphology, behavior, ecology, and others.

The determination of traditional morphological characters in systematic ornithology began with Thomas Henry Huxley in the mid-19th century and concluded with the massive *fin de siècle* works of Fürbringer (1888), Gadow and Selenka (1891), and Gadow (1893). In between, many investigators added to the characters which hopefully would be useful in unraveling avian relationships. None was universally successful, so it was the principal contribution of Hans Gadow to derive a list of "about 40" characters which, taken together and appropriately weighted, formed the basis for a technical diagnosis for each group of birds. In a sense Gadow's effort was a precursor to "numerical taxonomy" of the latter half of the 20th Century

The history of these discoveries, as well as the strengths of weaknesses of each character, have been reviewed in detail by Sibley and Ahlquist (1972, 1990). A generation ago, it was obligatory for a serious ornithologist to be able to "translate" any of Robert Ridgway's technical diagnoses. With the movement in biology away from anything traditional, probably fewer than 10% of practicing ornithologists can do so today. Nonetheless, such a diagnosis is critical to achieve an unambiguous meaning of the avian baramins.

Space prohibits the description, drawing, and details for these characters. The reader should consult a classical textbook on ornithology such as Van Tyne and Berger (1959, pp. 21–107, 559–586) or an anatomical compendium such as that edited by Baumel (1993).

We have taken the following from Ridgway and Friedmann (1946, pp. 2–3), condensed, and rearranged it to omit variable characters and eliminated the Hoatzin Kind.

Technical Diagnosis. Landfowl (Order Galliformes).

Terrestrial or arboreal rasorial birds with nares holorhinal, impervious; bill relatively short (much shorter than head) with maxilla vaulted, its tip overhanging that of the mandible, vaulted, not compressed; angle of mandible produced and recurved; rhamphotheca simple. Palate schizognathous; palatines without internal lamina; maxillopalatines not coalesced with each other or with the vomer; quadrate bone double; basipterygoid processes absent but represented by sessile facets on anterior part of sphenoidal rostrum. Sternum deeply 4-notched or cleft with median xiphoid process long and narrow, the internal processes much shorter, and external processes shorter still and bent over posterior ribs, their extremities expanded; coracoids without a subclavicular process and with basal ends overlapping or crossed; 16 cervical vertebrae; ankylosed sacral vertebrae preceded by a free vertebra, this by four ankylosed heterocoelus vertebrae. Hallux always present; deep plantar tendons of Type I (if reaching the hallux proceeding from flexor hallucis longus, not from flexor digitorum longus. Intestinal convolutions of Type V (plagiocoelus); crop present, globular, stomach a gizzard; gall bladder present; caeca large. Aftershaft present; neck without lateral apteria; adult downs on pterylae only. Young ptilopaedic and nidifugous. Distribution cosmopolitan except Polynesia, New Zealand, and Antarctica.